

10B13

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SEARCH REQUEST FORM

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Requestor's
Name: _____

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Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

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CPU time: _____

Total time: 17Number of Searches: 1Number of Databases: 7**Search Site**

____ STIC

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____ Pre-S

Type of Search☒ N.A. Sequence☒ A.A. Sequence

____ Structure

____ Bibliographic

Vendors☒ IG MPSACIT

____ STN

____ Dialog

____ APS

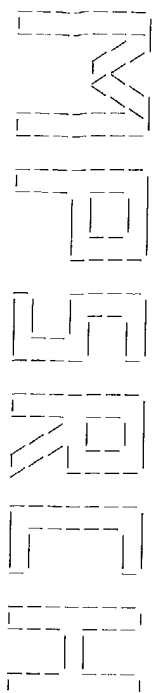
____ Geninfo

____ SDC

____ DARC/Questel

____ Other

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 (TM)

Release 3.0.4A John F. Collins, Bioinformatics Research Unit.
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MPsrch_nrn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Tue Apr 21 00:00:18 1998: Maspar time 145.06 Seconds

Tabular output not generated. 795.535 Million cell updates/sec

Title: >US-08-292-694A-11
 Description: (1-1000) from US08292694A.seq
 Perfect Score: 994
 N.A. Sequence: 1 AAGGAGGAGAAATCAGTATC.....CCAGTATGACTAGTCGTGGA 1000
 Comp: TTCCTCGTTTATGTCATTAG.....GGTCACTAGTATGACACACT

Scoring table: TABLE default

Gap 6

Mmatch STD : Dbase 0; Query 0

Searched: 159651 segs, 57698962 bases x 2

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: n-geneseq30

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
 14:part14 15:part15 16:part16 17:part17 18:part18
 19:part19 20:part20 21:part21 22:part22 23:part23
 24:part24 25:part25 26:part26 27:part27 28:part28
 29:part29 30:part30 31:part31 32:part32 33:part33

Statistics: Mean 9.090; Variance 5.438; scale 1.671

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	992	99.8	1000	13	Human kappa opioid re	0.00e+00
2	857	86.2	1142	20	Human kappa opioid re	0.00e+00
3	670	67.4	1410	13	Mouse kappa opioid re	0.00e+00
4	660	66.4	2481	15	Mammalian kappa opioi	0.00e+00
5	282	28.4	1610	14	Human mu opioid recep	3.87e-173
6	282	28.4	2160	15	Human mu opioid recep	3.52e-161
7	279	28.1	2070	12	Rat mu opiod recepto	1.28e-169
8	277	27.9	1618	14	Rat mu opiod recepto	1.28e-169
9	277	27.9	1618	14	Rat mu opiod recepto	1.28e-169
10	265	26.7	1821	10	Transcription regulat	3.52e-161
11	265	26.7	1821	10	Transcription regulat	3.52e-161
12	265	26.7	1821	10	Transcription regulat	3.52e-161
13	248	24.9	2272	13	Mouse delta opioid re	3.01e-149
14	245	24.6	829	11	Murine delta opioid r	3.82e-147
15	245	24.6	2447	10	Partial sequence of t	3.82e-147

16	210	21.1	1567	14	089233	Rat opiod receptor c	1.10e-122
17	208	20.9	2706	15	092972	Rat opiod receptor	2.72e-111
18	202	20.3	1330	13	075928	Mouse opiod receptor	4.07e-117
19	191	19.2	2800	14	090096	Mouse kappa-3 opiod	1.78e-109
20	74	7.4	1047	2	020572	Human Natruietic Pep	2.35e-30
21	73	7.3	1118	14	083682	Epsilon opiod recept	1.03e-29
22	70	7.0	1047	2	010572	Human Natruietic Pep	8.61e-28
23	70	7.0	1634	7	045653	Human somatostatin re	8.61e-28
24	69	6.9	1265	7	045654	Murine somatostatin r	3.74e-27
25	63	6.3	1244	7	045656	Murine somatostatin r	3.74e-27
26	61	6.1	726	31	T77788	Murine somatostatin r	2.36e-23
27	61	6.1	1110	5	Q29155	G-protein coupled rec	4.25e-22
28	61	6.1	1130	23	T09250	Pituitary somatostati	4.25e-22
29	61	6.1	1351	7	045655	Human somatostatin re	4.25e-22
30	52	5.2	1054	14	083681	Human somatostatin re	4.25e-22
31	51	5.1	1796	7	045658	Epsilon opiod recept	1.35e-16
32	47	4.7	1296	7	045657	Murine somatostatin r	6.28e-16
33	44	4.4	130	10	056701	Human somatostatin re	1.60e-13
34	43	4.3	91	9	051746	Partial sequence (seq	9.61e-12
35	42	4.2	204	1	N81164	Oligonucleotide probe	3.71e-11
36	42	4.2	204	1	N81164	Base substituted B.co	1.42e-10
37	41	4.1	723	31	T77787	Base substituted B.co	1.42e-10
38	40	4.0	91	9	Q51745	G-protein coupled rec	5.40e-10
39	40	4.0	563	9	Q50505	Oligonucleotide probe	2.04e-09
40	40	4.0	678	9	Q50506	Sequence of orphan re	2.04e-09
41	39	3.9	114	12	070468	Sequence of mouse som	2.04e-09
42	38	3.8	822	5	Q29156	Brain somatostatin re	7.61e-09
43	37	3.7	114	12	070466	Generic DNA sequence	2.82e-08
44	36	3.6	114	12	070467	Generic DNA sequence	1.04e-07
45	36	3.6	1378	17	T10666	Human bradykinin B2 r	3.76e-07

ALIGNMENTS

RESULT 1
 ID 075931 Standard; DNA; 1000 bp.
 AC 075931;
 DT 18-AUG-1995 (first entry)
 DE Human kappa opiod receptor partial cDNA fragment.
 KW Mouse; kappa; delta; mu; opiod; receptor; brain; primer; PCR; amplify;
 KW transmembrane domain; somatostatin; receptor; human; expression vector;
 KW truncate; chimere; assay; probe; ss.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT CDS 102..989
 FT /tag= a
 FT /product= partial human kappa opiod receptor
 FT /gene= 075931-A.
 FT /date= 08-DEC-1994.
 FT /r= 20-MAY-1994; U05747.
 FT /r= 20-MAY-1993; US-066296.
 FT /r= 30-JUL-1993; US-100694.
 FT /r= 05-NOV-1993; US-147592.
 FT /r= (ARCH-) ARCH DEV CORP.
 FT /r= Bell GI, Reisine T, Yasuda K;
 FT /r= WPI; 95-022804/03.
 FT /r= P-PDB; R67672.
 FT /r= Polynucleotides and peptides derived from opiod receptor
 FT /r= screening assays for useful drug substances.
 FT /r= Claim 10; Page 236-239; 300pp; English.
 FT /r= The partial nucleotide sequence of the novel human kappa opiod receptor
 FT /r= using a probe from the mouse kappa opiod receptor gene (075926). The
 FT /r= gene is similar to the mouse kappa opiod receptor sequence. Of the
 FT /r= very similar to the mouse kappa opiod receptor sequence. Of the
 FT /r= C-terminal 293 amino acids, 281 residues are identical and 6 residues
 FT /r= have conservative substitutions. The gene encoding the human opiod
 FT /r= receptor can be placed in a suitable expression vector for production of
 FT /r= the protein in a cell. The opiod receptors thus produced are useful for
 FT /r= the development of novel assays designed to select or improve substances,
 FT /r= capable of interacting with the opiod receptor proteins, for use in
 FT /r= diagnosis, drug design and therapeutic applications.

SQ Sequence 1000 BP; 238 A; 253 C; 225 G; 278 T;
 Query Match 99.8%; Score 992; DB 13; Length 1000;
 Best Local Similarity 99.9%; Pred. No. 0.00e+00;
 Matches 999; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Db 1 aagaagcaaaatcaatgaatccaaagcctacacaaacattacattatggtttgac 60
 1 AAGAGCAAAATCAATGATCCAAAGGCTATCACAAACATCACTTATGGGGTTCAC 60
 Db 61 ttaaaatgagaggaatgctatgtttctttcttttaataacaaaatgaagcaag 120
 61 TTAATAATGAGGGAATGCTATGTTCTTTCTTTTATATACAAATAATGAAGCAG 120
 Db 121 caaacacattacattacattacattacattacattacattacattacattac 180
 121 CAACCAACATTTACATATTTAACTGGCTTTGGAGATGCTTATGATACAAACATGC 180
 Db 181 ccttcaagagtaagcttacttgaatgaattcctggcctttggggatgctgtgcaaga 240
 181 CCTTCAGAGTACGCTACTTGAATGATTCCTGGCTTTGGGAGATGCTGTGCAAGA 240
 Db 241 tagtaatttcattgattacttaaacatgcttaccacatcttaccattacattac 300
 241 TAGTAATTTCCATTGATTACTACAAACATGTTACCAACATCTTACCTTGACCATGATGA 300
 Db 301 ggcgtgagacgctacattgctgctgtgccaacccgtgaagccttggacttccgacaccc 360
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 Db 361 tgaagcaaaatcaatgaatccaaagcctacattacattacattacattacattac 420
 361 TGAAGCAAAATCAATGATCCAAAGGCTATCACAAACATCACTTATGGGGTTCAC 420
 Db 421 caatagtccttggagagcaccacaaagtgaggaggtgtcgaatgagagtcgttcgc 480
 421 CAATAGTCCTTGGAGGACCAAAAGTCAAGGAGGAGTGTGATGATGAGTGGCTTGC 480
 Db 481 agttccacagatgatactacccctgctgtgagaccccttcaatgaatcctgcttccat 540
 481 AGTTCACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
 Db 541 ttgcttcgtatcccttctctcatcatcatcatcatcatcatcatcatcatcatcat 600
 541 TTGCTTCGTATCCCTTCTCTCATCATCATCATCATCATCATCATCATCATCATCATCAT 600
 Db 601 tcaaganngtccgctccttctctgctcccgagagaaagaaagaaagaaagaaagaa 660
 601 TCAAGANNGTCCGCTCCTTCTCTGCTCCCGAGAGAAAGAAAGAAAGAAAGAAAGAAAG 660
 Db 661 ccaagactgctcgt 720
 661 CCAAGACTGCTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
 Db 721 tcaatcctgt 780
 721 TCAATCCTGT 780
 Db 781 acttcgtatgagccttgaagctatatacaacagtagctgaatccattctctcaagcttcc 840
 781 ACTTCGTATGAGCCTTGAAGCTATATACAAACAGTAGCTGATCCCTTCTCTCAAGCTTTC 840
 Db 841 ttgatgaaacttcaagcgtgttcccggaacttctgttccattgaagatgaaatgag 900
 841 TTGATGAANAATCAAGCGGTGTTCCGGGACTTCTGCTTCCACTGAAGATGAGANATGG 900
 Db 901 agcgcnagagcaatgacagagtcggaataacagttccaggaatcctctacccgaagga 960
 901 AGCGCNAGAGCAATGACAGAGTCGGAATAACAGTTCCAGATCCTGCTTACCTGAGGAGA 960
 Db 961 tggatgagatgataaataacagatgataatgataatgataatgataatgataatgata 1000
 961 TGGATGAGATGATGATAAACAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1000

RESULT 2
 ID T12550 standard; cDNA; 1142 BP.
 AC T12550;
 DT 03-SEP-1996 (first entry)
 DE Human kappa opioid receptor cDNA.
 KW Human; kappa opioid receptor; psychiatric disorder; cardiovascular;
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT CDS 1..1142
 FT /tag= a
 FT /product= kappa-opioid_receptor
 FT /note= "incomplete termination codon"
 PN WO9601898-A1.
 PD 25-JAN-1996.
 PF 07-JUL-1995; F00912.
 PR 11-JUL-1994; FR-008531.
 PA (UYST-) UNIV PASTEUR STRASBOURG LOTIS.
 PI Kieffer B, Simonin F;
 DR WPI; 96-097628/10.
 DR P-PSDB; R88722.
 PT New nucleic acid encoding the human kappa opioid receptor - useful
 PT in diagnosis and therapy, and for isolating receptor ligands and
 PT modulators
 PS Claim 3; Page 13-15; 30pp; French.
 CC This sequence codes for the human kappa opioid receptor and was
 CC obtained from two overlapping cDNA fragments isolated from a
 CC human placental cDNA library. The fragments were amplified from
 CC the library using PCR primers based on the sequence of human
 CC genomic clones which hybridised with a murine delta receptor cDNA
 CC probe. Nucleotide probes derived from the kappa opioid receptor
 CC coding sequence are useful for diagnosis of neurological, cardio-
 CC vascular and psychiatric disorders associated with opioid
 CC receptors.
 SQ Sequence 1142 BP; 236 A; 337 C; 283 G; 286 T;
 Query Match 86.2%; Score 857; DB 20; Length 1142;
 Best Local Similarity 98.7%; Pred. No. 0.00e+00;
 Matches 862; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
 Db 257 gatcacaaagatgaagacagcaacacacattacattacattacattacattacattac 316
 100 GATCACAAAGATGAAGACAGCAACACACATTACATTACATTACATTACATTACATTACATT 159
 Db 317 cttaagttactacaacatgctccttccagagtaggtctactgaatgaattcctgacct 376
 160 CTTAAGTTACTACAACATGCTCCTTCCAGAGTAGGTCCTACTGATGATGATGATGATGAT 219
 Db 377 ttggggatgctgt 436
 220 TTGGGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 279
 Db 437 tcttccacttaccatgtagtgagcgtgtgacccgtacattgcccgtgtgacacccgtgaag 496
 280 TCTTCCACTTACCATGATGATGAGCGGTGACCCGTATATGCTGCTGCTGCTGCTGCTGCT 339
 Db 497 cttagtactccgacacaccccttgaagcaaatcatatcatctgcatctgtgctgtgt 556
 340 CTTTGGATTCGCGACACCCCTTGAAGCAAAAGATCATCAATATGCAATGCGGCTGCTGT 399
 Db 557 cgtcatcctgttgacatcctctgcaatagtccttggagggacacaaatgaaggaagcgtcg 616
 400 CGTCATCTGTTGGGACATCTCTGCAATAGTCTTGGAGGACCAAAAGTCAAGGAGGAGTGTG 459
 Db 617 atgtcatgagtgccctcttgacagttccagatgatactacattcctcgtgtgagacccttca 676
 460 ATGTCAATGAGTGCCTTGTGACGCTTCCAGATGATGATGATGATGATGATGATGATGAT 519
 Db 677 tgaagatcgtgcttctcatcttctgcttctgctgtagatccctgtctcatcatcatctgtctgt 736
 520 TGAAGATCGCTCTTCACTTGTGCTTGTGATGATGATGATGATGATGATGATGATGATGATGAT 579

Db 737 acaccctgatctcctgctctcaagagcgctccgctctcttctgctcccgagagaag 796
 QY 580 ACACCCATATATCTCTGGCTCTCAGANNNGTCGGCTCTTCTTGCTCCGAGAGAAAG 639
 Db 797 atcgcaactcgttagatgacaccagactgctctgtgtgtgtgacgtctctctcgtct 856
 QY 640 ATNNCAACCTGCTGATGATCAACAGACTGTCCTGCTGCTGCTGCTGCTGCTGCT 699
 Db 857 gctgactcccatcaccatcaccatcctgtgtgagagctctggtgagacacccaccagca 916
 QY 700 GCTGACCTCCATTCACATATTCATCTCGTGAGAGCTCTGAGGAGCACTCCACACCA 759
 Db 917 cagctgctctcctcagctctcctcctctctctctctctctctctctctctctctct 976
 QY 760 CAGCTGCTCTCTCCAGCTATATCTCTCTCATGCTTATGAGCTATACCAACAGTAGCTCTGA 819
 Db 977 atccatctctcagct 1036
 QY 820 ATCCCATTCCTACGCTCTTCTTATGAAACTTCACAGCTGTTCTCCGGAGCTTCTGCT 879
 Db 1037 ttccacgaagatgagatgagatgagacgagacagactagacagatccgaatacagttcag 1096
 QY 880 TTCACGTAAGATGAGATGAGAGCGCAGCACTACAGAGTCCGAATAACAGTTTCAGG 939
 Db 1097 atcctgcttacctgagagacatgcatgagatga 1129
 QY 940 ATCCTGCTTACCTGAGGAGATGATGAGATGA 972

RESULT 3
 ID 075926 standard; DNA; 1410 BP.
 AC 075926;
 DT 17-AUG-1995 (first entry)
 DE Mouse kappa opioid receptor MOR1 cDNA.
 KW Mouse; kappa; delta; mu; opioid receptor; brain; primer: PCR: amplify;
 KW transmembrane domain; somatostatin; receptor; human; expression vector;
 KW truncate; chimeric; assay; probe; ss.
 OS Mus musculus.
 FS Key Location/Qualifiers
 FT CDS 186..1328
 FT /flag= a
 FT /product= mouse kappa opioid receptor
 PN W09428132-A.
 PD 08-DEC-1994.
 PF 20-MAY-1994; 005747.
 PR 20-MAY-1993; US-066296.
 PR 30-JUL-1993; US-100694.
 PR 05-NOV-1993; US-147592.
 PA (ARCH-) ARCH DEV CORP.
 PI Bell GI, Reisine T, Yasuda K;
 DR WPI: 95-022804/03.
 DR P-PSDB: R67669.

PT Polynucleotides and peptides derived from opioid receptor
 PT polypeptides - for use in therapeutic compositions and in
 PT screening assays for useful drug substances.
 PS Claim 10: Page 207-211; 300pp; English.
 CC The nucleotide sequence of the novel mouse kappa opioid receptor gene
 CC MOR1. The gene was isolated from a mouse brain cDNA library using a
 CC fragment (amplified from the cDNA library with primers 075926-30) as a
 CC probe. The primers are based on the conserved sequences present in the
 CC second and third transmembrane domains of somatostatin (SRII) receptor
 CC subtypes SSTR1, SSTR2 and SSTR3. The 1.2 kb PstI fragment from the mouse
 CC kappa opioid receptor clone, lambda ms1-1, was subcloned into the CMV
 CC promoter-based expression vector pCMV-6b. The resultant construct
 CC pCMV-ms1-1 was transfected into COS-1 cells for protein production. The
 CC gene encoding the opioid receptor can be used to produce complete,
 CC truncated or chimeric opioid receptor proteins. The opioid receptors
 CC thus produced are useful for the development of novel assays designed to
 CC select or improve substances, capable of interacting with the opioid
 CC receptor proteins, for use in diagnosis, drug design and therapeutic
 CC applications.

CC Sequence 1410 BP; 322 A; 360 C; 337 G; 391 T;
 SQ

Query Match 67.4%; Score 670; DB 13; Length 1410;
 Best Local Similarity 87.7%; Pred. No. 0.00e+00;
 Matches 790; Conservative 0; Mismatches 108; Indels 3; Gaps 2;

Db 442 gatcacgaagaatgaagacgcgaacacacacatcatatattacacgtcttgacagt 501
 QY 100 GATACACAAAGATGAAGACAGACACCAACATTATACATTATTAACCTGGCTTGGCAGATG 159
 Db 502 ctgtgttaccacacacatgaccttcaagagtgtcttctactgtatgtatcttggcctt 561
 QY 160 CTGTAGTACTACCAACCATGCGCTTTCAGATAGCGTCTACTGATGATATTCGCGCCTT 219
 Db 562 ttgagagtgtgcatgcaagaatgttcatctccatctgactactacaatgtttcccgca 621
 QY 220 TTGGGGAATGTCCTGCAAGATAGTAAATTCATTTGATTAATCTACCAATGTTCACAGCA 279
 Db 622 tattacacttgacacatgatgatgtgagacgctacatctgtgtgtgtgacacctgtgaag 681
 QY 280 TCTTCACCTTGACCATGATGAGCGTGAACGCTACATTGCGGTGTGCCACCCGCTGAAG 339
 Db 682 ctltggacttccgagacaccttgaagcgaagatcatcaaatctgtcatlttgctctctg 741
 QY 340 CTTTGGACTTCGCGACACCCCTTGAAGGCAAAAGATCAATATCTGCATCTGGCTGCTCT 399
 Db 742 catcatctgttgatatacagcgatagctcttgaggacacaaagtacgagagatgtg 801
 QY 400 CGTCATCTGTGTTGGCATCTCTGCATTAATCTCTTGAGGACCAAAAGTGAAGGATGCTG 459
 Db 802 atgtccattgaatgtctccttgatgcttctcctgatgatacgaatactcctgtgtgactcttca 861
 QY 460 ATGTCAATGAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 519
 Db 862 ttgaagatctgtctctcctgtcttctgtcttctgtcttctcctcctcctcctcctcct 921
 QY 520 TGAAGATCTGCGCTTCAATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 579
 Db 922 acaccctgatgatctcctgagcgtgaagagtgctcgtctcctgtctgctcctcctgagagag 981
 QY 580 ACACCTGATGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 639
 Db 982 accgaatctcgcgcgcac 1041
 QY 640 ATNNCAACCTGCTGATGATCAACAGACTGTCCTGCTGCTGCTGCTGCTGCTGCTGCT 699
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 QY 700 GCTGGACTCCCATTCACATTAATTCATCTGCTGAGAGCTCTGGGGAGACACTCCCAAGCA 759
 Db 1102 cagctgccccctccac 1161
 QY 760 CAGCTGCTCTCTCCACCTATTCCTTCTGATGCTGCTTATGCTGCTGCTGCTGCTGCTGCT 819
 Db 1162 atcctgttctctatgctcctctctgtatgataacacacacacacacacacacacacac 1221
 QY 820 ATCCCATTCCTACGCTCTTCTTGAATGAATCTTCAAGGGGCTTTCGGGACTTCTGCT 879
 Db 1222 tcccatatagatgagatgagagcgccagacacacacacacacacacacacacacacac 1281
 QY 880 TTCCACTGAGATGAGNATGAGAGCCGACGACACTAGAGATCGGAATACAGTTCAAG 939
 Db 1282 atccggttccatgag--agat-gtggagagatgaataaagacacatgactagctcgtg 1338
 QY 940 ATCTGCTTACTCTGAGGAGATGATGAGATGATGAATAAACCAATATGACTAGCTGAG 999
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 QY 1000 A 1000

RESULT 4
 ID 086725 standard; cDNA; 2481 BP.
 AC 086725;

[illegible]


```

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      /product= Mu-subtype-opioid_receptor
      EP-612845-A.
      PD 31-AUG-1994.
      PF 09-FEB-1994; US-026140.
      PR 26-FEB-1993; US-026140.
      PA (AMCY ) AMERICAN CYANAMID CO.
      PI Corbett MJ, Eppeler CM, Shieh H, Zysk JR;
      DR WPI; 94-265963/33.
      DR P-PSDB; R65188.
      PT Pure mu-type opioid receptor protein - and nucleic acid coding
      PS for it.
      PS Claim 1: Fig 11; 39pp; English.
      CC R65188 is the rat mu-subtype opioid receptor protein purified
      CC from rat brain membranes, with biotinyl-b-endorphin (R5656)
      CC as its ligand. It is encoded by the nucleotide sequence 079199
      CC which was synthesised using 071022 and 071023 as PCR primers.
      CC R65188 is useful for identifying other receptor subtypes, for
      CC screening new opioid ligands and for studying mechanisms of
      CC opioi.d action, e.g. drug addiction.
      SQ Sequence 2070 BP; 526 A; 564 C; 423 G; 557 T;

Query Match 28.1%; Score 279; DB 12; Length 2070;
Best Local Similarity 70.4%; Pred. No. 5.01e-171;
Matches 553; Conservative 0; Mismatches 224; Indels 9; Gaps 7;

Db 248 agataccacaaatgaagactgcccacacatctacatttcaacctgtctgagac 307
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 99 AGATACCAAGAGATGAGACAGACACCAACATTTACATTATTACCTGGCTTGCGAGAT 158

Db 308 gcccttagcgcgcgtacacacgccccttccagagtgcaactacccctgaggaacatgccc 367
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 159 GCTTTACTTCTACAAACCATGCCCCCTTTCAGAGTACGGTCTACTTGATGAATTCCTGGCCT 218

Db 368 ttggaacacccctcctgacagatggtatctccaatagattactacaacatggtaccagc 427
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 219 TTGCGGATGTCGTGTCAGATAGTATTTCCATTATTTCTACACATGTTCCAGC 278

Db 428 attaccacctctgacacatgagcgtggaacgctacattgtctgtccacacatgtaaa 487
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 279 ATCTTCACCTTGACATGAGAGGCGTGACCGGTACATTCGCCGTGTCACCCCGTGAAG 338

Db 488 gccctgatttcgttacccccccaatgccaataatgccaagctctgacatgtatctc 547
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 339 GCTTTGACTTCCGACACCCCTTGAAGGCAAGATCATATCTTCATCTGGCTCTG 398

Db 548 tctcttgccatcggctcgcgtgtaattgtaacgcaacacaaatacgaagcagg-gtc 606
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 399 TCGTCATCTGTGGCATCTCTGCATAGTCTCTTGAGGSCACCAAGTCAAGGAGGTGTC 458

Db 607 catag-attgacacct-cagttct-cccacccaac--ctggtactgaggaaactgctc 661
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Qy 459 GATTCATATGAGTCTGCTGGTTCAGTCCAGATGATGATGATGATGATGATGATGATG 518

Db 662 a--aa-atcgtgtcttatcttgcgttctcatgcccgtctccatcatcagtggtgt 718
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Qy 519 ATGAAGATCGCGCTTCATCTTCCTTCCTGATCCCTGCTCATCATCATATGCTGTC 578

Db 719 taaggccatgatacttaacgaactcaagaagcgttcgacatgatacgggtccaaagaaag 778
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Qy 579 TACACCTCGATGATCTCGCTGCTCAAGANNCTCCGGCTCTTCTGATCCCGCAGAGAA 638

Db 779 gaccggaatctgacagatcaccccgatggtgctggtgctggtgctggtatctatcgtc 838
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Qy 759 ACAGCTGCTCTCTCCAGCTATTACTTCTGCATCGCTTACGCTATACCAAGATAGAGCTG 818

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      /product= Mu-subtype-opioid_receptor
      EP-612845-A.
      PD 31-AUG-1994.
      PF 09-FEB-1994; US-026140.
      PR 26-FEB-1993; US-026140.
      PA (AMCY ) AMERICAN CYANAMID CO.
      PI Corbett MJ, Eppeler CM, Shieh H, Zysk JR;
      DR WPI; 94-265963/33.
      DR P-PSDB; R65188.
      PT Pure mu-type opioid receptor protein - and nucleic acid coding
      PS for it.
      PS Claim 1: Fig 11; 39pp; English.
      CC R65188 is the rat mu-subtype opioid receptor protein purified
      CC from rat brain membranes, with biotinyl-b-endorphin (R5656)
      CC as its ligand. It is encoded by the nucleotide sequence 079199
      CC which was synthesised using 071022 and 071023 as PCR primers.
      CC R65188 is useful for identifying other receptor subtypes, for
      CC screening new opioid ligands and for studying mechanisms of
      CC opioi.d action, e.g. drug addiction.
      SQ Sequence 2070 BP; 526 A; 564 C; 423 G; 557 T;

Query Match 27.9%; Score 277; DB 14; Length 1618;
Best Local Similarity 70.2%; Pred. No. 1.28e-169;
Matches 552; Conservative 0; Mismatches 225; Indels 9; Gaps 7;

Db 496 agataccacaaatgaagactgcccacacatctacatttcaacctgtctgagac 555
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 99 AGATACCAAGAGATGAGACAGACACCAACATTTACATTATTACCTGGCTTGCGAGAT 158

Db 556 gcccttagcgcgcgtacacacgccccttccagagtgcaactacccctgaggaacatgccc 615
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Qy 159 GCTTTACTTCTACAAACCATGCCCCCTTTCAGAGTACGGTCTACTTGATGAATTCCTGGCCT 218

Db 616 ttggaacacccctcctgacagatggtatctccaatagattactacaacatggtaccagc 675
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 219 TTGCGGATGTCGTGTCAGATAGTATTTCCATTATTTCTACACATGTTCCAGC 278

Db 676 attaccacctctgacacatgagcgtggaacgctacattgtctgtccacacaggtcaaa 735
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Qy 279 ATCTTCACCTTGACATGAGAGGCGTGACCGGTACATTCGCTGTCACCCCGTGAAG 338

Db 736 gccctgatttcgttacccccccaatgccaataatgccaagctctgacatgtatctc 795
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Qy 339 GCTTTGACTTCCGACACCCCTTGAAGGCAAGATCATATCTTCATCTGGCTCTG 398

Db 796 tctcttgccatcggctcgcgtgtaattgtaacgcaacacaaatacgaagcagg-gtc 854
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Qy 399 TCGTCATCTGTGGCATCTCTGCATAGTCTCTTGAGAGCACCACCAAGTCAAGGAGGTGTC 458

Db 855 catag-attgacacct-cagttct-cccacccaac--ctggtactgaggaaactgctc 909
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Db 910 a--aa-atcgtgtcttatcttgcgttctcatgcccagaccccatcatcactgtgtgt 966
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QY 519 ATGAAGATCTGAGTCTCATCTTTGCTTCGATGCCGTCGTCATCATCTGCTGC 578
 Db 967 taagcccttgatctctacgactcaagagcgcttcgactatgctatcggtcccaagaag 1026
 QY 579 TACACCCGATGATGATCCCTGCTCAGANNHCCGCGCTCTTTCGCTCCCGAGAGAA 638
 Db 1027 gacaggaatctggagagatcacccggatgctgctgctgctgctgctgctgctgctgct 1086
 QY 639 GATNNCAACCTGCGTGGATGATCAGAGATGCTGCTGGTGGTGGTGGTGGTGGTGGTGG 698
 Db 1087 tgcctgagcccccatacattacgctacatcaacagcgctgatalcagattccagaacc 1146
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 Db 1207 aatccagctctttagccttccctctgctgctgctgctgctgctgctgctgctgctg 1266
 QY 819 AATCCCATCTCTCTAGCGCTTCTTGTGATGAATAACTCAAGCGGTGTTCCGGGACTCTGC 878
 Db 1267 atccca 1272
 QY 879 TTTCGA 884

RESULT 9
 ID Q89223 standard; cDNA; 1618 BP.
 AC Q89223;
 DT 20-OCT-1995 (first entry)
 DE Transcription regulatory protein cDNA.
 KW Mu opioid receptor; MOR-1; gene therapy; diagnostic;
 KW Transcription regulatory protein; ss.
 OS Rattus sp.
 FH Key Location/Qualifiers
 FT CDS 339..1235
 PN W09507983-A.
 PD 23-MAR-1995.
 PF 13-SEP-1994; U10358.
 PR 13-SEP-1993; US-120601.
 PA (INDV) UNIV INDIANA FOUND.
 PI Yu L;
 DR WPI: 95-131351/17.
 DR P-PSDB; R1965.
 PT New nucleic acid encoding new human mu opioid receptor - and
 PT related vectors, transformed cells, antibodies etc., useful in
 PT diagnosis, treatment and drug screening.
 PS Disclosure: Page 199-203; 266pp; English.
 CC A 365 bp fragment of the mouse delta opioid receptor was used to
 CC screen a rat brain cDNA library under low stringency conditions.
 CC One positive clone included the sequence given in Q89223, encoding a
 CC mu opioid receptor, MOR-1 (R71964). Sequence analysis revealed a
 CC alternative reading frame (Q89223) encoding a zinc
 CC finger-containing transcription regulatory protein (R71965).
 SQ Sequence 1618 BP; 390 A; 486 C; 370 G; 372 T;

Query Match 27.9%; Score 277; DB 14; Length 1618;
 Best Local Similarity 70.2%; Pred. No. 1,28e-169; Indels 9; Gaps 7;
 Matches 552; Conservative 0; Mismatches 225; Trdeals 9; Gaps 7;

Db 496 agatacaccacaatgaagactgcccacacacattacattcaacctgtctgcaagac 555
 QY 99 AGATACACAAGATGAGAGACAGACCAACATTTATATTAACTTACCGCTTGGCAGAT 158
 Db 556 gcccttagcgcgcgtacacgtgccccttcaagagtgtaactacgtgatggaatggccc 615
 QY 159 GCTTAACTTACTACAAACCAACCGCTTTCAGAGTACGCTTACTGATGATATTCCTGCT 218
 Db 616 ttggagccctctctcaagatgctgatatcatatagatactatacacaacatgcttcacagc 675
 QY 219 TTGGGGAGATGTGCTGCTCAAGATAGTATTTCCATTACTTACACACAGATGTTACACAGC 278

Db 676 atattaccctctgacacatgagcgtggaccgctacattgctgtctgcaccacagtleaa 735
 QY 279 ATCTTCACTTGACCATATATATAGGCTGACCGCTACATCTGCTGCTGCTGCTGCTGAG 338
 Db 736 gccctgatttcgcttacccccccgaatgccaatctgtaacagctgtgtaacatgctc 795
 QY 339 GCTTGGACTTCCGACACCGCTTGAAGCAAGATCATCATATCTGATCTGGGTGGTGG 398
 Db 796 tctctgcacatgctgtgctcgtatgttcttcaatggaacacacaaatatacagaggg-gtc 854
 QY 399 TCGTATCTGTGGATCTCTGCAATGATGCTTGGAGGACACAAAGACAGGAGAGGCTC 458
 Db 855 catag-attgaccct-cagcttct-cccacccaac--ctgtaactggaagaaactgctc 909
 QY 459 GATGTCAATGAGTGTGCTGCTTCAATTCOCATGATGACATCTCTGCTGCTGCTGCTC 518
 Db 910 a-aa-atcgtgcttattctctgcttctcattcagtcagatccatcatcatcactgctgt 966
 QY 519 ATGAAGATCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 578
 Db 967 taagccttgatgattcttaagactcaagagcgcttcgactgctatcggtcccaagaag 1026
 QY 579 TACACCTGATGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 638
 Db 1027 gacaggaatctgagcagatcacaccggatgctgctgctgctgctgctgctgctgctgct 1086
 QY 639 GATNNCAACCTGCGTGGATGATCAGAGATGCTGCTGGTGGTGGTGGTGGTGGTGGTGG 698
 Db 1087 tgcctgagcccccatacattacgctacatcaacagcgctgatalcagattccagaacc 1146
 QY 699 TCGTGAGATCCCATCATCATATTTATCTCTGTGTGAGAGCTCTGGAGACACCTCCACAGC 758
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 QY 759 AAGCTGCTCTCTCCAGCTATTTACTTGCATGCGCTTGGCTTAGGCTATACACAGATAGCTG 818
 Db 1207 aatccagctctttagccttccctctgctgctgctgctgctgctgctgctgctgctg 1266
 QY 819 AATCCCATCTCTCTAGCGCTTCTTGTGATGAATAACTCAAGCGGTGTTCCGGGACTCTGC 878
 Db 1267 atccca 1272
 QY 879 TTTCGA 884

RESULT 10
 ID Q56700 standard; cDNA; 1821 BP.
 AC Q56700;
 DT 15-SEP-1994 (first entry)
 DE Sequence of murine delta opioid receptor in the DOR-1 cDNA clone.
 KW Opioid receptor; morphine; opiate; ss.
 OS Mus musculus.
 FH Key Location/Qualifiers
 FT CDS 29..1139
 PN W09404552-A.
 PD 03-MAR-1994.
 PF 13-AUG-1993; U07665.
 PR 13-AUG-1992; US-929200.
 PA (REGC) UNIV CALIFORNIA.
 PI Edwards RH, Evans CJ, Kaufman D, Keith DE;
 DR WPI: 94-083099/10.
 DR P-PSDB; R48629.
 PT DNA encoding opioid receptors and antibodies against this
 PT receptor - used to express and locate these receptors, and screen
 PT opds. for opioid (ant)agonist activity
 PS Claim 1; Fig 5; 74pp; English.
 CC A cDNA library was constructed using mRNA isolated from the NG109-15
 CC cell line. A single clone, named the DOR-1 clone was isolated.
 CC Comparisons with known sequences in Genbank showed highest homology
 CC between DOR-1 and the G-protein-coupled somatostatin receptor. Other
 CC features of the DOR-1 clone AA sequence deduced from the cDNA

CC Sequence include 3 consensus glycosylation sites at residues 18 and
 CC 33 (predicted to be in the extracellular N-terminal domain), and at
 CC residue 310 (close to the C-terminus and predicted to be
 CC intracellular). Phosphokinase C consensus sites are present within
 CC predicted intracellular domains, at residues 242,255, 344 & 352.
 CC Seven putative membrane-spanning regions were identified. The DOR-1
 CC clone produces a delta receptor with a predicted mol. wt. of 40,558
 CC kDaltons prior to post-translational modifications.
 SQ Sequence 1821 BP; 339 A; 559 C; 341 G; 362 T;

Query Match 26.7%; Score 265; DB 10; Length 1821;
 Best Local Similarity 70.6%; Pred. No. 3,52e-161;
 Matches 550; Conservative 0; Mismatches 217; Indels 12; Gaps 10;

Db 257 tacacaaatgaagaccgcaacaacatcacatcattcattcgtcttggtcgatgcg 316
 Qy 102 TACACAAAGATGAGACAGACAGACCAACATTACATTAACTGGCTTGGCAGATGCT 161
 Db 317 ctggccacgagacgctgccttcagagcgcaagtaacttgtaggaagtgccgtt 376
 Qy 162 TTAGTTACTACACCAATGACCTTTCAGATAGGTTACTTATGATGAAATTCCTGCTTTT 221
 Db 377 ggcagctgctgtgcaaggctgctcctcattcactactacaacatgttactagatc 436
 Qy 222 GGGAGTGTGCTGTGCAAGATGATTTCCATTACTTACACATGTTTACAGCATC 281
 Db 437 ttcaacctcaocatgatgagcgttggaacgctacattgctctgcacatcctgtcaaac 496
 Qy 282 TTCACCTTGACCATGAGAGAGCGTGACCGGTACATTGCGCGTGCCACCCCGTGAAGCT 341
 Db 497 ctgagactcggagacacagcaagcgcaagctgataatcattcattcgtctgttgc 556
 Qy 342 TTGAGACTTCCGCAACCTTGAGGCAAGATCATATCTGCACTGTGCTCTCTGCG 401
 Db 557 tcaagtgctgggtgcccatcatgctatgctgcaatgcaacacccggagatgctgacgt 616
 Qy 402 TCATCTGTGGCATCTCTGCATATGTCCTTGGAGGCAACCAAGTCAAGGAGATGTCGAT 461
 Db 617 gt-atgca-tgct-c---cagttccc-a-g-tccagctgtgtaactggagacgtgac 667
 Qy 462 GTCAATGAGTGTGCTGTCAGTTCACGATGATGATGATGATGATGATGATGATGATG 521
 Db 668 aagatctgctgttctccttcttcttcttcttcttcttcttcttcttcttcttctt 727
 Qy 522 AAGATCTGCGCTTCAATCTTTCCTTCTGATTCCTGCTCTCTCTCTCTCTCTCTCT 581
 Db 728 ggcctcatgctactgctgctgctgctgctgctgctgctgctgctgctgctgctg 787
 Qy 582 AACCTGATGATCTGCGCTGCTCAGANNGTCCGGCTCTTCTGAGCTCCGAGAGAAAT 641
 Db 788 cgcagcctggcgagcatcaagcgcatgtgtgtgtgtgtgtgtgtgtgtgtgtgt 847
 Qy 642 NNCAACCTGCTAGGATACCAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 701
 Db 848 tggggcgccacacacatctgtcatctgtctgagcgtggtgagacatccggcgagac 907
 Qy 702 TGGACTCCCATTCACATTTATCTGTGTGAGGCTTGGGGAGACCTCCACAGC-AC 760
 Db 908 coacttggtgtgagcagcatgcaactgtcatctgtcgtgggtctaacgcaacagcagc 967
 Qy 761 AG-CTGCTCTCTCCAGCTATT-ACCTTTCAGANCGCTTAGGCTATACCAAGTAGCTG 818
 Db 968 aaccggttctctacgcttcccttgagagaaactcaagcgtctgttccgcagctctg 1026
 Qy 819 AATCCATTTCTACGCTCTTCTGATGAAAACTTCAAGCGGCTGTTCCGGGACTTCTG 877

RESULT 11
 ID Q56705 standard; cDNA; 1981 BP.
 AC Q56705;
 DT 15-SEP-1994 (first entry)
 DE Partial sequence of the murine mu-receptor clone DOR-2
 DE (MOR-1, MOR-1alpha)

KW Opioid receptor; morphine; opiate; ss.
 OS Mus musculus.
 PN W09404552-A.
 PD 03-MAR-1994.
 PR 13-AUG-1993; 007665.
 PR 13-AUG-1992; US-929200.
 PA (REGC) UNIV CALIFORNIA.
 PI Edwards RH, Evans CJ, Kaufman D, Keith DE;
 DR WPT; 94-08309/10.
 PT DNA encoding opioid receptors and antibodies against this
 PT receptor - used to express and locate these receptors, and screen
 PT cDNAs for opioid (ant)agonist activity
 PS Example: Fig 9: 74bp; English.
 CC A cDNA library prep. from mouse brain was probed using DOR-1 (see
 CC Q56704) as a probe. One clone was recovered and sequenced. This
 CC clone, designated DOR-2, represented a new gene. DOR-2 hybridised
 CC to a different pattern of neurons than did DOR-1 and showed greater
 CC labeling of the striatum. The identity of DOR-2 (mOR-1) as that of
 CC a mu receptor was confirmed.
 SQ Sequence 1981 BP; 499 A; 549 C; 436 G; 496 T;

Query Match 26.7%; Score 265; DB 10; Length 1981;
 Best Local Similarity 69.5%; Pred. No. 3,52e-161;
 Matches 546; Conservative 0; Mismatches 231; Indels 9; Gaps 7;

Db 538 agatataccaaatgaagactgcccacacatcattcattcattcgtctgctgagat 597
 Qy 99 AGATTAACAAGATGAGAGAGACAGACCAACATTACATTAACTGCTTGGCAGAT 158
 Db 598 ggccttagcactagacacgctgccttcagagtgtaactacactgtagggagcgcgc 657
 Qy 159 GCTTTATTTACTACACCATGCCCCCTTTCAGATAGGCTTACTTGAATTCCTGAGCT 218
 Db 658 ttggaaacatcctctgcaagatgctgctcattcattcattcattcattcattcatt 717
 Qy 219 TTGGGAGTGTGCTGTCAGATGATGATGATGATGATGATGATGATGATGATGATG 278
 Db 718 attctacccctctgacacatgagtgtagcagcgttagcttccgtctgcccggatga 777
 Qy 279 ATCTTACCTTGGACCAAGATGAGGCTGAGCGCTACATGCTGCTGCTGCTGCTG 338
 Db 778 ggcctgattctcgttaccccgccgaatgccaatctcattcattcattcattcattc 837
 Qy 339 GCTTTGAGACTTCCGCAACCTTGAAGCAAGATCATCATCTGATTTGGCTGGTG 398
 Db 838 tctctgcacatgctctgcccgtatgttcaatggcaacacaaatcaagcaggg-gtc 896
 Qy 399 TCGTCATCTGTGCACTCTGCAATAGTCTTGGAGGCAACCAAGTCAAGGAGGCTG 458
 Db 897 catag-attgacct-ca--c-gttctcctcaccatgtagtctggagaaactgtc 951
 Qy 459 GATGTCAATTGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 518
 Db 952 a--aa-attctgtctcattcattcattcattcattcattcattcattcattcattc 1008
 Qy 519 ATGAAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 578
 Db 1009 tatggaactgattcattcattcattcattcattcattcattcattcattcattcatt 1068
 Qy 579 TACACCTGATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 638
 Db 1069 gaacggaacctgagcagatcaccgagatgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1128
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 Db 1129 tgcctgaacccatccacatcattcattcattcattcattcattcattcattcattc 1188
 Qy 699 TGTGAGATCTCCATTCATATTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 758
 Db 1189 acttccagactgttctctgagacttctgatttgccttgggtttacacaaagctgtctg 1248
 Qy 759 ACAGTGTCTCTCTGCAATTTACTTTCGATGCGCTTAGGCTATACCAAGTAGGCTG 818

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Msrch_n n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Mon Apr 20 23:31:55 1998; Maspar time 908.25 seconds

Tabular output not generated. 1301.894 Million cell updates/sec

Title: >US-08-292-694A-11
 Description: (1-1000) from US08292694A.seq
 Perfect Score: 994
 N.A. Sequence: 1 AAGAGCGAATACAGTATC.....CCAGTATGACAGTCGCGA 1000
 Comp: TTTCTCTTTAGTCATTAG.....GGTCATACATGATGACACCT

Scoring table: TABLE default
 Gap 6

Mmatch STD : Dbase 0; Query 0

Searched: 354530 seqs, 591221332 bases x 2

Post-processing: Minimum Match 08
 Listing first 45 summaries

Database:

emb153
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 7:em_hum1 8:em_hum2 9:em_da 10:em_ro 11:em_un 12:em_vi
 13:em_pat
 genbank105
 14:gs_ro 15:gb_om 16:gb_ov 17:gb_in 18:gb_pl 19:gb_da
 20:gs_st 21:gb_vi 22:gb_ph 23:gb_sy 24:gb_un 25:gb_pat
 26:gb_htg

Statistics: Mean 11.021; Variance 5.890; scale 1.871

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	857	86.2	1142	25	A48343	Sequence 1 from Patent
2	703	70.7	1733	14	CEU04092	Cavia porcellus Hartle
3	670	67.4	1288	14	S81111	kappa-opioid receptor
4	670	67.4	1410	14	MUSKAPOPRE	Mouse kappa opioid rec
5	662	66.6	1273	14	RATRODR	Rat kappa opioid recep
6	662	66.6	1358	14	RATRORIA	Rattus norvegicus kapp
7	660	66.4	2094	14	RATROB	Rattus norvegicus kapp
8	660	66.4	2481	14	RATROB	Rattus norvegicus kapp
9	660	66.4	2481	14	RATROB	Rattus norvegicus kapp
10	660	66.4	4742	14	RNU00442	CDNA coding rat kappa-
11	383	38.5	1186	14	S778683	Rattus norvegicus kapp
12	378	38.0	638	14	MUSMORDEP3	Mouse MORDE gene for k
13	375	37.7	4048	14	RNKROR	Rattus norvegicus kapp
14	316	31.8	1109	14	S77868S2	kappa opioid receptor

Result	LOCUS	DEFINITION	ACCESSION	NID	KEYWORDS	SOURCE	ORGANISM	REFERENCE	ATTNORS	TITLE	JOURNAL	COMMENT	FEATURES	source	CDS	BASE COUNT	ORIGIN
1	A48343	Sequence 1 from Patent	A48343	g2302133	unidentified.	unidentified.	unidentified.	1 (bases 1 to 1142)	Kieffer,B. and Simonin,F.	HUMAN KAPPA OPIOID RECEPTOR, NUCLEIC ACIDS AND USES THEREOF	Patent: WO 9601898-A 1 25-DAN-1996;	UNIV PASTEUR (FR)	Other publication ER 2722209 960112.	location	1..1142	236 a	337 c

ALIGNMENTS

Result	LOCUS	DEFINITION	ACCESSION	NID	KEYWORDS	SOURCE	ORGANISM	REFERENCE	ATTNORS	TITLE	JOURNAL	COMMENT	FEATURES	source	CDS	BASE COUNT	ORIGIN
1	A48343	Sequence 1 from Patent	A48343	g2302133	unidentified.	unidentified.	unidentified.	1 (bases 1 to 1142)	Kieffer,B. and Simonin,F.	HUMAN KAPPA OPIOID RECEPTOR, NUCLEIC ACIDS AND USES THEREOF	Patent: WO 9601898-A 1 25-DAN-1996;	UNIV PASTEUR (FR)	Other publication ER 2722209 960112.	location	1..1142	236 a	337 c

Query Match: 86.2%; Score 857; DB 25; Length 1142;
 Best Local Similarity 98.7%; Pred. No. 0.00e+00;
 Matches 862; Conservative 0; Mismatches 11; Indels 0; Gaps 0;


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Db 257 GATACAGAAAGATGAGACAGACACCAACATTTCATATTTAACTGGCTTGGCAGATG 316
QY 100 GATACAGAAAGATGAGACAGACCAACATTTCATATTTAACTGGCTTGGCAGATG 159
Db 317 CTTCAGTACTACACCATGCCCCCTTCAGAGATGAGTCTACTATGATATCTGGCCCTT 376
QY 160 CTTCAGTACTACACCATGCCCCCTTCAGAGATGAGTCTACTATGATATCTGGCCCTT 219
Db 377 TTGGGGATGTCTCTGCAAGATAGTAAATTTCCATTGATTTACTACAGCTTCCACGCA 436
QY 220 TTGGGGATGTCTCTGCAAGATAGTAAATTTCCATTGATTTACTACAGCTTCCACGCA 279
Db 437 TCTCCACCTTGACCATGATGAGAGCTGAGACGCTACATTTGCGGTGTCACCCCGTGAAG 496
QY 280 TCTCCACCTTGACCATGATGAGAGCTGAGACGCTACATTTGCGGTGTCACCCCGTGAAG 339
Db 497 CTTCGACCTTCCGACACACCTTGAAGGCAGAAAGATCATATATGTCATCTGGCTGT 556
QY 340 CTTCGACCTTCCGACACACCTTGAAGGCAGAAAGATCATATATGTCATCTGGCTGT 399
Db 557 CGTATCTCTGGCATCTCTGCATATAGTCTCTGAGAGGACCAAGTACAGGAGAGAGCTG 616
QY 400 CGTATCTCTGGCATCTCTGCATATAGTCTCTGAGAGGACCAAGTACAGGAGAGAGCTG 459
Db 617 ATGTCATTGAGTCTCTCTGAGTTCACCATGATGATGATGATGATGATGATGATGATGAT 676
QY 460 ATGTCATTGAGTCTCTCTGAGTTCACCATGATGATGATGATGATGATGATGATGATGAT 519
Db 677 TGAAGATCTGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 736
QY 520 TGAAGATCTGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 579
Db 737 ACACCTCTGATGATCTCTGCTCTCAAGACGCTCGGCTCTCTCTCTCTCTCTCTCTCT 796
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QY 640 ATGCGACCTCTGATGATCTCTGCTCTCAAGACGCTCGGCTCTCTCTCTCTCTCTCTCT 699
Db 857 GCTGGACCTCCCATTCACATATTCATCTCTGATGAGGCTCTGGGAGACACCTCCACAGCA 916
QY 700 GCTGGACCTCCCATTCACATATTCATCTCTGATGAGGCTCTGGGAGACACCTCCACAGCA 759
Db 917 CAGCTGCTCTCTCAGCTATTTACTTTCGATCTGCTAGGCTATACCAACAGTACGCTG 976
QY 760 CAGCTGCTCTCTCAGCTATTTACTTTCGATCTGCTAGGCTATACCAACAGTACGCTG 819
Db 977 ATCCATCTCTCTCAGCTATTTACTTTCGATCTGCTAGGCTATACCAACAGTACGCTG 1036
QY 820 ATCCATCTCTCTCAGCTATTTACTTTCGATCTGCTAGGCTATACCAACAGTACGCTG 879
Db 1037 TTCCAGTGAAGATGAGATGAGAGCGGACGAGCTAGAGAGAGTCCGAATACAGTTCAGG 1096
QY 880 TTCCAGTGAAGATGAGATGAGAGCGGACGAGCTAGAGAGAGTCCGAATACAGTTCAGG 939
Db 1097 ATCTGCTTACCTAGAGGAGCATTCATGAGGATGA 1129
QY 940 ATCTGCTTACCTAGAGGAGCATTCATGAGGATGA 972

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RESULT 2
LOCUS 2 CP004092 1733 bp mRNA ROD 24-MAY-1995
DEFINITION Cavia porcellus Hartley kappa opiod receptor mRNA, complete cds.
ACCESSION 004092
NID 9476106
KEYWORDS
SOURCE
ORGANISM
Cavia porcellus
guinea pig.
Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Euteria; Rodentia; Hystrioonathi; Cavidae; Cavia.
REFERENCE
1 (bases 1 to 1733)
Xle,G.X., Meng,F., Mansour,A., Thompson,R.C., Hovestien,M.T.,
AUTHORS

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TITLE
JOURNAL
MEDLINE
REFERENCE
AUTHORS
JOURNAL
FEATURES
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/db_xref="taxon:10141"
/clone="gpk10R"
/sex="male"
/tissue="brain"
/dev_stage="adult"
1..239
5'UTR
240..1382
CDS
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high affinity to dynorphin A"
/product="kappa opiod receptor"
/db_xref="pid:9476107"
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CHEVYALDRTPKAKINICTLSSVGSVITLITAGTVRSDVDIIESDLPDD
YSWVDLFRKICVVFAPVLPVITIVCYTMTILKSVRLSRRDRRLRITLV
LVVAVFIICWPDHIFLIVEAGSISHTAALSYFCIALGYTNSLNPDIYALD
ENKRCRFRDFCFPIKRMERQSTRVNTVODPAVRYNDGVNKPV"
1383..1733
3'UTR
polyA_site
BASE COUNT 409 a 416 c 505 g 403 t
ORIGIN
Query Match 70.7%; Score 703; DB 14; Length 1733;
Best local Similarity 89.5%; Pred. No. 0.00e+00;
Matches 807; Conservative 0; Mismatches 92; Indels 3; Gaps 2;

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[illegible]


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RESULT 4
LOCUS MUSKAPORRE 1410 bp mRNA ROD 13-DEC-1993
DEFINITION Mouse kappa opiod receptor mRNA, complete cds.
ACCESSION L11065
NID 9348248
KEYWORDS kappa opiod receptor.
SOURCE Mus musculus (library: Clontech #ML1036a) brain cDNA to mRNA.
ORGANISM Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
Murinae; Mus.
1 (bases 1 to 1410)
Yasuda,K., Raynor,K., Kong,H., Breder,C.D., Takeda,J., Reisine,T.
and Bell,G.-I.
Cloning and functional comparison of kappa and delta opiod
receptors from mouse brain
Proc. Natl. Acad. Sci. U.S.A. 90, 6736-6740 (1993)
JOURNAL 93342064
MEDLINE
FEATURES
source
Location/Qualifiers
1..1410
/organism="Mus musculus"
/db_xref="taxon:10090"
/tissue_type="brain"
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186..1328
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/db_xref="PID:g348249"
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LVVAVFTTCWPIPHIFILVEADGSTSHSTALSTYFIALGTYNSSLNPLVLAFLD
ENFKRCFRCFPCIKMERQSTNRVNTVODPASRVDVGNNKPY"

BASE COUNT 322 a 360 c 337 g 391 t
ORIGIN
Query Match 67.4%; Score 670; DB 14; Length 1410;
Best Local Similarity 87.7%; Pred. No. 0.00e+00;
Matches 790; Conservative 0; Mismatches 108; Indels 3; Gaps 2;

Db 442 GATACAGGAAGATGAGACGCGCAACCACTACATATATACCTGGCTTGGAGATG 501
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QY 100 GATACAGGAAGATGAGACGCGCAACCACTTACATATATACCTGGAGATG 159
|||||
Db 502 CTTTGGTTCACCTACCTATGCTTCAGAGTGTCTGCTACCTGATGATTCCTTGGCCTT 561
|||||
QY 160 CTTTACTTACTACACCAATGCCCTTCAGAGTACGGTCTACTGATGATTCCTGGCCTT 219
|||||
Db 562 TTGGAGATGCGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 621
|||||
QY 220 TTGGGATGCGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 279
|||||
Db 622 TATTCACCTGACCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 681
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QY 280 TCTTCACCTGACCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 339
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Db 682 CTTTGACCTCGGACACCTTGAAGCAAGATCAATCAATCTGATTCCTTGGCTCTGG 741
|||||
QY 340 CTTTGACCTCGGACACCTTGAAGCAAGATCAATCAATCTGATTCCTTGGCTCTGG 399
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Db 742 CATCATCTGTGTATATAGCATATGCTTGGAGGACCAAGTCAAGGAAAGATGTGG 801
|||||
QY 400 CGTCATCTGTGGACATCTGTGCAATATGCTTGGAGGACCAAGTCAAGGAAAGATGTGG 459
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Db 802 ATGTCAATGAATGCTCTGCAATTCCTGATGATGATGATGATGATGATGATGATGATGATG 861
|||||
QY 460 ATGTCAATGAATGCTCTGCAATTCCTGATGATGATGATGATGATGATGATGATGATGATG 519
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Db 862 TGAAGATCTGTGTCTGCTGCTTGGCTTGTGATCCCAAGTCCATCATCATCTGTGTGTCT 921
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QY 520 TGAAGATCTGTGTCTGCTGCTTGTGATCCCTGCTGATCCCTGCTCATCATCATCTGCTGCT 579
Db 922 ACACCTGATGATCTGCGCCTTGAAGAGTGTCCGCTCTGCTGCTGCTCCCGAGAGAG 981
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QY 580 ACACCTGATGATCTGCGCCTTGAAGAGTGTCCGCTCTGCTGCTGCTCCCGAGAGAG 639
|||||
Db 982 ACGGAATCTCGCGCCTTGAAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1041
|||||
QY 640 ATNNCACTGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 699
|||||
Db 1042 GTTGAACCCCATTCACATCTTATCTGTTGAGAGGCTGTGAGAGACCTCCACAGCA 1101
|||||
QY 700 GTGGAACCCCATTCACATCTTATCTGTTGAGAGGCTGTGAGAGACCTCCACAGCA 759
|||||
Db 1102 CAGCTGCTCTGCGCCTTGAAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1161
|||||
QY 760 CAGCTGCTCTGCGCCTTGAAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 819
|||||
Db 1162 ATCTGCTCTGCTGCTGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATG 1221
|||||
QY 820 ATCCATCTCTGATGCTGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATG 879
|||||
Db 1222 TCCCATTTAGATGCGATGAGCGCCAGACCAATAGATTAGAAACACAGTTCAG 1281
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QY 880 TTCCATTTAGATGAGATGAGCGCCAGACCAATAGATTAGAAACACAGTTCAG 939
|||||
Db 1282 ATCTGCTCTGATGCTGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATG 1338
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QY 940 ATCTGCTCTGATGCTGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATG 999
|||||
Db 1339 A 1339
QY 1000 A 1000

RESULT 5
LOCUS R4TRORD 1273 bp mRNA ROD 21-DEC-1993
DEFINITION Rat mRNA for opiod receptor, complete cds.
ACCESSION D16534
NID 9409390
KEYWORDS G-protein coupled receptor; opiod receptor; transmembrane protein.
SOURCE Rattus norvegicus (strain Wistar) adult brain cDNA to mRNA, clone
PROR2.
ORGANISM Rattus norvegicus
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
Murinae; Rattus.
1 (bases 1 to 1273)
Nishi,M., Takeshima,H., Fukuda,K., Kato,S. and Mori,K.
cDNA cloning and pharmacological characterization of an opiod
receptor with high affinities for kappa-subtype-selective ligands
FEBS Lett. 330 (1), 77-80 (1993)
2 (bases 1 to 1273)
Takeshima,H.
Direct Submission
Submitted (19-JUN-1993) to the DDBJ/EMBL/GenBank databases. Hiroshi
Takeshima, International Institute for Advanced Studies; c/o
Shimadzu Corporation N-80, 1 Nishinokyo-Kuawahara-cho, Kyoto 604,
Japan (Tel:075-823-1208, Fax:075-811-8186)
Submitted (19-JUN-1993) to DDBJ by:
Hiroshi Takeshima
International Institute
for Advanced Studies
c/o Shimadzu Corporation
N-80
1 Nishinokyo-Kuawahara-cho
Kyoto 604
Japan
Japan
Phone: 075-823-1208
Fax: 075-811-8186.
FEATURES
source
Location/Qualifiers
1..1273

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Query Match	66.6%	Score 653	DB 14	Length 1273
Best Local Similarity	87.2%	Pred. No. 0.00e+00		
Matches 786	Conservative 0	Mismatches 112	Indels 3	Gaps 1

Db	305	GATACACAAAGATGAGAGCCGACACCAACATCTACATATTTAACTGGCTTGGCAGATG	364
QY	100	GATACACAAAGATGAGAGCCGACACCAACATTTACATTTTAACTGGCTTGGCAGATG	159
Db	365	CTTTGGTTACTACCACTATGGCCCTTCAGAGTGTCTGTACTTGATGAATTTGTGGCTT	424
QY	160	CTTTAGTTACTACCAACCATGGCCCTTCAGAGTGTCTGTACTTGATGAATTTGTGGCTT	219
Db	425	TTGGAGATGTCTGGCAGAAATTTGTCATTTCCATTTGCTACTACACAGATTTTACACCA	484
QY	220	TTGGGAGTGTCTGGCAGAGATAGTAATTTCCATTGATTTACTACACAGATTTTACACCA	279
Db	485	TATTCACCTTGCACCATGATGATGTGTGAGCCGCTACATTTGCCGTGTGCCACCCCTGGAAG	544
QY	280	TCTTCACCTTGCACCATGATGAGCCGCTGAGCCGCTACATTTGCCGTGTGCCACCCGCTGAAG	339
Db	545	CTTTGGATTTCCGAAACACTTTGAAAGAAAGATATCAATATCTGCATTTTGGCTACTGG	604
QY	340	CTTTGGATTTCCGCAACCCCTTGAAGGAAAGATATCAATTTCTGCATTTTGGCTACTGG	399
Db	605	CATCATCTGTTGGTATATCAGCGATATGTCCTTGGAGCACCAGAAAGTCAGGAGATGTGG	664
QY	400	CGTCATCTGTTGGCATCTCTGCAATATGTCTTGGAGGACACCAGAAATCAGGAGATGTGG	459
Db	665	ATGTGATGGAATGCTCCCTCTTGACGTTTCTCTGATGATGAATATTTCTGTGGGGACCTCTTCA	724
QY	460	ATGTATTTGAGATGCTCCCTCTTGAGTCCGACGATGATGATGATCTCTGTGGGGACCTCTTCA	519
Db	725	TGAAGATCTGTCTCTCTCTCTTGGCTTTGATCCCTGTGTATTCATCAATGTCTCTCT	784
QY	520	TGAAGATCTGTCTCTCTCTCTCTTGGCTTTGATCCCTGTGTATTCATCAATGTCTCTCT	579
Db	785	ACACCCGTGATATCTCGCGCTTGAAGAGTGTGTCGCTCTCTCGGGGCTCTGAGAGAAAG	844
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Db	845	ACCGAATCTCCGCGGATCAACAGAGCTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	904
QY	640	ATTNCAATCTCGGTGATGATCAACAGAGCTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	699
Db	905	GTTGACACCCCATCCACATCTTTATCTCGGTGTGAGAGCTCTTGGAGCAGACCTGCCACACA	964
QY	700	GTTGACACCCCATCCACATTTTCACTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	759
Db	965	CAGCTGTCTCTTACGCTATTACATTTTGCATTTGCCCTTGGTTATACCAACAGACCTTGA	1024

RESULT	LOCUS	6	1358 bp	mRNA	ROD	21-OCT-1993
DEFINITION	Rat kappa opioid receptor mRNA, complete cds.					
ACCESSION	L22001					
KEYWORDS	kappa opioid receptor; opioid receptor.					
SOURCE	Rattus norvegicus whole brain cDNA to mRNA.					
ORGANISM	Rattus norvegicus					
	Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;					
REFERENCE	Murinae; Rattus.					
AUTHORS	1 (bases 1 to 1358)					
TITLE	Chen, Y., Mestek, A., Liu, J. and Yu, L.					
JOURNAL	Molecular cloning of a rat kappa opioid receptor reveals sequences					
MEDLINE	similarities to the mu and delta opioid receptors					
FEATURES	Biochem. J. 295, 625-628 (1993)					
source	94039008					
	Location/Qualifiers					
	1..1358					

BASE COUNT	304 a	353 c	320 g	381 t
ORIGIN				
Query Match	56.6%	Score 662;	DB 14;	Length 1358;
Best Local Similarity	87.2%;	Pred. No. 0.00e+00;		
Matches 789	Conservative	0;	Mismatches 112;	Indels 3; Gaps 1;
Db	337	GATACCAAGATGAGAGACCGCAACCAACATCTACANATTAACTGGCTTTGGCAGATG	386	
Oy	100	GATACACAAAGATGAGAGACCAACCAACATCTACANATTAACTGGCTTTGGCAGATG	159	
Db	387	CTTGGTGTACACACATATGCGCTTCAGAGTGGTGTGCTGACATTTGGCTT	446	
Oy	160	CTTGGTGTACACACATGCGCTTTAGAGTACGGTGTCTTGATGATTAATTCCTGGCTT	219	
Db	447	TTGAGATGTTCTGGCAGATTGTCAATTCACATTGACTACTCAACATGTTTACAGCA	506	
Oy	220	TTGGGAGATGTCCTGGCAGATGATTTCCATTGATTCTCAACATGTTTACAGCA	279	
Db	507	TATTCACCTTGACCATGATGATGTGGACGCGCATTTGGCGGTGGCCACCGCTGTGAAG	566	


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QY      280 TCTTACCTTGACATATATAGCTGGACCGCTACATTCGCGTGTGCCACCCCTGAGG 339
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QY      340 CTTTGGATTTCOCAGACACCTTTGAAGCAAGATCATCAATCTGCATTTGGCTACTGG 399
Db      627 CATCATCTGTGGTATATGACGCGATAGCTTGGAGGACCAAGTCAAGGAAATGTGG 686
QY      400 CGTCATCTGTGGATCTGCATATATCTCTGGAGGACCAAGTCAAGGAAATGTGG 459
Db      687 ATGTCATATGATATCTCTCTGCAAGTTCCTGATGATGATATTCCTGTGGGAGCCTCTTCA 746
QY      460 ATGTCATATGATATCTCTCTGCAAGTTCCTGATGATGATATTCCTGTGGGAGCCTCTTCA 519
Db      747 TGAAGATCTGTGCTTGTGCTTGTGCTTGTATCCCTGTCTATATCATATCTGTGCT 806
QY      520 TGAAGATCTGTGCTTGTGCTTGTGCTTGTATCCCTGTCTATATCATATCTGTGCT 579
Db      807 ACACCCGTGATGATCTGCGCTTGAAGAGTGTGCGGCTCTCTGTGGGCTCTGAGAGAG 866
QY      580 ACACCCGTGATGATCTGCGCTTGAAGAGTGTGCGGCTCTCTGTGGGCTCTGAGAGAG 639
Db      867 ACCGAATCTCCGCGGATGACCAAGCTGTGCTGTGATGTGATGATCTCTCATCTCT 926
QY      640 ATNNCAACCTGCGTAGATACACAGACTGTGCTGTGTGTGTGTGTGTGTGTGTGTGT 699
Db      927 GTTGGACCCCATCCACATCTTTATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 986
QY      700 GCTGGATCCCATCATCATATCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 759
Db      987 CAGGTGCTCTGTAGTATCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1046
QY      760 CAGGTGCTCTGTAGTATCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 819
Db      1047 ATCTGTTCTCTATAGCTTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1106
QY      820 ATCCATCTCTCTAGCTTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 879
Db      1107 TCCCATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1166
QY      880 TCCCATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 939
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QY      940 ATCTGTTCTCTATAGCTTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 999
Db      1224 A 1224
QY      1000 A 1000

RESULT 7
LOCUS   RAIKOR1B      2094 bp      mRNA      ROD      19-NOV-1993
DEFINITION Rattus norvegicus kappa opioid receptor (KOR-1) mRNA, complete cds.
ACCESSION L22536
NID      6425188
KEYWORDS G-protein coupled receptor; kappa opioid receptor; transmembrane protein.
SOURCE   Rattus norvegicus (strain Sprague-Dawley) (library: lambda gt10)
          adult brain (striatum) cDNA to mRNA.
ORGANISM Rattus norvegicus
          Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
          Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
          Murinae; Rattus.
REFERENCE 1 (bases 1 to 2094)
          Li,S., Zhu,J., Chen,C., Chen,Y.-W., de Riel,J.K., Ashby,B. and
          Liu-Chen,L.-Y.
          Molecular cloning and expression of a rat k opioid receptor
          Biochem. J. 295, 629-633 (1993)
          94059009
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          Location/Qualifiers
          1..2094
source

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223..1365
/codon_start=1
/product="kappa opioid receptor"
/db_xref="pid:425189"
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CHPVKALDEPRLKAKIINICIMLASVGSIALVGGTREVEDVIECSLOEPDE
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2094
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Query Match      66.4%      Score 660; DB 14; Length 2094;
Best Local Similarity 87.1%      Pred. No. 0.00e+00;
Matches 785; Conservative 0; Mismatches 113; Indels 3; Gaps 1;

Db      479 GATACAAAGATGAGAGACCGCAACCAACATCTACATATTTAACCTGGCTTGACAGATG 538
QY      100 GATACAAAGATGAGAGACCGCAACCAACATTTACATATTTAACCTGGCTTGACAGATG 159
Db      539 CTTTGGTCTTACCACTATGACCTTCCAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 598
QY      160 CTTTGGTCTTACCACTATGACCTTCCAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 219
Db      599 TTGAGATGTCCTGTGCAATATGTCTATTTCCATGTGACTCTACACATGTTTACCGACA 658
QY      220 TTGAGATGTCCTGTGCAATATGTCTATTTCCATGTGACTCTACACATGTTTACCGACA 279
Db      659 TATTCACCTGACCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 718
QY      280 TCTTACCTTGACCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 339
Db      719 CTTTGGATTTCOCAGACACCTTTGAAGCAAGATCATCAATCTGCATTTGGCTACTGG 778
QY      340 CTTTGGATTTCOCAGACACCTTTGAAGCAAGATCATCAATCTGCATTTGGCTACTGG 399
Db      779 CATCATCTGTGGTATATGACGCGATAGCTTGGAGGACCAAGTCAAGGAAATGTGG 838
QY      400 CGTCATCTGTGGATCTGCATATATCTCTGGAGGACCAAGTCAAGGAAATGTGG 459
Db      839 ATGTCATATGATATCTCTCTGCAAGTTCCTGATGATGATATTCCTGTGGGAGCCTCTTCA 898
QY      460 ATGTCATATGATATCTCTCTGCAAGTTCCTGATGATGATATTCCTGTGGGAGCCTCTTCA 519
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QY      520 TGAAGATCTGTGCTTGTGCTTGTGCTTGTATCCCTGTCTATATCATATCTGTGCT 579
Db      959 ACACCCGTGATGATCTGCGCTTGAAGAGTGTGCGGCTCTCTGTGGGCTCTGAGAGAG 1018
QY      580 ACACCCGTGATGATCTGCGCTTGAAGAGTGTGCGGCTCTCTGTGGGCTCTGAGAGAG 639
Db      1019 ACCGAATCTCCGCGGATGACCAAGCTGTGCTGTGATGTGATGATCTCTCATCTCT 1078
QY      640 ATNNCAACCTGCGTAGATACACAGACTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 699
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Query Match	66.4%;	Score 660;	DB 14;	Length 2481;
Best Local Similarity	87.1%;	Pred. No. 0.00e+00;		
Matches 785;	Conservative	0;	Mismatches 113;	Indels 3; Gaps 1;
Db	367	GATACACAAATATGAAGCCCGCACACCAACATCTACATATTTAACTGGCTTTGGAGATG	426	
QY	100	GATACACAAATATGAAGCCCGCACACCAACATTTAACTGGCTTTGGAGATG	159	
Db	427	CTTGGTACTACCACTTTCGCCCTTCCAGAGCGCTGTACTGTGAATCTTGGCCT	486	
QY	160	CTTTAGTTACTACCAACCATGCCCTTTGAGAGCGCTTACTTGAATCTTGGCCT	219	
Db	487	TTGAGATGTTCTGTGCAAGATTGTCAATTCATTTAGTACTACACAAATGTTTACAGCA	546	
QY	220	TTGGGATGTGCTGTGCAAGATAGTAATTTTCATTTAGTACTACAAATGTTTACAGCA	279	
Db	547	TATTCACCTTTGACCATGTATGAGTGTGAGCCGCTACATTTGCCGTGTGCCACCTGTGAAAG	606	
QY	280	TCTTCACCTTTGACCATGTATGAGCCGCTACATTTGCCGTGTGCCACCTGTGAAAG	339	
Db	607	CTTTCGATTTTCGCAACACCTTTGAAAGCAAGATCATCAATACATTCGCAATTTGGCTACAGG	666	
QY	340	CTTTGCACTTTCCGACACACCTTTGAAAGCAAGATCATCAATTCGCAATTTGGCTACAGG	399	
Db	667	CATCATCTGTTGATATATACAGGATAGTCTTTGAGGACCAACCAATTCAGGAGATGTGG	726	
QY	400	CGTCACTGTGTGGCATCTCTGTGCATATAGTCTTTGAGGACCAACCAATTCAGGAGATGTGG	459	
Db	727	ATGTATTTGAATGCTCTCTTTCGAGTTTCTGTATGATGATATATCTCTGTGTGGACCTCTTCA	786	
QY	460	ATGTATTTGAATGCTCTCTTTCGAGTTTCTGTATGATGATATATCTCTGTGTGGACCTCTTCA	519	
Db	787	TGAAGATCTGTCTCTGCTCTTGGCTTTGTATCCCTGTATCCCTGTATTCATATGTCCTGT	846	
QY	520	TGAAGATCTGTCTCTTTCATCTTGGCTTTGTATCCCTGTATCCCTGTATTCATATGTCCTGT	579	
Db	847	ACACCTGATGATCTCTGCTCTTGAAGAGTGTCCGCTCTCTCGGCGCTCTGAGAGAGG	906	
QY	580	ACACCTGATGATCTCTGCTCTTGAAGAGTGTCCGCTCTCTCGGCGCTCTGAGAGAGG	639	
Db	907	ACCGAATCTCCGCGGATACACCAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	966	
QY	640	ATNNCAACCTGCTGT	599	
Db	967	GTTGACCCCGCATTCACATCTTATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1026	
QY	700	GTTGACCCCGCATTCACATCTTATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	759	
Db	1027	CAGTGTCTCTCTGATATTTACTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1086	
QY	760	CAGTGTCTCTCTGATATTTACTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	819	
Db	1087	ATTCGTCTCTCTGATATTTACTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1146	
QY	820	ATTCGTCTCTCTGATATTTACTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	879	
Db	1147	TCCCATTTAAGTGTGATGTGAGCCCGCACACCAACGAGTTTGAACCAAGTTTCAGG	1206	
QY	880	TTCACCTGAGATGTGAGTGTGAGCCCGCACACCAACGAGTTTGAACCAAGTTTCAGG	939	
Db	1207	ATTCGTCTCTCTGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGG	1263	
QY	940	ATTCGTCTCTCTGAGGAGATCGATGGATATGATTAACCAAGATATGACTAGTCGTGG	999	
Db	1264	A 1264		
QY	1000	A 1000		
RESULT	9			
LOCUS	E08874	2481 bp	RNA	PAT
DEFINITION	CDNA coding rat kappa-opioid receptor.			
				26-NOV-1996

ACCESSION E08874
 NID 92176978
 KEYWORDS JP 1995070191-A/1.
 SOURCE Rattus sp.
 ORGANISM Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 1 (bases 1 to 2481)
 Kimimichi, S.
 RECEPTOR PROTEIN, ITS PRODUCTION AND USE THEREOF
 Patent: JP 1995070191-A 1 14-MAR-1995;
 TAKEDA CHEM IND LTD
 OS Rattus sp. (rat)
 PN JP 1995070191-A/1
 PD 14-MAR-1995 JP 1993190261
 PR 30-JUL-1993 JP 1993190261
 PR 09-JUL-1993 JP 93P 170591
 PI SATO KIMIMICHI
 PC C07K14/47, C12N1/21, C12N1/09, C12P21/02//A61K38/00, A61K38/00, C12R1.19, C12P21/02, C12R1.19, C07K99:00;
 CC strandedness: Double;
 CC topology: Linear;
 FH Key
 FH Location/Qualifiers
 FT source 1..2481
 FT /organism="Rattus sp."
 FT /db_xref="taxon:10118"
 FT CDS 111..1253
 FT /product="rat kappa-opioid receptor".
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 source 1..2481
 Location/Qualifiers
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 /db_xref="taxon:10118"
 /product="rat kappa-opioid receptor".
 BASE COUNT 629 a 588 c 344 g 720 t
 ORIGIN
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 Best Local Similarity 87.1%; Pred. No. 0.00e+00;
 Matches 785; Conservative 0; Mismatches 113; Indels 3; Gaps 1;
 Db 367 GATACACAAGATGAAGACCGCAACACATCTACATATTTAACTGGCTTTGGCAGATG 426
 QY 100 GATACACAAGATGAAGACCGCAACACATCTACATATTTAACTGGCTTTGGCAGATG 159
 Db 427 CTTTGGTACTACACATGCCCCCTCCAGAGTGTCTCTACTTGTATGATTTCTTGGCCCTT 486
 QY 160 CTTTGGTACTACACATGCCCCCTCCAGAGTGTCTCTACTTGTATGATTTCTTGGCCCTT 219
 Db 487 TTGGAGATGTTCTGTGCAAGATTTGCTTCATTTGCTACTGCTACTGCAACATGTTTACCGACA 546
 QY 220 TTGGAGATGTTCTGTGCAAGATTTGCTTCATTTGCTACTGCTACTGCAACATGTTTACCGACA 279
 Db 547 TATTACCTTGACACATGATGATGTGGACCGCTACATTTGCCGTGTGGCACCTGTGAAG 606
 QY 280 TATTACCTTGACACATGATGATGTGGACCGCTACATTTGCCGTGTGGCACCTGTGAAG 339
 Db 607 CTTTGGATTTCCCAACACCTTTGAAGAAGATCATCAACATCTGCAATTTGGCTACTGG 666
 QY 340 CTTTGGATTTCCCAACACCTTTGAAGAAGATCATCAACATCTGCAATTTGGCTACTGG 339
 Db 667 CATTACCTTTGGATTTGCAAGATTTGCTTCATTTGCTACTGCTACTGCAACATGTTTACCGACA 726
 QY 400 CATTACCTTTGGATTTGCAAGATTTGCTTCATTTGCTACTGCTACTGCAACATGTTTACCGACA 459
 Db 727 ATGTCAATGGAATGCTCTGTCGACATTTCCGATGATGATGATGATTTCCCTGGTGGACCTCTTCA 786
 QY 460 ATGTCAATGGAATGCTCTGTCGACATTTCCGATGATGATGATGATGATTTCCCTGGTGGACCTCTTCA 519
 Db 787 TGAAGATCTGTCTGCTTCTGCTTTGCTTTTATTCCTGCTTTATTCATTCATGCTGCT 846
 QY 520 TGAAGATCTGTCTGCTTCTGCTTTGCTTTTATTCCTGCTTTATTCATTCATGCTGCT 579

Db 847 ACACCTTGATGCTCTGCTTGAAGATGTGGGCTCTCTGCGGCTCTGAGCAAG 906
 QY 580 ACACCTTGATGCTCTGCTTGAAGATGTGGGCTCTCTGCGGCTCTGAGCAAG 639
 Db 907 ACCGAATCTCCGCGGATGATCAACCAAGCGGTAGGTGTTGACGCTTCATCT 966
 QY 640 AATNCACTCCGCGGATGATCAACCAAGCGGTAGGTGTTGACGCTTCATCT 699
 Db 967 GTTGACCCCATCCACATCTTATCTCGTGAAGCTTAGCGCAGCACTCTACACA 1026
 QY 700 GTTGACCCCATCCACATCTTATCTCGTGAAGCTTAGCGCAGCACTCTACACA 759
 Db 1027 CAGCTGCTCTCAGTATTTACTTCTGCAATGCTTGGGTATACCAACAGCACTTGA 1086
 QY 760 CAGCTGCTCTCAGTATTTACTTCTGCAATGCTTGGGTATACCAACAGCACTTGA 819
 Db 1087 ATCTGTTCTCTAATGCTTCTGATGAAGCTTCAAGCGTGTGTTAGGACCTTCTGCT 1146
 QY 820 ATCTGTTCTCTAATGCTTCTGATGAAGCTTCAAGCGTGTGTTAGGACCTTCTGCT 879
 Db 1147 TCCCATTAAGATGCGATGAGGCGCCAGACCAACAGATTTAGAACAGCTTCAGG 1206
 QY 880 TCCCATTAAGATGCGATGAGGCGCCAGACCAACAGATTTAGAACAGCTTCAGG 939
 Db 1207 ATCTGTTCTCTAATGCTTCTGATGAAGCTTCAAGCGTGTGTTAGGACCTTCTGCT 1263
 QY 940 ATCTGTTCTCTAATGCTTCTGATGAAGCTTCAAGCGTGTGTTAGGACCTTCTGCT 999
 Db 1264 A 1264
 QY 1000 A 1000

RESULT 10
 LOCUS RND00442 4742 bp mRNA ROD 25-MAY-1994
 DEFINITION Rattus norvegicus kappa1 opioid receptor mRNA, complete cds.
 ACCESSION U00442
 NID 9403486
 KEYWORDS Norway rat.
 SOURCE Rattus norvegicus
 ORGANISM Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae; Murinae; Rattus.
 1 (bases 1 to 4742)
 Meng, F., Xie, G.-X., Thompson, R.C., Mansour, A., Goldstein, A., Watson, S.J. and Akil, H.
 Cloning and pharmacological characterization of a rat kappa opioid receptor
 Proc. Natl. Acad. Sci. U.S.A. 90, 9954-9958 (1993)
 JOURNAL 94032210
 MEDLINE 2 (bases 1 to 4742)
 REFERENCE Meng, F.
 TITLE Direct Submission
 JOURNAL Submitted (05-AUG-1993) Fan Meng, Mental Health Research Institute, University of Michigan, 205 Zina Fitcher Place, Ann Arbor, Michigan 48109, USA
 FEATURES
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 Location/Qualifiers
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 /evidence=experimental
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 /db_xref="pid:9403487"
 /translation="MESPQIFRGEGRPCASACILPNSSSWEPWMAEDSGSYGS EDOQLPAHISPAIVITIAVSYFVGLVGNLSVMFVITITKKTATINITINFLA

QY 629 CCGAGAGAAAGATNNCAACCTGGGAGATGACACAGACTGGTGGTGAGGAGT 688
 DB 524 CTTCATCATGCTGGTGGAGCCCATTCATCATCTTATCTGCTGGAGCTTGGAGAC 583
 QY 689 CTTCGCTGCTGCTGGAGCTCCATCATATTCATCTGCTGGAGCTTGGAGAC 748
 DB 584 CTCCACAGCAGCAGCTGGCCCTCCACATCTTATCTGCTGGAGCTTGGAGAC 643
 QY 749 CTCCACAGCAGCAGCTGGCCCTCCACATCTTATCTGCTGGAGCTTGGAGAC 808
 DB 644 CACAGACCTGATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 703
 QY 809 CAGTACGCTGATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 868
 DB 704 GAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 763
 QY 869 GAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 928
 DB 764 CACAGTTCAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 820
 QY 929 TACAGTTCAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 988
 DB 821 ACTAGTCTGGA 832
 QY 989 ACTAGTCTGGA 1000

RESULT 12
 LOCUS MTSORBDP3 638 bp DNA ROD 12-APR-1996
 DEFINITION Mouse MORGD gene for kappa-opioid receptor, exon 3.
 ACCESSION D31665
 NID 9643595
 KEYWORDS G-protein associated; kappa opioid receptor; opioid drugs and
 peptides-binding; transmembrane protein.
 SEGMENT 3 of 3
 SOURCE Mus musculus
 ORGANISM Mus musculus
 Eukaryota; Mitochondrial eukaryotes; Metazoa; Chordata;
 Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
 Murinae; Mus.
 REFERENCE 1 (bases 1 to 638)
 AUTHORS Nishi, M., Takeshima, H., Mori, M., Nakagawa, K. and Takeuchi, T.
 TITLE Structure and chromosomal mapping of genes for the mouse
 +kappa-opioid receptor and an opioid receptor homolog (MOR-C)
 JOURNAL Biochemical and Biophysical Research Communication 205, 1353-1357
 (1994)
 REFERENCE 2 (bases 1 to 638)
 AUTHORS Takeshima, H.
 TITLE Direct Submission
 JOURNAL Submitted (28-MAY-1994) to the DDBJ/EMBL/GenBank databases. Hiroshi
 Takeshima, Tokyo Institute of Psychiatry, Department of
 Neurochemistry; 2-1-8 Kamikitazawa, Setagaya-ku, Tokyo 156, Japan
 (Tel:03-3304-5701(ex.312), Fax:03-3329-8035)
 COMMENT Submitted (28-May-1994) to DDBJ by:
 Hiroshi Takeshima
 Department of Neurochemistry
 Tokyo Institute of Psychiatry
 2-1-8 Kamikitazawa, Setagaya-ku
 Tokyo 156
 Japan
 Phone: 03-3304-5701 x312
 Fax: 03-3329-8035.
 FEATURES
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 1. 638
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 /db_xref="PID:9808876"
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exon
 /note="third protein coding sequence (P3)"
 /number=3
 BASE COUNT 141 a 154 c 151 g 192 t
 ORIGIN Chromosome 1 A2-3.
 Query Match 38.0%; Score 378; DB 14; Length 638;
 Best Local Similarity 84.98; Pred. No. 5,14e-264;
 Matches 471; Conservative 0; Mismatches 81; Indels 3; Gaps 2;
 DB 20 CACGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 79
 QY 446 CAGGAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 505
 DB 80 GTGGATCTCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATG 139
 QY 506 GTGGATCTCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATG 565
 DB 140 CATCATCTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 199
 QY 566 CATCATCTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 625
 DB 200 CTCCGAG 259
 QY 626 CTCCGAG 685
 DB 260 AGCTTCATCATCTGATGATGATGATGATGATGATGATGATGATGATGATG 319
 QY 686 AGCTTCATCATCTGATGATGATGATGATGATGATGATGATGATGATGATG 745
 DB 320 CACCTCCACAG 379
 QY 746 CACCTCCACAG 805
 DB 380 CACAGACCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 439
 QY 806 CACAGACCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 865
 DB 440 TAGGACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 499
 QY 866 CCGGACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 925
 DB 500 AAGACAGTTCAGATGATGATGATGATGATGATGATGATGATGATGATGATG 556
 QY 926 AAGACAGTTCAGATGATGATGATGATGATGATGATGATGATGATGATGATG 985
 DB 557 AAGACAGTTCAGATGATGATGATGATGATGATGATGATGATGATGATGATG 571
 QY 986 AAGACAGTTCAGATGATGATGATGATGATGATGATGATGATGATGATGATG 1000

RESULT 13
 LOCUS RNROR3 4048 bp DNA ROD 25-MAR-1995
 DEFINITION Rattus norvegicus kappa opioid receptor gene, exon 4 and complete
 cds.
 ACCESSION U17995
 NID 9727258
 KEYWORDS 3 of 3
 SEGMENT Norway rat.
 SOURCE Rattus norvegicus
 ORGANISM Eukaryota; Mitochondrial eukaryotes; Metazoa; Chordata;
 Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
 Murinae; Rattus.
 REFERENCE 1 (bases 1 to 4048)
 AUTHORS Yakovlev, A.G., Krueger, K.E. and Faden, A.I.
 TITLE Structure and expression of a rat kappa opioid receptor gene

JOURNAL
MEDLINE
95204422
REFERENCE
2 (bases 1 to 4048)
AUTHORS
Yakovlev, A.G.
TITLE
Direct Submision
Submitted (02-DEC-1994) Alexander G. Yakovlev, George G. Tom
University School of Medicine, Neurology, 3900 Reservoir Rd.,
Washington, DC 20007, USA

FEATURES
source
Location/Qualifiers
1..4048
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/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/sex="male"
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89..3951)
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2, 3, and 4"
join(U17993:1083..11707,U17994:226..578,89..3951)
/note="second of two alternate transcripts; does not use
exon 1, and the 5' end of exon 2 is extended into Intron
1"
join(U17993:1451..1707,U17994:226..578,89..621)
/codon_start=1
/product="kappa opiate receptor"
/db_xref="PID:g727260"
/translation="MESPQIFRGEPPTCPASACILPNSSWEPFNWMSDNGSVGS
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CHPKVADFRPTLKAKIINCTIMLLASVGSIAIVYGGTKEVDVEDVCECSOPDDE
YSWMLDFMKICVFAFVFPVPIITVCTILMLIRKSVRLSGSRKDNLRIRIKLV
LVVAVFTICMTPIHFTILVEKDGSHSTAVLSSTFICIAIGYINSSNPVIAFLD
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89..3951
/number=4
/evidence=experimental
/product="kappa opiod receptor"

BASE COUNT 1196 a 783 c 798 g 1271 t
ORIGIN

Query Match 37.7%; Score 375; DB 14; Length 4048;
Best Local Similarity 84.8%; Pred. No. 1,21e-261;
Matches 468; Conservative 0; Mismatches 81; Indels 3; Gaps 1;

Db 84 GGCAGATGGATGTCATGTAATGCTGCTGAGTTCCTCGATGATGAATATTCCTGCTG 143
QY 449 GGAAGGTGTGATGTCATGTAATGCTGCTGAGTTCCTCGATGATGAATATTCCTGCTG 508
Db 144 GGAACCTTCATGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 203
QY 509 GGACCTTCATGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 568
Db 204 CATTTGCTGTACACCTGATGATCTGCGCTGGAAGAGTGTCCGGCTCCTCTCGGGCTC 263
QY 569 CARGCTGTGTACACCTGATGATCTGCGCTGGAAGAGTGTCCGGCTCCTCTCGGGCTC 628
Db 264 TCGAGAAAGAGCCGAATCTCCCGCGGATCACCAAGCTGGTGTAGTGGTGTAGT 323
QY 629 CCGAGAAAGAGCCGAATCTCCCGCGGATCACCAAGCTGGTGTAGTGGTGTAGT 688
Db 324 CTCATCATGCTGTGAGCCCGATCCACATCTTATCTGCTGAGGCTCTAGGACAGAC 383
QY 689 CTTCGTGTGTGCTGAGCTCCCATTCATCATATTCCTGCTGAGGCTCTAGGACAGAC 748
Db 384 CTCACACAGACAGCTCTGCTGTAGCTATTAATCTGCAATGCTGGGTATACCAA 443
QY 749 CTCACACAGACAGCTCTGCTGTAGCTATTAATCTGCAATGCTGGGTATACCAA 808
Db 444 CAGAGCTTGAATCTGCTGTAGCTATTAATCTGCAATGCTGGGTATACCAA 503

QY 809 CAGTAGCCCTGAATCCCATTCCTCTACGCCCTTCTGATGAATAACTCAAGCGGTGTTCCG 868
Db 504 GCACCTTCCTGCTCCCATTAAGATGAGATGAGCGCCAGACACAAAGAGCTTAGAAA 563
QY 869 GGACCTTCCTGCTCCCATTAAGATGAGATGAGCGCCAGACACAAAGAGCTTAGAAA 928
Db 564 CACAGTTCAGATTCCTGCTCCCATTAAGATGAGATGAGCGCCAGACACAAAGAGCTTAG 620
QY 928 TACAGTTCAGATTCCTGCTCCCATTAAGATGAGATGAGCGCCAGACACAAAGAGCTTAG 988
Db 621 ACTAGTCATGGA 632
QY 989 ACTAGTCATGGA 1000

RESULT 14
LOCUS S7786852 1109 bp DNA ROD 26-SEP-1995
DEFINITION kappa opiod receptor [mice, Genomic, 1109 nt, segment 2 of 3].
ACCESSION S77869
NID 9998530
KEYWORDS
2 of 3
SEGMENT
SOURCE
Mus sp.
ORGANISM
Mus sp.
Eukaryotae; Mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathu; Muridae; Murinae;
Mus.
REFERENCE
1 (bases 1 to 1109)
AUTHORS
Lin, H.C., Lu, S., Augustin, L.B., Felsheim, R.F., Chen, H.C., Loh, H.H.
and Wei, L.N.
Cloning and promoter mapping of mouse kappa opiod receptor gene
JOURNAL
Biochem. Biophys. Res. Commun. 209 (2), 639-647 (1995)
MEDLINE
95251653
REMARK
Genbank staff at the National Library of Medicine created this
entry [NCBI gi58316534] from the original journal article.
This sequence comes from Fig. 2.
FEATURES
source
1..1109
/organism="Mus sp."
/db_xref="taxon:10095"

BASE COUNT 331 a 213 c 204 g 361 t
ORIGIN

Query Match 31.8%; Score 316; DB 14; Length 1109;
Best Local Similarity 86.5%; Pred. No. 3,71e-215;
Matches 392; Conservative 0; Mismatches 58; Indels 3; Gaps 2;

Db 275 AAGCAAAATTAATTAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 332
QY 4 AAGCAAAATTAATTAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 63
Db 333 AGACATGAGAGAAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 392
QY 64 AAGATGAGAGAAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 122
Db 393 ACGACATCTACATATTAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 452
QY 123 ACGACATCTACATATTAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 182
Db 453 TTTGAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 512
QY 183 TTTGAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 572
Db 513 GTGATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 632
QY 243 GTGATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 748
Db 573 GTGATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 808
QY 303 GTGATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 868
Db 633 AAGCAAAATTAATTAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 692

QY 363 AAGCAAGAATCATCATATCTGCATCGGCTGCTGTCATCTGTTGGCATCTCTGCA 422

Db 693 ATATCTCTGGAGGACCAAGTACGGCAAGT 725

QY 423 ATATCTCTGGAGGACCAAGTACGGCAAGT 455

RESULT 15

LOCUS MUSMORGP2 488 bp DNA ROD 12-APR-1996

DEFINITION Mouse MORGD gene for kappa-opioid receptor, exon 2.

ACCESSION D31664

KEYWORDS 9643594

KEYWORDS G-protein associated; kappa opioid receptor; opioid drugs and peptides-binding; transmembrane protein.

SEGMENT 2 of 3

SOURCE Mus musculus DNA, clone_lib:phage lambda fix11.

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 488)

AUTHORS Nishi, M., Takeshima, H., Mori, M., Nakagawara, K. and Takeuchi, T.

TITLE Structure and chromosomal mapping of genes for the mouse kappa-opioid receptor and an opioid receptor homolog (MOR-C)

JOURNAL Biochemical and Biophysical Research Communication 205, 1353-1357 (1994)

REFERENCE 2 (bases 1 to 488)

AUTHORS Takeshima, H.

TITLE Direct Submision

JOURNAL Submitted (28-MAY-1994) to the DDBJ/EMBL/Genbank databases. Hiroshi Takeshima, Tokyo Institute of Psychiatry, Department of Neurochemistry, 2-1-8 Kamikitazawa, Setagaya-Ku, Tokyo 156, Japan (Tel:03-3304-5701(ex.312); Fax:03-3329-8035)

COMMENT Submitted (28-May-1994) to DDBJ by: Hiroshi Takeshima

Department of Neurochemistry

Tokyo Institute of Psychiatry

2-1-8 Kamikitazawa, Setagaya-Ku

Tokyo 156

Japan

Phone: 03-3304-5701 x312

Fax: 03-3329-8035.

FEATURES

source

1.488

Location/Qualifiers

/organism="Mus musculus"

/db_xref="taxon:10090"

/clone_lib="phage lambda fix11"

89..441

/note="second protein coding sequence (P2)"

exon

number=2

BASE COUNT 129 a 103 c 97 g 159 t

ORIGIN Chromosome 1 A2-3.

Query Match 31.7%; Score 315; DB 14; Length 488;

Best Local Similarity 90.5%; Pred. No. 2.27e-214;

Matches 352; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

Db 55 AUGGAGGAAGAAATCTGTTCTTTCTTTTATTTTATGATACAGAGATGAGACCGCAACCA 114

QY 67 AUGGAGGAAGAAATCTGTTCTTTCTTTTATGATACAGAGATGAGACCGCAACCA 126

Db 115 ACATCTACATATTTAATCTGCTTGGAGATGCTTGGTACTACCATGATGCTTTC 174

QY 127 ACATTTACATATTTAATCTGCTTGGAGATGCTTGGTACTACCATGATGCTTTC 186

Db 175 AGAGTCTCTCTACTGATGATGAAATCTTGGCTTTTGGAGATGCTTATGCAAGATGTCA 234

QY 187 AGAGTACGGCTCTGATGATGAAATCTTGGCTTTTGGAGATGCTTATGCAAGATGTCA 246

Db 235 TTTCATTTGACTCTACAGATGTTTACGACATATTCACCTTGACCAAGATGATGTGG 294

QY 247 TTTCATTTGACTCTACAGATGTTTACGACATATTCACCTTGACCAAGATGATGTGG 306

Db 295 ACCGCTACATTTGCTGTGTGCCACCCCTGTGAAGGCTTGGACTTCGACACCTTTGAAG 354

QY 307 ACCGCTACATTTGCTGTGTGCCACCCCTGTGAAGGCTTGGACTTCGACACCTTTGAAG 366

Db 355 CAAGATCATCAATCATCTGATTTGGCTCTCGGATCATCTGTGTATTCAGCGATAG 414

QY 367 CAAGATCATCAATCATCTGATTTGGCTCTCGGATCATCTGTGTATTCAGCGATAG 426

Db 415 TCCTTGGAGGACCAAGTACGAGGAGT 443

QY 427 TCCTTGGAGGACCAAGTACGAGGAGT 455

Search completed: Mon Apr 20 23:47:15 1998

Job time : 920 secs.

(TW)

Release 3.0.4A John F. Collins, Biocomputing Research Unit.
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MPsrch_n n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Mon Apr 20 23:10:34 1998; Maspar time 1013.06 Seconds

Tabular output not generated. 1172.160 Million cell updates/sec

Title: >US-08-292-694A-1
Description: (1-1410) from US08292694A.seq
Perfect Score: 1410
N.A. Sequence: 1 GCGCAGCCTTGCTGATCCGAA.....AACCCGATTCACAGTCGAG 1410
Comp: CCGCTGGAGAGACTAGGGTT.....TTGGGTCTATGTTGACGTC

Scoring table: TABLE default
Gap 6

Mmatch STD : Dbase 0; Query 0

Searched: 1126798 seqs, 421087984 bases x 2

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database:

emb1-est
1:em_est1 2:em_est2 3:em_est3 4:em_est4 5:em_est5
6:em_est6 7:em_est7 8:em_est8
Database: genbank-est
9:gb_est1 10:gb_est2 11:gb_est3 12:gb_est4 13:gb_est5
14:gb_est6 15:gb_est7 16:gb_est8 17:gb_est9 18:gb_est10
19:gb_est11 20:gb_est12 21:gb_est13

Statistics: Mean 11.354; Variance 1.916; scale 5.926

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	123	8.7	183	10	R81583 yj04b04.r1 Homo sapien	2.22e-214
2	103	7.3	153	10	R31984 yh62c10.r1 Homo sapien	5.21e-168
3	78	5.5	433	10	R81332 yj04b04.s1 Homo sapien	1.17e-111
4	42	3.0	373	9	T08926 BSM06818 Homo sapien	9.14e-37
5	41	2.9	450	13	W04836 za81f05.r1 Soares feta	6.99e-35
6	32	2.3	324	9	T77094 ycg3b07.r1 Homo sapien	8.30e-19
7	30	2.1	435	10	R31938 yh62c10.s1 Homo sapien	1.67e-15
8	29	2.1	3055	20	G28604 human STS SHG-35403	6.76e-14
9	27	1.9	249	11	H29103 ym31f07.r1 Homo sapien	8.71e-11
10	27	1.9	319	13	HSC27C021 H. sapiens partial cDN	8.71e-11
11	27	1.9	386	11	H14301 ym63c04.r1 Homo sapien	8.71e-11
12	27	1.9	416	16	AA182250 mt83h08.r1 Soares mous	8.71e-11
13	27	1.9	478	17	AA189997 mt98e07.r1 Soares mous	8.71e-11
14	27	1.9	492	21	B50064 CT978SK-2206.TV C197	8.71e-11
15	27	1.9	602	23	AA51931 vgl1f07.r1 Soares mous	8.71e-11

16	27	1.9	1664	20	G28514 human STS SHG-31461	8.71e-11
17	25	1.8	217	22	C10515 C.elegans cDNA clone y	7.87e-08
18	24	1.7	249	11	T29782 BS194762 Homo sapiens	2.04e-06
19	24	1.7	391	22	AA436714 zvs96d05.s1 Soares test	2.04e-06
20	24	1.7	391	11	N93987 za66c09.r1 Homo sapien	2.04e-06
21	24	1.7	442	15	W56386 zc57a06.r1 Soares para	2.04e-06
22	24	1.7	442	15	W79255 zdf75c02.r1 Soares feta	2.04e-06
23	24	1.7	453	15	W63664 zc57g11.r1 Soares para	2.04e-06
24	24	1.7	514	22	HMW42E11B human fetal brain cDNA	2.04e-06
25	24	1.7	598	15	W37328 zc11h02.r1 Soares para	2.04e-06
26	24	1.7	2856	20	G28560 human STS SHG-35278	2.04e-06
27	22	1.6	255	10	R15444 y46a09.s2 Homo sapien	9.66e-04
28	23	1.6	261	18	AA331167 ES352121 Embryo, 8 wee	4.71e-05
29	23	1.6	300	22	C11312 C.elegans cDNA clone y	4.71e-05
30	23	1.6	315	19	AA386021 yb53d01.r1 Homo sapien	4.71e-05
31	23	1.6	327	10	R27256 ES199944 Pancreas tumo	4.71e-05
32	23	1.6	339	13	HSB18A052 H. sapiens partial cDN	4.71e-05
33	23	1.6	370	23	RCS16541A Rice cDNA, partial seq	4.71e-05
34	23	1.6	385	11	R31585 yj126a04.r1 Homo sapien	4.71e-05
35	23	1.6	404	11	H14901 yj126a04.r1 Homo sapien	4.71e-05
36	23	1.6	416	11	H44713 yj15b08.s1 Homo sapien	4.71e-05
37	23	1.6	420	11	H26756 yf05g04.r1 Knowles SOL	9.66e-04
38	22	1.6	443	20	AA467444 human STS CHRC GGAA20B	4.71e-05
39	22	1.6	443	20	G09917 y064e04.r1 Homo sapien	4.71e-05
40	22	1.6	501	11	H43475 ym15c07.r1 Bartstead mo	4.71e-05
41	23	1.6	559	17	AA239704 zK8404.r1 Soares preg	4.71e-05
42	23	1.6	580	19	AA084783 F.rubripes GSS sequenc	4.71e-05
43	23	1.6	598	21	FR0027571 44al Human retina cDNA	4.71e-05
44	23	1.6	791	13	W28236	

ALIGNMENTS

RESULT 1
LOCUS R81583 183 bp mRNA
DEFINITION yj04b04.r1 Homo sapiens cDNA clone 147727 5' similar to gb:L5119
ACCESSION R81583
NID 9858186
KEYWORDS SOURCE
human clone=147727 library=Soares placenta Nb2HP vector=PT793D
(Pharmacia) with a modified polylinker host=DH10B (ampicillin
resistant) primer=M13Rp1 Rsite1=Not I Rsite2=Eco RI female placenta
obtained at birth (full term). 1st strand cDNA was primed with a
Not I - oligo(dT) primer '5'
AAGTGGAGAAATTCGCGCGCGAGAAATTTTCTTTTCTTTT 3', double-stranded
cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not
I and cloned into the Not I and Eco RI sites of the modified pT73
vector. Library went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaldo.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Choroata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Hominoide; Homo.
1 (bases 1 to 183)
Hillier, L., Clark, N., Dubouque, T., Elliston, K., Hawkins, M.,
Holman, M., Hulman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Irevaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and
Wilson, R.
The Washu-Merck EST Project
Unpublished (1995)

REFERENCE
AUTHORS

TITLE JOURNAL
COMMENT
Contact: Wilson RK
Washu-Merck EST Project
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence starts: 1

[illegible]

REFERENCE 1 (bases 1 to 435) Dubeau, T., Elliston, R., Hawkins, M.,
AUTHORS Hilder, L., Clark, N.,
Holman, M., Hulman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohling, T., Soares, M., Tan, F.,
Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and
Wilson, R.
TITLE The Washu-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT
Contact: Wilson RK
Washu-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: leste@watscn.wustl.edu
High quality sequence stops: 255
Source: IMAGE Consortium, LNLU
This clone is available royalty-free through LNLU ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
FEATURES
Source
1..435
/organism="Homo sapiens"
/clone="134322"
BASE COUNT 102 a 98 c 108 g 120 t 7 others
ORIGIN
Query Match 2.1%; Score 30; DB 10; Length 435;
Best Local Similarity 77.8%; Pred. No. 1.67e-15; Indels 3; Gaps 3
Matches 63; Conservative 0; Mismatches 15;
Db 293 GGTAACTGAGATGATGACCTGCTCTCTCCGAGGAACTGACGAGGCATCTCC 352
|||||
Cp 1394 GGTAAACCAAG-AICATGTGACCTCTCTACTCGAGAAACATTAAGAGA-CATTCC 1337
|||||
Db 353 ACGGCTAGGTCATACGGGGTT 373
|||||
Cp 1336 ACGACTAG-TCATACTGGCTT 1317
|||||
RESULT 8
LOCUS G28604 3055 bp DNA STS 01-JUL-1996
DEFINITION human STS SHGC-35403.
ACCESSION G28604
G1408419
NID STS; STS sequence; primer; sequence tagged site.
KEYWORDS human.
SOURCE
ORGANISM Homo sapiens
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 3055)
Myers, R.N.
Unpublished (1996)
COMMENT
Contact: Richard M. Myers
Stanford Human Genome Center (SHGC)
Stanford University School of Medicine
Department of Genetics, M-344, Stanford, CA 94305, USA
Tel: 4157259687
Fax: 4157259689
Email: myers@shgc.stanford.edu
Primer A: AGGACAAAGATCTCCCAAGA
Primer B: AGAAGGAAGAGACTGTGAAGC
STS size: 201
PCR Profile:
Initial incubation: 94 degrees C for 90 seconds
Denaturation: 94 degrees C for 15 seconds
Annealing: 62 degrees C for 23 seconds
Polymerization: 72 degrees C for 30 seconds
PCR Cycles: 30
Thermal Cycler: Perkin Elmer 9600

Protocol:

Template: 25 ng
 Primer: each 1 uM
 dNTPs: each 200 uM
 Taq Polymerase: 0.05 units/uL
 Total Vol: 10 uL

Buffer:

MgCl₂: 2.5 mM
 KCl: 50 mM
 Tris-HCl: 20 mM
 pH: 8.3

Prepared with primer pairs provided by Sandoz, derived from Z49205
 -- Washington University/Merck EST sequence.

FEATURES
 source
 1..3035
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /map="3"
 STS
 primer_bind 1969..2169
 primer_bind complement(2146..2169)
 BASE COUNT 725 a 775 c 769 g 786 t
 ORIGIN

Query Match 2.1%; Score 29; DB 20; Length 3055;
 Best Local Similarity 61.6%; Pred. No. 6.76e-14;
 Matches 77; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

Db 1015 GCAGTCAATCTGATTCATCATCGGCTTCCTGGACAGCGGCGCATCTGGATG 1074
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 375 GCTGTCTACCTGTGTATTTGGTGGGCTTGTAGTGGGCAATCTCTGGTCACTTTGTC 434
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1075 TTGCTTCCACATGAACCCCTGGAGCGCATCTCGTTCATGTTCAATTTGGCTCG 1134
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 435 ATCATCCGATACAGAGATGAAGACCGACCAACATCATATTTAACTGCTTTGG 494
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1135 GCCGA 1139
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 495 GCCGA 499

RESULT 9
 LOCUS H29103 249 bp mRNA EST 17-JUL-1995
 DEFINITION Ym31f07.r1 Homo sapiens cDNA clone 49725 5' similar to gp:1L06797
 PROBABLE G PROTEIN-COUPLED RECEPTOR LCRI HOMOLOG (HUMAN).
 ACCESSION H29103
 NID 9900013
 KEYWORDS EST.
 SOURCE human clone-49725 library-soares infant brain 1MB vector-Lafrmid BA
 host=PH108 (ampicillin resistant) primer-M3RPI Rsite=Not I
 Rsite2-Hind III whole brain from a 73 days post natal female. 1st
 strand cDNA was primed with a Not I - oligo(dT) primer [5',
 AACTGGAGATTCGGCGCGCAGAGATTTTCTTTTCTTTT 3']; double-stranded
 cDNA was ligated to Hind III adaptors (pharmacia), digested with
 Not I and directionally cloned into the Not I and Hind III sites of
 the lafrmid BA vector. Library went through one round of
 normalization. Library constructed by Bento Soares and M.Fatima
 BonaIbo.

ORGANISM Homo sapiens
 Eukaryotes; Metazoa; Eumetazoa; Bilateria; Coelomata;
 Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
 Sarcopterygii; Chonadata; Tetrapoda; Amniota; Mammalia; Theria;
 Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 249)
 Hillier, L., Clark, N., Dubuque, T., Ellis, K., Hawkins, M.,
 Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
 Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
 Trevisan, E., Waterston, R., Williamson, A., Wohlmann, P., and
 Wilson, R.
 TITLE The WashU-Merck EST Project
 JOURNAL Unpublished (1995)

COMMENT

GDB: G00-422-535
 Contact: Wilson RK
 WashU-Merck EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@wustl.edu
 High quality sequence stops: 198
 Source: IMAGE Consortium, LIND
 This clone is available royalty-free through LIND; contact the
 IMAGE Consortium (info@image.lind.gov) for further information.
 Location/Qualifiers
 1..249
 source
 /organism="Homo sapiens"
 /clone="49725"

BASE COUNT 58 a 75 c 55 g 56 t 5 others

ORIGIN

Query Match 1.9%; Score 27; DB 11; Length 249;
 Best Local Similarity 60.4%; Pred. No. 8.71e-11;
 Matches 67; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

Db 116 TTTCGAACTTCCTATGCAAGGAGTCATGTCATCAACAGTCACCTACAGCA 175
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 561 TTGGAGATGTCGTATGCAAGATTTGCATTTGCATGACTACACATGTTACCA 620
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 176 GTTCCTATCTGGCCTTCATACAGTCTGACCGTACCTGGCATCTCCAC 226
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 621 AATTCACCTTGACATGATGATGTGACCGCCTACATGCTGTGTCCAC 671
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 10
 LOCUS HSC27C021 319 bp RNA EST 21-SEP-1995
 DEFINITION H. sapiens partial cDNA sequence; clone c-27c02.
 ACCESSION Z44696
 NID 9573854
 KEYWORDS EST; partial cDNA sequence; transcribed sequence fragment.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
 Vertebrata; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 319)
 Genexpress.
 Direct Submission
 Submitted (24-OCT-1994) Genethon, B.P. 60, 91002 Evry Cedex France
 and Genetique Molculaire et Biologie du developpement, CNRS UPR420
 B.P. 8, 94801 Villejuif Cedex France.E-mail: genexpress@genethon.fr
 2 (bases 1 to 319)
 Genexpress.
 The Genexpress cDNA program
 Unpublished
 3 (bases 1 to 319)
 Auffray, C., Behar, G., Bois, F., Bouchier, C., da Silva, C.,
 Devignes, M.D., Duprat, S., Houliette, R., Jumeau, M.N., Lamy, B.,
 Lorenzo, F., Mitchell, H., Mariage-Samson, R., Pietu, G., Poullot, Y.,
 Sebastien-Kabatichs, C. and Tessier, A.
 IMAGS: molecular integration of the analysis of the human genome
 and its expression
 C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)
 95277534
 Clone library from B.Souares, Psychiatry Dept. Columbia University
 USA.

TITLE
 JOURNAL
 MEDLINE
 COMMENT

Cloning_method: total mRNA was oligo-(dT) primed and directionally
 cloned 5' -> 3' into the HindIII -> NotI sites of the lafrmid BA
 vector;
 Sequencing_method: single read, full automatic;
 Primer: M13_reverse
 cDNA sequence colinear to mRNA
 Stretch_removed: nothing
 Normalization_method: Bento Soares, P.N.A.S in press;

Genexpress_library_id: C;
Genexpress_sequence_id: y1c-27c02;

No significant homology found with:
genbank release 81 swissprot release 28.

FEATURES

Source
1..319
/organism="Homo sapiens"
/isolate="muscular atrophy patient"
/db_xref="taxon:9606"
/dev_stage="3 months old"
/tissue_type="total brain"
/clone_lib="normalized infant brain cDNA"
/sex="Female"
BASE COUNT 59 a 107 c 81 g 69 t 3 others
ORIGIN

Query Match 1.9%; Score 27; DB 13; Length 319;
Best Local Similarity 61.2%; Pred. No. 8.71e-11;
Matches 74; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

D 195 TCGCCCTTACCTTCGATTTTATCCCTTGTAGTTGTAATACCTGCTCTGT 254
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Q 370 TCACCGCTCTACTCTGTGTATTGTGTGGCTTATGGGCAATTCGTGCAATG 429
D 255 GGCCTTTCATCCGAGACCAAGTCGGGACCCCGGCAACGTGTCTGATGATCTG 314
| ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Q 430 TGTGATATCCGATACGAGATGAGACCGCAACACATCTACATATTTAACCTGG 489
D 315 C 315
Q 490 C 490

RESULT 11
LOCUS H14301 385 bp mRNA EST 10-JUL-1995
DEFINITION YM63C04.r1 Homo sapiens cDNA clone 163590 5' similar to
gb:003642_cds1 PROBABLE G PROTEIN-COUPLED RECEPTOR AP2 (HUMAN);.
ACCESSION H14301
KEYWORDS 9879121
SOURCE

human clone=163590 library=Soares adult brain N24AB55Y
vector=PT73D (Pharmacia) with a modified polylinker host=DH10B
(ampicillin resistant) primer=MI3RPI Rsite1-Not I Rsite2-Eco RI
55-year old male. 1st strand cDNA was primed with a Not I -
oligo(dT) primer [5',
TGTACCATCTGGAAGTGGGACGCGCGCTTTTCTTTTCTTTTCTTTT 3'],
double-stranded cDNA was size selected, ligated into the Not I and
(Pharmacia), digested with Not I and cloned into the Eco RI adapters
RI sites of a modified pT73 vector (Pharmacia). Library went
through one round of normalization to a Cot = 35. Library
constructed by Bento Soares and M.Fatima Bonaldo. The adult brain
RNA was provided by Dr. Donald H. Gilden. Tissue was acquired 17-18
hours after death which occurred in consequence of a ruptured
aortic aneurysm. RNA was prepared from a pool of tissues
representing the following areas of the brain: frontal, parietal,
temporal and occipital cortex from the left and right hemispheres,
subcortical white matter, basal ganglia, thalamus, cerebellum,
midbrain, pons and medulla.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 386)

REFERENCE

Haller, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hulman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, B., Rohlfing, T., Soares, M., Tan, F.,
Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and
Wilson, R.

TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT

Contact: Wilson R
WashU-Merck EST Project

Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800
Fax: 314 286 1810

Email: est@watson.wustl.edu

High quality sequence stops: 212

Source: IMAGE Consortium, LBNL
This clone is available royalty-free through LBNL; contact the
IMAGE Consortium (info@image.lbnl.gov) for further information.

FEATURES

Source
1..386
/organism="Homo sapiens"
/clone="163590"
BASE COUNT 58 a 122 c 104 g 98 t 4 others
ORIGIN

Query Match 1.9%; Score 27; DB 11; Length 386;
Best Local Similarity 73.7%; Pred. No. 8.71e-11;
Matches 42; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

D 107 CAACATGTACACAGCAGCTTCTTCTCCTGACGAGAGACCTTGACCGTACATGCG 163
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Q 605 CAACATGTACACAGATATTCACCTTGACGAGATGATGTGGACCGCTACATTCG 661

RESULT 12
LOCUS AA182250 416 bp mRNA EST 06-JAN-1997
DEFINITION mt83h08.r1 Soares mouse lymph node N6MLN Mus musculus cDNA clone
636543 5' similar to gb:M60626 FMT-DEU-PHE RECEPTOR (HUMAN);.
ACCESSION AA182250
KEYWORDS 91765715
NID
EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Mus

REFERENCE

1 (bases 1 to 416)
Marra, M., Haller, L., Allen, K., Bowles, M., Dietrich, N., Dubuque, T.,
Gessel, S., Kucaba, T., Lacy, K., Le, M., Martin, J., Morris, K.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theisinger, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.

TITLE The WashU-Merck Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT

Contact: Marra M/Mouse EST Project

WashU-Merck Mouse EST Project

Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800
Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LBNL; contact the
IMAGE Consortium (info@image.lbnl.gov) for further information.

Seq primer: -28M13 rev2 from Amersham

High quality sequence stop: 372.

FEATURES

Source

1..416
/organism="Mus musculus"
/strain="C57BL/6J"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 15
TGTACCATCTGGAAGTGGGACGCGGATACCTTTTCTTTTCTTTTCTTTT
3'; double-stranded cDNA was ligated to Eco RI adapters
(Pharmacia), digested with Not I and cloned into the Not
I and Eco RI sites of the modified pT73 vector. RNA
provided by Dr. Bertrand Jordan. Library constructed and
normalized by Bento Soares and M.Fatima Bonaldo."
/db_xref="taxon:10090"

ACCESSION AA511931
 NID 92249785
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata;
 Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
 Murinae; Mus.
 1 (bases 1 to 602)
 Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
 Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,D., Morris,M.,
 Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
 Theisinger,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
 Waterston,R.
 The WashU-HMI Mouse EST Project
 Unpublished (1996)

TITLE
 JOURNAL
 COMMENT
 Contact: Marra M/Mouse EST Project
 WashU-HMI Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 850L, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@wustl.edu
 This clone is available royalty-free through INL; contact the
 IMAGE Consortium (info@image.lnl.gov) for further information.
 MGI:505725
 Seg primer: -28m3 rev2 ET from Amersham
 High quality sequence stop: 388.

FEATURES
 source
 1..602
 location/Qualifiers
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /note="Vector: pT7T3-D-Pac (Pharmacia) with a modified
 polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
 was primed with a Not I - oligo(dT) primer 15/
 TCTTACCATCTGAGTGGAGGAGCGCGGAGATTTTCTTTTCTTTTCTTTT
 3']; double-stranded cDNA was ligated to Eco RI adaptors
 (Pharmacia), digested with Not I and cloned into the Not
 I and Eco RI sites of the modified pT7T3 vector. RNA
 provided by Dr. Minoru Ko, Wayne State Univ. Library
 constructed and normalized by Bento Soares and M.Fatima
 Bonaldo."
 /db_xref="taxon:10090"
 /clone="961637"
 /clone_lib="Soares mouse NbME"
 /sex="male"
 /issue_type="heart"
 /dev_stage="4 weeks"
 /lab_host="DH10B"
 <1..>602

tRNA
 BASE COUNT 142 a 164 c 144 g 152 t
 ORIGIN

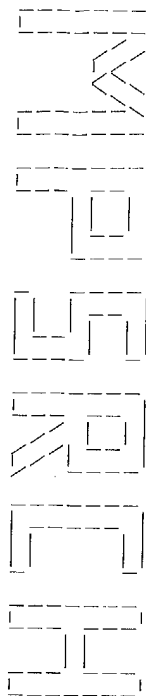
Query Match 1.9%; Score 27; DB 23; Length 602;
 Best Local Similarity 66.3%; Pred. No. 8.71e-11;
 Matches 55; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

Db 355 TGGGAGACAGCTGCTGATTCAGTGTGCTGATTCGAAACAAGAGGATCGGACTGTCAACA 414
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 409 TGGGCAATTTCTGTCGTATGTTTGTCAATCCATACAGCAAGATGAGAGCCCAACA 468
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 415 ACATCTTCCTGCTGTCCTGGCT 437
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 469 ACATCTACATATTTAACCTGGCT 491

Search completed: Mon Apr 20 23:27:43 1998
 Job time : 1029 secs.



(TM)

 Release 3.0.4a John F. Collins, Biocomputing Research Unit.
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MPearch_n n.a. - n.a. database search, using Smith-Waterman algorithm
 Run on: Mon Apr 20 22:47:25 1998; Maspar time 1272.37 Seconds
 Tabular output not generated. 1310.345 Million cell updates/sec

Title: >US-08-292-694A-1
 Description: (1-1410) from US08292694A.seq
 Perfect Score: 1410
 N.A. Sequence: 1 GGGGACCTTGCTGATGTCGCA.....AACCCGATTACTGACGAG 1410
 Comp: CGCGTGCAGACGACATAGGCTT.....TTGGGTCTATGTTGACGTC

Scoring table: TABLE default

Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 354530 seqs, 591221332 bases x 2

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database:

emb153

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 26:gb_hlg

Statistics: Mean 11.183; Variance 5.314; scale 2.105

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	1410	100.0	1410	14	MUSKAPOPRE	Mouse kappa oploid rec	0.00e+00
2	11208	85.7	1288	14	S81111	kappa-oploid receptor	0.00e+00
3	1133	80.4	1273	14	RATROBP	Rat kappa for oploid re	0.00e+00
4	1133	80.4	1358	14	RATKOR1A	Rattus norvegicus kapp	0.00e+00
5	1131	80.2	2094	14	RATKOR1B	Rattus norvegicus kapp	0.00e+00
6	1131	80.2	4742	14	RATKOR1B	Rattus norvegicus kapp	0.00e+00
7	1129	80.1	2481	14	RATKOR	Rattus norvegicus kapp	0.00e+00
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9	857	59.4	1733	14	CDNA coding rat kappa-	0.00e+00	
10	838	59.4	1142	25	A48343	Cavia porcellus hattle	0.00e+00
11	618	43.8	1186	14	S778683	Sequence 1 from Patent	0.00e+00
12	607	43.0	638	14	MUSMORGDp3	Mouse MORGD gene for k	0.00e+00
13	558	36.6	4048	14	RNKR03	Rattus norvegicus kapp	0.00e+00
14	354	25.1	488	14	MUSMORGDp2	Mouse MORGD gene for k	1.77e-275

15	354	25.1	1109	14	S7786832	kappa oploid receptor	1.77e-275
16	348	24.7	432	14	MKU16998	Mus musculus kappa op	3.67e-270
17	341	24.2	658	14	RNKR02	Rattus norvegicus kapp	5.82e-264
18	315	22.3	1610	14	MWU26915	Mus musculus mu oploid	5.68e-241
19	313	22.2	2229	14	MWU19380	Mus musculus mu oploid	3.31e-239
20	311	22.1	1231	16	CCMDOP1	C.comersoni mRNA for	1.93e-237
21	311	22.1	2135	14	RATMOR1A	Rattus norvegicus Mu o	1.93e-237
22	311	22.1	2397	14	RATMOR1B	Rattus norvegicus Mu o	1.93e-237
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25	309	21.9	1586	14	RATMOR1A	Rattus norvegicus mu o	1.12e-235
26	307	21.8	1367	14	RATMOR1A	Rattus norvegicus mu o	1.12e-235
27	291	20.6	1835	14	RNKR03	Rattus norvegicus mu o	6.54e-220
28	291	20.6	2203	14	MUSMORGDp3	Mouse delta oploid recep	8.25e-220
29	291	20.6	2203	14	MUSMORGDp3	Mouse delta oploid recep	8.25e-220
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32	291	20.6	2272	14	MUSMORGDp3	Mus musculus delta op	8.25e-220
33	289	20.5	1415	15	BTU89677	Bos taurus mu oploid r	4.76e-218
34	285	20.2	1366	14	RATMOR1A	Rattus norvegicus kapp	1.58e-214
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36	283	20.1	1458	16	DRU1596	Danio rerio mRNA for o	9.05e-213
37	283	20.1	1861	15	PIGMOOPR	Pig musculus mu oploid r	9.05e-213
38	273	19.4	2074	14	MUSMORGDp1	Mouse MORGD gene for k	5.56e-204
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40	261	18.5	998	25	A38530	Sequence 3 from Patent	1.88e-193
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ALIGNMENTS

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 DEFINITION Mouse kappa oploid receptor mRNA, complete cds.
 ACCESSION L11065
 NID G348248
 KEYWORDS kappa oploid receptor.
 SOURCE Mus musculus (Library: Clontech #ML1036a) brain cDNA to mRNA.
 ORGANISM Mus musculus
 Eukaryotes; mitochondria; eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae; Mus.
 1 (bases 1 to 1410)
 Yasuda,K., Raynor,K., Kong,H., Breder,C.D., Takeda,J., Reisine,T.
 and Bell,G.I.
 Cloning and functional comparison of kappa and delta oploid
 receptors from mouse brain
 JOURNAL Proc Natl. Acad. Sci. U.S.A. 90, 6736-6740 (1993)
 MEDLINE 93342064
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source

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RESULT 3
LOCUS 3
DEFINITION Rat mRNA for opiod receptor, complete cds.
ACCESSION D16534
KEYWORDS G-protein coupled receptor; opiod receptor; transmembrane protein.
SOURCE Rattus norvegicus (strain Wistar) adult brain cDNA to mRNA, clone
PROB2.
ORGANISM Rattus norvegicus
Eukaryote; mitochondria; eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae;
Murinae; Rattus.
REFERENCE 1 (bases 1 to 1273)
AUTHORS Nishikawa, H., Fukuda, K., Kato, S. and Mori, K.
TITLE CDNA cloning and pharmacological characterization of an opiod
receptor with high affinities for kappa-subtype-selective ligands
FEBs Lett. 330 (1), 77-80 (1993)
JOURNAL 93380575
MEDLINE 2 (bases 1 to 1273)
REFERENCE 2 (bases 1 to 1273)
AUTHORS Nishikawa, H.
TITLE Direct Submission
COMMENT Submitted (19-JUN-1993) to the DDBJ/EMBL/Genbank databases. Hiroshi
Takeshima, International Institute for Advanced Studies, c/o
Shimadzu Corporation N-80, 1 Nishinokyo-Kuwarehara-cho, Kyoto 604,
Japan (Tel:075-823-1208, Fax:075-811-8186)
Hiroshi Takeshima
International Institute
for Advanced Studies
c/o Shimadzu Corporation
N-80
1 Nishinokyo-Kuwarehara-cho
Kyoto 604
Japan
Phone: 075-823-1208
Fax: 075-811-8186.
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 530 GAGTCTGTAT 589
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RESULT 4
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 DEFINITION Rat kappa opiod receptor mRNA, complete cds.
 ACCESSION L22001
 MID 9409236
 KEYWORDS kappa opiod receptor; opiod receptor.
 SOURCE Rattus norvegicus whole brain cDNA to mRNA.
 ORGANISM Rattus norvegicus
 Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae; Murinae; Rattus.
 REFERENCE 1 (bases 1 to 1358)
 AUTHORS Chen, Y., Mestek, A., Liu, J., and Yu, L.
 TITLE Molecular cloning of a rat kappa opiod receptor reveals sequence similarities to the mu and delta opiod receptors
 JOURNAL Biochem. J. 295, 625-628 (1993)
 MEDLINE 94059008
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RESULT 5
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DEFINITION Rattus norvegicus kappa opiod receptor (KOR-1) mRNA, complete cds.

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ACCESSION L22536
NID 542518
KEYWORDS G-protein coupled receptor; kappa opiod receptor; transmembrane protein.
SOURCE Rattus norvegicus (strain Sprague-Dawley) (library: lambda gt10) adult brain (striatum) cDNA to mRNA.
ORGANISM Rattus norvegicus
REFERENCE 1 (bases 1 to 2094)
AUTHORS Li,S., Zhu,Y., Chen,C., Chen,Y.-W., de Riel,J.K., Ashby,B. and Liu-Chen,L.-Y.
TITLE Molecular cloning and expression of a rat kappa opiod receptor
JOURNAL Biochem. J. 295, 629-633 (1993)
MEDLINE 9405909
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JOURNAL Submitted (21-Jul-1993) to the DDBJ/EMBL/Genbank databases.
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Fax: 075-753-4586)
COMMENT Submitted (21-Jul-1993) to DDBJ by:
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Department of Pharmacology
Faculty of Pharmaceutical Sciences
Kyoto University
Kyoto, Kyoto 606-01
Japan
Phone: 075-753-4546
Fax: 075-753-4586.

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BASE COUNT 629 a 588 c 544 g 720 t

ORIGIN

Query Match 80.1%; Score 1129; DB 14; Length 2481;
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ACCESSION	92176978		
NID	JP 1995070191-A/1.		
KEYWORDS	Rattus sp.		
SOURCE	Rattus sp.		
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REFERENCE	Kimimichi, S.		
AUTHORS	RECEPTOR PROTEIN, ITS PRODUCTION AND USE THEREOF		
TIME	Patent: JP 1995070191-A 1 14-MAR-1995;		
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REFERENCE
AUTHORS Xie,G.X., Meng,Z., Mansour,A., Thompson,R.C., Hovesteren,M.T.,
Goldstein,A., Watson,S.J. and Akil,H.E.
TITLE Primary structure and functional expression of a guinea pig kappa
opioid (dynorphin) receptor
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 91 (3), 3779-3783 (1994)
MEDLINE 94224825
REFERENCE 2 (bases 1 to 1733)
AUTHORS Xie,G.
TITLE Direct Submission
JOURNAL Submitted (07-DEC-1993) Guo-Xi Xie, Mental Health Research
Institute, The University of Michigan, 205 Zina Pitcher Place, Ann
Arbor, MI 48109-0720, USA
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 ACCESSION S77872


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Db 564 CAGAGTTACGAGATCTGCTCCATGAGAGGATGTTGGTGGGANTAAATAGCCATAGACT 623
QY 1271 CACAGTTACGAGATCTGCTCCATGAGAGGATGTTGGTGGGANTAAATAGCCATAGACT 1330
Db 624 AGTACATGAGAAATCTGCTCCATGAGAGGATGTTGGTGGGANTAAATAGCCATAGACT 683
QY 1331 AGTACATGAGAAATCTGCTCCATGAGAGGATGTTGGTGGGANTAAATAGCCATAGACT 1390
Db 684 AACCCAGATTACCATGCGAG 703
QY 1391 AACCCAGATTACCATGCGAG 1410

RESULT 14
LOCUS MUSMORBP2 488 bp DNA ROD 12-APR-1996
DEFINITION Mouse MORBP gene for kappa-opioid receptor, exon 2.
ACCESSION D31664
KEYWORDS G-protein associated; kappa opioid receptor; opioid drugs and
peptide-binding; transmembrane protein.
SEGMENT 2 of 3
SOURCE Mus musculus
ORGANISM Mus musculus
Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
Murinae; Mus.
REFERENCE 1 (bases 1 to 488)
AUTHORS Nishi, M., Takeshima, H., Mori, M., Nakagawa, K. and Takeuchi, T.
TITLE Structure and chromosomal mapping of genes for the mouse
kappa-opioid receptor and an opioid receptor homolog (MOR-C)
JOURNAL Biochemical and Biophysical Research Communication 205, 1353-1357
(1994)
REFERENCE 2 (bases 1 to 488)
AUTHORS Takeshima, H.
TITLE Direct Submission
JOURNAL Submitted (28-MAY-1994) to the DDBJ/EMBL/GenBank databases. Hiroshi
Takeshima, Tokyo Institute of Psychiatry, Department of
Neurochemistry; 2-1-8 Kamikita-za, Setagaya-Ku, Tokyo 156, Japan
(Tel:03-3304-5701(ex.312), Fax:03-3329-8035)
COMMENT Submitted (28-May-1994) to DDBJ by:
Hiroshi Takeshima
Department of Neurochemistry
Tokyo Institute of Psychiatry
2-1-8 Kamikita-za, Setagaya-Ku
Tokyo 156
Japan
Phone: 03-3304-5701 x312
Fax: 03-3329-8035.

FEATURES
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Best Local Similarity 100.0%; Pred. No. 1.77e-275;
Matches 354; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 502 CTTGGTACTACCACTATGCGCTTTGAGAGTGTGCTACTGATGATCTTGGCCTT 561
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QY 742 CATCATCTGTGGTATATACGAGATAGCTTGGAGGACCAAGCAGGAGAG 795

RESULT 15
LOCUS S77868S2 1109 bp DNA ROD 26-SEP-1995
DEFINITION Kappa opioid receptor [mice, genomic, 1109 nt, segment 2 of 3].
ACCESSION S77869
KEYWORDS 2 of 3
SEGMENT 2 of 3
SOURCE Mus sp.
ORGANISM Mus sp.
Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Mus.
REFERENCE 1 (bases 1 to 1109)
AUTHORS Liu, H.C., Lu, S., Augustin, L.B., Felsenfeld, R.F., Chen, H.C., Loh, H.H.
and Wei, L.N.
TITLE Cloning and promoter mapping of mouse kappa opioid receptor gene
JOURNAL Biochem. Biophys. Res. Commun. 209 (2), 639-647 (1995)
MEDLINE 9525163
REMARK GenBank staff at the National Library of Medicine created this
entry [NCBI gibbs 166534] from the original journal article.
This sequence comes from Fig. 2.

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Matches 354; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

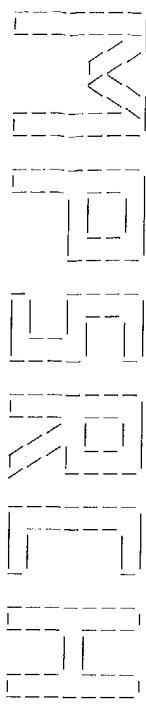
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QY 502 CTTGGTACTACCACTATGCGCTTTGAGAGTGTGCTACTGATGATCTTGGCCTT 561
Db 490 TTGAGATGTGCTATGCAAGATTTGCTATTTCCATTGACTACTACCAAGTGTACAGCA 549
QY 562 TTGAGATGTGCTATGCAAGATTTGCTATTTCCATTGACTACTACCAAGTGTACAGCA 621
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QY 622 TATTCACCTTGACCATGATGAGTGTGAGCGCTACATTCCTGTGTCACCCCTGTGAAG 681
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QY 742 CATCATCTGTGGTATATACGAGATAGCTTGGAGGACCAAGCAGGAGAG 795
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Tue Apr 21 08:03:54 1998

US-08-292-694A-1.rge

Page 14

Search completed: Mon Apr 20 23:10:13 1998
Job time : 1368 secs.



(TM)

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MSEARCH n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Mon Apr 20 23:28:06 1998; MasPar time 199.87 Seconds

Tubular output not generated. 814.103 Million cell updates/sec

Title: >US-08-292-694A-1

Description: (1-1410) from US08292694A.seq

Perfect score: 1410

N.A. Sequence: 1 GCGCACCTTCGTGATGCCAA.....AACCCAGATTCACACTGCAG 1410

Comp: CGCGTGAGACGACTGAGGTTT.....TTGGGTCATAGTTCACGTC

Scoring table: TABLE default

Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 159651 seqs, 57698962 bases x 2

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database:

n-geneseq30

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33

Statistics: Mean 9.344; Variance 5.218; scale 1.791

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	1410	100.0	1410	13	Q75926	Mouse kappa opioid re
2	1129	80.1	2481	15	Q86725	Mammalian kappa opioi
3	838	59.4	1142	20	T12550	Human kappa opioi re
4	668	47.4	1000	13	Q75931	Human kappa opioi re
5	311	22.1	2070	12	Q75199	Rat mu-subtype opioi
6	309	21.9	1618	14	Q85222	Rat mu opioi recepto
7	309	21.9	1618	14	Q85223	Transcription regulat
8	309	21.9	1821	10	Q56700	Partial sequence of t
9	291	20.6	1821	10	Q56705	Sequence of murine de
10	291	20.6	2272	13	Q75927	Mouse delta opioi re
11	289	20.5	1610	14	Q85226	Human mu opioi recep
12	289	20.5	2160	15	Q93102	Human mu opiate recep
13	276	19.6	2216	11	Q66566	Murine delta opioi r
14	230	16.3	829	10	Q56703	Partial sequence of t
15	220	15.6	1567	14	Q85233	Rat opioi receptor c

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
16	218	15.5	1330	13	Q75928	Mouse opioi receptor
17	218	15.5	2706	15	Q92972	Rat opioi receptor
18	207	14.7	2600	14	Q90906	Mouse kappa-3 opioi
19	195	13.8	2447	10	Q56702	Partial sequence of t
20	97	6.9	1265	7	Q45654	Murine somatostatin
21	91	6.5	1047	2	Q10572	Human Natluretic Pep
22	78	5.5	1047	2	Q10572	Human Natluretic Pep
23	77	5.5	1518	14	Q83682	Epsilon opioi recept
24	78	5.5	1634	7	Q45653	Human somatostatin
25	75	5.3	1110	5	Q29155	Human somatostatin
26	73	5.2	1244	7	Q45656	Murine somatostatin
27	67	4.8	832	5	Q29156	Brain somatostatin
28	68	4.8	1130	23	T09250	Human somatostatin
29	67	4.8	1296	7	Q45657	Human somatostatin
30	68	4.8	1351	7	Q45655	Human somatostatin
31	68	4.8	1796	7	Q45658	Murine somatostatin
32	56	4.0	1054	14	Q83681	Epsilon opioi recept
33	52	3.7	726	31	T77788	G-protein coupled rec
34	46	3.3	1162	11	Q66170	Seven transmembrane
35	46	3.3	2254	11	Q66167	Seven transmembrane
36	45	3.2	1200	16	Q95036	Rat hippocampal neuro
37	45	3.2	1556	16	Q95035	Rat hippocampal neuro
38	44	3.1	1065	33	T86154	Human MIP-1alpha/RAN
39	44	3.1	1495	11	Q62695	C-C chemokine recept
40	41	2.9	91	9	Q51746	Oligonucleotide probe
41	39	2.8	91	9	Q51746	Oligonucleotide probe
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ALIGNMENTS

RESULT 1
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DT 17-AUG-1995 (first entry)
DE Mouse kappa opioi receptor MOR1 cDNA.
KW Mouse; kappa; delta; mu; opioi receptor; brain; primer; PCR; amplify;
KW transmembrane domain; somatostatin; receptor; human; expression vector;
KW truncate; chimaeric; assay; probe; ss.
OS Mus musculus.
FH Key Location/Qualifiers
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FT /product= mouse kappa opioi receptor
FT W09428132-A.
FD 08-DEC-1994.
PD 20-MAY-1994; U05747.
PR 20-MAY-1993; US-066296.
PR 30-JUL-1993; US-100694.
PR 05-NOV-1993; US-147592.
PA (ARCH-) ARCH DEV CORP.
PI Bell GI, Reisine T, Yasuda K;
DR WPI; 95-022804/03.
DR P-PSDB; R67669.
PT Polynucleotides and peptides derived from opioi receptor
PT polypeptides - for use in therapeutic compositions and in
PT screening assays for useful drug substances.
PS Claim 10; Page 207-211; 300pp; English.
CC The nucleotide sequence of the novel mouse kappa opioi receptor gene
CC MOR1. The gene was isolated from a mouse brain cDNA library using a
CC fragment (amplified from the cDNA library with primers Q75929-30) as a
CC probe. The primers are based on the conserved sequences present in the
CC second and third transmembrane domains of somatostatin (SMT) receptor
CC subtypes SSTR1, SSTR2 and SSTR3. The 1.2 kb pSI fragment from the mouse
CC kappa opioi receptor clone, lambda ms1-1, was subcloned into the CMV
CC promoter-based expression vector pCMV-Eb. The resultant construct
CC pCMV-ms1-1 was transfected into COS-1 cells for protein production. The
CC gene encoding the opioi receptor can be used to produce complete,
CC truncated or chimaeric opioi receptor proteins. The opioi receptors
CC thus produced are useful for the development of novel assays designed to

CC select or improve substances, capable of interacting with the opioid
 CC receptor proteins, for use in diagnosis, drug design and therapeutic
 CC applications.
 SQ Sequence 1410 BP; 322 A; 360 C; 337 G; 391 T;

Query Match 100.0%; Score 1410; DB 13; Length 1410;
 Best Local Similarity 100.0%; Pred. No. 0.00e+00;
 Matches 1410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
 ID Q86725 standard; cDNA; 2481 BP.
 AC Q86725;
 DT 01-DEC-1995 (first entry)
 DE Mammalian kappa opioid receptor protein cDNA.
 KM Mammalian kappa opioid receptor; mouse delta opioid receptor; analgesic;
 KN amplification; primer; rat; probe; E.coli; RT-PCR; hypnotic compound; ds.
 OS Rattus rattus.
 FH key Location/Qualifiers
 FT CDS 111..1253
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 FT /product= kappa opioid receptor
 FT J07070191-A.
 PD 14-MAR-1995.
 PE 30-JUL-1993; 190261.
 PR 09-JUL-1993; JP-170591.
 PA (TAKE) TAKEDA CHEM IND LTD.
 DR WPI: 95-144857/19.
 DR P-PSDB: R72591.
 PT kappa opioid receptor protein and cells expressing it - useful
 PT for the screening of compounds for analgesic and hypnotic
 PT properties
 PS Claim 2; Page 9-10; 15pp; Japanese.
 CC The nucleotide sequence of the novel mammalian kappa opioid receptor
 CC cDNA. The gene was isolated by amplifying a fragment from rat brain mRNA
 CC by reverse transcriptase-PCR (RT-PCR) using primers Q86726-7 derived from
 CC the mouse delta-opioid receptor gene. This fragment was cloned into the
 CC plasmid pCRIT to produce pRI. The plasmid pRI was used to probe a rat
 CC brain DNA library in lambda ZAPIT to obtain a clone of the rat kappa
 CC opioid receptor gene, designated pXOPR2. This clone was introduced into
 CC E.coli JM109 for production of the receptor protein. The receptor protein
 CC is useful for screening of analgesic and hypnotic compounds including
 CC peptides and proteins.
 SQ Sequence 2481 BP; 629 A; 588 C; 544 G; 720 T;

Query Match 80.13; Score 1129; DB 15; Length 2481;
 Best Local Similarity 95.5%; Pred. No. 0.00e+00;
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Db 95 agctgagcactacatcagatgagctcccatccagatttcccgagagagcagccctac 154


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575 ccgtgacattgctgctgtgcccaccccgtaaaagcttggattccgaacacotttgaagc
650 CCGCTACATGTGTGTGTCCACCCGTGTAAGCTTGGACTTGGACACACCTTTGAAAGC
635 aaagatcacacaatctcatattgttgcctactgctacatcatctgtgttatatcgcatgt
710 AAAGATCATCAACATCTGATTTGCTCTCTGCTCATCATCTGTTGATATTCAGCATAGT
695 ccttgagagacaaagatcaggaagatgtgaltcatattgaatctctcttgcattcc
770 CCTTGAGAGCAACAAAGTACAGGAGATGTGATGTCAATGAACTCCTTTCATTTCC
829
755 tgaatataatctctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt
830 TGAATATAATCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
815 tttatccctgtcttaacatcatctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt
890 TGTGATCCCACTCTCTCATCATCATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
949
875 tttccgctctctctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt
950 TGTCCGCTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
934
935 ggtctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt
1010 GGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
1069
995 ggtcgaagctctagagcagacactctcaacagcagctgtctctctgtgtgtgtgtgtgt
1070 GGTGAGAGCTCTGTGGAACACACTCTCCACAGCAGCTGTCTCTCCACATTTATTTCTG
1129
1055 catgtccttgggtatacaacaacagcagcttgaatcgtgttctcatgtgtgtgtgtgt
1130 TATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
1189
1115 aaacttaagaggtgtttttagagctctgtctcccaatlaagatgagatgagagcgcca
1190 AACTTTAAGAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
1249
1175 gagacaacaagatgtagaacaacagctcagatcctgtgtgtgtgtgtgtgtgtgtgtgt
1254

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1250 GAGCACCAATAGATTGAAACACAGATTCCAGTCTGCTTCATGAGATGTGGAG
1235 gatgaataagccaagatgctgtatgtaaatgtcttcttcttcttccggttagaga
1310 GATGATTAAGCCAGATATGACATGTGTGGAATGTCTTTATTTGTTCACAGTAGAGA
1295 agatccaatgactctgtttaccacagattacccttag
1370 AGAGTTCAATGATCTTTGTTTACCCAGATTACACTGAG
1410

RESULT
3
ID T12550 standard; cDNA; 1142 bp.
AC T12550;
DI 03-SEP-1996 (first entry)
DE Human kappa opioid receptor cDNA.
KM Human; kappa opioid receptor; psychiatric disorder; cardiovascular;
neurology; diagnosis; ds.
OS Homo sapiens.
FH Key
FT CDS
FT 1..1142
FT Location/Qualifiers
FT
FT /*tag= a
FT /product= kappa-opioid_receptor
FT /note= "incomplete termination codon"
FT PN W09601898-A1.
FT PD 25-JAN-1996.
FT PF 07-JUL-1995; F00912.
FT PR 11-JUL-1994; FR-008531.
FT RA (UTST-) UNIV PASTEUR STRASBOURG LOUIS.
FT PI Kieffer B, Simolin F;
FT WP1: 96-097628/10.
FT DR P-PSDB: R88722.
FT PT New nucleic acid encoding the human Kappa opioid receptor - useful
in diagnosis and therapy, and for isolating receptor ligands and
PT modulators
PS Claim 3; Page 13-15; 30pp; French.
CC This sequence codes for the human kappa opioid receptor and was
CC obtained from two overlapping cDNA fragments isolated from a
CC human placental cDNA library. The fragments were amplified from
CC the library using PCR primers based on the sequence of human
CC genomic clones which hybridized with a murine delta receptor cDNA
CC probe. Nucleotide probes derived from the kappa opioid receptor
CC coding sequence are useful for diagnosis of neurological, cardio-
CC vascular and psychiatric disorders associated with opioid
CC receptors.
SQ Sequence 1142 bp; 236 A; 337 C; 283 G; 286 T;

Query Match 59.4%; Score 838; DB 20; Length 1142;
Best Local Similarity 86.7%; Pred. No. 0.00e+00;
Matches 990; Conservative 0; Mismatches 152; Indels 0; Gaps 0;

Db 1 atggaatcccccagatccagatcttcgcgagggagccgccttaactgcgcagagcgc 60
QY 186 ATGGAATCCCCCATTCAGATCTTCGAGGAGATCCAGGCCCTTACCTGCTCTCCAGTCT 245
Db 61 tgcctgcccccaacagcagcgcctgtttcccgcgctggcgccgcgcgaagaagcgcgc 120
QY 246 TGCCTTCTCCCAACAGCAGCTCTTGTGTCCCAACTGGGCGAGATCCGAGATGAAGGC 305
Db 121 agcgcgcgtcggagagcgcgcagctgagagccgcgcagacatctccgcgcacatcccggtc 180
QY 306 AGTGTGGGCTCAGAGGATCAGACAGCTGAGAGCCGCGACATCTCTCCGGCATCTCCGT 365
Db 181 atatacagcggtctactcctcgtatgttgcgtgtgtgtgtgtgtgtgtgtgtgtgtgt 240
QY 366 ATCATACCGCTGTCTACTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 425
Db 241 atgtcgtgataccagatatacaaaagatgaagacacacacattcatatttaac 300
QY 426 ATGTGTTCATATCCATACACAGATGAAGAGCCGACACCAACATCTCAATATTTAAC 485
Db 301 ctggtcttgcagatgttttagtactacaacacatgcccttgaagatgaagcttactgt 360

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QY 486 CTGGCTTTGGCAGATGCTTTGGTTACTACCACTATAGCCCTTTCAGAGTGTCTACTTGG 545
 Db 361 atgaattctggccttttggggatgtgtgtcaagaaagaaatttccattgattactac 420
 QY 546 ATGAATTTCTGCTTTGGAGATGTGTATGCAAGATTTCATTTCATTGACTATAC 605
 Db 421 aacatgttcaaccagatcttcaacttgaccatgtatgagcgtggaccgttaattgacctg 480
 QY 606 AACATGTTTACAGATATATACCTTGACCATGATGATGTGGACCGGTACATGCTGTGG 665
 Db 481 tggcaacccctggaaagcttggacttgcgcacaccccttgaaggcaaatatcaatc 540
 QY 666 TGGCAACCTTGGAAGCTTTGGACTTCCGACACCTTTGGAAGCAAAATATCATCATC 725
 Db 541 tgcacatctgtctgtctgtcatctgttggcatctgttgaatagttccttggagcaacaa 600
 QY 726 TGCATTGCTGCTTGGCTGCAATGCTGTGTATATCAGCGATAGTCTTGGAGGACACAA 785
 Db 601 gtcaagggaagagctgcatgtcatcttgaagtgtctcttgcagcttcccgatgatactcc 660
 QY 786 GTCAAGGGAAGATGTGATGTATGATTAATGCTCTTGACAGTTTCCATGATTAATATCC 845
 Db 661 tgggtggaccccttcatgaagatgtgtcttcatcttgccttgccttgccttgcctc 720
 QY 846 TGGTGGATCTCTTATTAAGATCTGTGTCTTCTGCTTCTTGGCTTTGTGATCCAGTCTC 905
 Db 721 atccatcatctgtctgtcaacccctgtatgtactgtgtctcaagaagcgtccgctcttct 780
 QY 906 ATCATCATGTCTGCTACACCTGTGATGATCCGCGCTGGAAGAGTCCGCGCTCTGCT 965
 Db 761 ggtctcccgagaaagatgcgcacactgtgtatgataccacagactgtctgtgtgtgt 840
 QY 966 GCTCTCCGAGAAAGAGCGAATCTCGCGCCGATCCAGCTGATGCTGTGTAGTAGT 1025
 Db 841 ggaagcttcgtctgtctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 900
 QY 1026 GCAAGCTTCATCATCTGT 1085
 Db 901 agacaccccccacagacagctgtctctccagctattacttctgtcagcttgaagctat 960
 QY 1086 AACACCTCCCAACAGACACAGCTGCCCTCCACACCTATATTTCTGTAATTCCTTGGGTAT 1145
 Db 961 accaacaagtagcttaacccatctctacgaccttctgtgaagaaacttgaagcgtgt 1020
 QY 1146 AACCAACGAGAGCTGATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1205
 Db 1021 ttccgggaacttctgtcttccactgaagatgagatgagcggcagagcactagcagatc 1080
 QY 1206 TTTAAGGACTTCTGCTTCCCTATTAAGATGCGAATGAGCGCAGAGCAACATAGATT 1265
 Db 1081 cgaataacagttcagagatctctgtacttaccgtgagggacatcgatgggataataacagta 1140
 QY 1266 AAGAAACACAGTTCAGAGATCCTTCTTCATGAGAGATGGGAGATGATAAGCCAGTA 1325
 Db 1141 tg 1142
 QY 1326 TG 1327

RESULT 4
 ID Q75931 standard; DNA; 1000 BP.
 AC Q75931;
 DE Human kappa oploid receptor partial cDNA fragment.
 KW Mouse; kappa; delta; mu; oploid receptor; brain; primer; PCR; amplify;
 KW transmembrane domain; somatostatin receptor; human; expression vector;
 KW truncate; chimeric; assay; probe; ss.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT CDS 102..989
 FT /*tag= a
 FT /product= partial human kappa oploid receptor
 PN M09428132-A.

PD 08-DEC-1994.
 PF 20-MAY-1994; U05747.
 PR 20-MAY-1993; US-066296.
 PR 30-JUL-1993; US-100694.
 PR 05-NOV-1993; US-147592.
 PA (ARCH-) ARCH DEV CORP.
 PI Bell GI, Reisine T, Yasuda K;
 DR WPI; 95-022804/03.
 DR P-PSDB; K67672.
 PT Polynucleotides and peptides derived from opiod receptor
 PT polypeptides - for use in therapeutic compositions and in
 PT screening assays for useful drug substances.
 PS Claim 10; Page 236-239; 300pp; English.
 CC The partial nucleotide sequence of the novel human kappa oploid receptor
 CC gene. The gene was isolated from a human brain hippocampus cDNA library
 CC using a probe from the mouse kappa oploid receptor gene (Q75926). The
 CC gene is missing the N-terminal sequence. The C-terminal sequence is
 CC very similar to the mouse kappa oploid receptor sequence. Of the
 CC C-terminal 293 amino acids, 281 residues are identical and 6 residues
 CC have conservative substitutions. The gene encoding the human opiod
 CC receptor can be placed in a suitable expression vector for production of
 CC the protein in a cell. The opiod receptors thus produced are useful for
 CC the development of novel assays designed to select or improve substances,
 CC capable of interacting with the opiod receptor proteins, for use in
 CC diagnosis, drug design and therapeutic applications.
 SQ Sequence 1000 BP; 238 A; 253 C; 225 G; 278 T;

Query Match 47.4%; Score 668; DB 13; Length 1000;
 Best local similarity 87.6%; Pred. No. 0.0e+00;
 Matches 789; Conservative 0; Mismatches 109; Indels 3; Gaps 2;

Db 100 gatacaagaatggaagacgaacacacattacatatattacctgcttggagatg 159
 QY 442 GATACACGAAGTGAAGACCGACCAACATATACATTTTACCTGGCTTGGCAGATG 501
 Db 160 cttaagttactcaacacatgccccttcagagtagcgttacttgaattgaattcctgtg 219
 QY 502 CTTGGTTACTACACATATGCTTCCCTTTCAGAGTGTGTCTACTGTATGAAATCTTGCCCT 561
 Db 220 ttggagatgtgtgtgtgaagatgaatttccattgattgaattgaattgaattgaatt 279
 QY 562 TTGGAGATGTGTATGCAAGATTTGATTTCCATTTGATGATCAACATGATTTACACGA 621
 Db 280 tcttaaccttgacacatgtagagcgtggaacgtacattgcgtgtgtgcaaccccgtaag 339
 QY 622 TATTCACCTTGAACATGATGATGTGTGACCGCTACATTCCTGTGTGCCACCTGTGAAG 681
 Db 340 ctltggaacttcgcaacaccccttgaaggaagacatcaatactgcacatgtgtgtgt 399
 QY 682 CTTGGACTTCCGAACACCTTGAAGGCAAGATCATCAACATCTGCAATTGGCTCTGG 741
 Db 400 ggtcatctgtgtgcatcttgcataatgtctctggaggagacaaagtcagaggatgtgt 459
 QY 742 CATCATCTGTGTATATGAGGATATGCTTGGAGGACCAAGATCAAGGAGATG 801
 Db 460 atgtcaatgagtcgtctggaagttccagatgatactacccctgtgtggaaccttca 519
 QY 802 ATGTCAATTAATGCTCTTGCAGTTTCCGATGATGAATATTCCTGTGTGGAATCTTCA 861
 Db 520 tgaagatctgtcttcaatcttgccttgccttgccttgccttgccttgccttgccttgcct 579
 QY 862 TGAAGATCTGTGTCTGCTGCTTGTGATCCCACTCTCCATCATCATATGCTGCT 921
 Db 580 acaacctgatgacctgtgtctcaaanngtcgggtctcttctgtgtctccgagagaag 639
 QY 922 AACACCTGATGATCTGCGCCCTGGAAGTGTCCGCTGCTGTGTGCTCCGAGAGAG 981
 Db 640 atnnaaacctgtagagacacacagactgtctgtgtgtgtgtgtgtgtgtgtgtgtgt 699
 QY 982 ACCGAATCTCCGCCCATACCAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1041
 Db 700 gctggaactccatcaatattcatctgtgtggaagctctgaggagaacctcccaagca 759

QY 1042 GTTGAACCCCATTCACATCTTATCCTGAGGAGCTGTGGAGAGCACTCCACAGCA 1101
 Db 760 caactctctctccacacttactcttgcctgcgccttaagctataccaagaagcctga 819
 QY 1102 CAGCTGCCCTCTCCAGCTATTATTTCTGTATTCCTGGGTATTAACCAACAGAGCCTGA 1161
 Db 820 atccattctctacgcctctcttgatgaactcaagcgctgttccggactctcgt 879
 QY 1162 ATCCCTTCTCTATGCTCTTCTTGATGAAACTTCAAGCGGTGTTAGGACTCTGCT 1221
 Db 880 ttccactgaagatgagatgagagcagacactagcagatccgaataacagctcag 939
 QY 1222 TCCCTATTAGATGCAATGAGACGCGACAGCACTAGAGTTAAACACAGTTCAG 1281
 Db 940 atctctgcttaacctgagagatcgatgagatgataataaccagatagctgctg 999
 QY 1282 ATCTCTCTTCCATGAG-AGAT-GTGGAGAGGATGATTAAGCAGATATGCTGTGG 1338
 Db 1000 a 1000
 QY 1339 A 1339

RESULT 5
 ID Q79199 standard; cDNA; 2070 BP.
 AC Q79199;
 DE 19-APR-1995 (first entry)
 DE Rat mu-subtype opioid receptor cDNA.
 KM Mu-subtype opioid receptor; MSOR; drug addiction; ds.
 OS Rattus rattus.
 FH Key
 FT CDS Location/Qualifiers
 FT /*tag= a 83..1154
 FT /product= Mu-subtype-opioid_receptor
 PN EP-612845-A.
 PD 31-AUG-1994.
 PE 09-FEB-1994; 101968.
 PR 26-FEB-1993; US-026140.
 PA (AMCY) AMERICAN CYANAMID CO.
 PI Corbett M, Eppler CM, Shieh H, Zysk JR;
 DR WPI; 94-265965/33.
 DR P-PSDB; R65188.
 PT Pure mu-type opioid receptor protein - and nucleic acid coding
 PT for it
 PS Claim 1; Fig 11, 39pp; English.
 CC R65188 is the rat mu-subtype opioid receptor protein purified
 CC from rat brain membranes, with biotinyl-b-endorphin (R5666)
 CC as its ligand. It is encoded by the nucleotide sequence Q79199
 CC which was synthesised using Q71022 and Q71023 as PCR primers.
 CC R65188 is useful for identifying other receptor subtypes, for
 CC screening new opioid ligands, and for studying mechanisms of
 CC opioid action, e.g. drug addiction.
 SQ Sequence 2070 BP; 526 A; 564 C; 423 G; 557 T;

Query Match 22.1%; Score 311; DB 12; Length 2070;
 Best Local Similarity 70.6%; Pred. No. 6,98e-207;
 Matches 605; Conservative 0; Mismatches 244; Indels 9; Gaps 8;

Db 171 ttacatcatgagccctactactatcgtctgtagtggcctctcggaactctcgtg 230
 QY 364 TTATATCATACCGGCTGTCTACTCTGTGTAATTTGTGTGGCTTATGGGCAATTTCTGG 423
 Db 231 tcatatgtagtctgtaagatacaccacaaatgaagactgcccacacatactattcca 290
 QY 424 TCATGTTTGTCATCTCCGATACAGAGATGAAAGACGCAACCAACATCTCAATTTA 483
 Db 291 acctgctctggaagacgcttagagaccagctacccctttagagtgtaactacc 350
 QY 484 ACGTGGCTTTGGCAAGTCTTTGGTACTACCACTATGCCCTTTAGAGTGTCTACT 543
 Db 331 ttagtgaagacatgagccctcggaacatcctctgcaagatcgtgtaactcaatgaact 410
 QY 544 TGATGATTTCTGGCCTTTGGAGATGTGCTATGCAAGATTTGCTATTTGCTACT 603

Db 411 acacaa tgttaccacagcatattcaccctctgcacacatgagcgtggaacgctacattgc- 470
 QY 604 AACATATGTTTACACATATTCACCTTGACCATGATGATGTGAGACCGCTATATTGCTG 663
 Db 471 tctgcacaccagtaacaaagcctgatttccgttaccoccccaaatgcaaatcgttaacg 530
 QY 664 TGTGCCACCCCTGTGGAAGCTTTGAACTTCCGAACACCTTTGAAAGCAATGATCATACCA 723
 Db 531 tctgcacactggtatccctcttctgcacatcgtgtcctgttaatgtcaatgcaaccaa 590
 QY 724 TCTGCATTTGGCTCTGGCATATCTGTGTATATACAGATATGCTCTGGAGGACACA 783
 Db 591 aatacagaga-g--g-gg--tc--catagattgaacccctcaagcttcccccacacactgtr 644
 QY 784 AAGTCAGGAAGATGTGATGTGATGATGATGCTCTCTGAGTITCTGTATGATGAATAT 843
 Db 645 actgg-gagaac-clyc--tcaaatctgtcttcttctctcttcatcatcagccggtcc 701
 QY 844 CCGTGGGAGATCTCTCATGAAGATCTGTCTGCTTTGGCTTTGGATCCAGCTCC 903
 Db 702 tcatctacactgtgtttagcggcctgatatctttagactcaagagcgttgcagtcat 761
 QY 904 TCATCATCTATGTCTGTCTACACCTGATATGCTGTGGCTTGAAGATGTCCGGCTCTGT 963
 Db 762 cgggtccaaagaagaagcagaatctgcgagagatccacggatggtgctggtgctg 821
 QY 964 CTGGCTCCCGAAGAGAAGACCCAAATCTCCGCGATCACCAAGCTGTGGTGTGATG 1023
 Db 822 tggcgtgatttatctgctcgtctgtagaccccatccaatctacgtcatcatcaaacgctga 881
 QY 1024 TTGCAGTCTTTCATCATMCTGTGTGACCCCATTCACATCTTTATCCMGATGGAGGCTCTG 1083
 Db 882 ttagcttccaaacacacatttcaagcgttcttctgcactcttgcattgcttgggtt 941
 QY 1084 GAAGACCTCCACAGACAGACGCTGCCCTCCAGATATTTCTGTCTGTTGCTTGGGT 1143
 Db 942 aacagacagctgcttgaatccagttctttagccttctctgataaactcaagcgat 1001
 QY 1144 ATACCAACAGCAGCTGTGATCTGTCTCTTCTGTATGCTCTTCTGTGATGAATCAAGCGGT 1203
 Db 1002 gcttcaagagctctgcacacc 1023
 QY 1204 GTTTAGGAGCTTCTGTCTGCC 1225

RESULT 6
 ID Q89222 standard; cDNA; 1618 BP.
 AC Q89222;
 DE 20-OCT-1995 (first entry)
 DE Rat mu opioid receptor cDNA.
 KM Mu opioid receptor; MOR-1; gene therapy; diagnostic; ss.
 OS Rattus sp.
 FH Key
 FT CDS Location/Qualifiers
 FT /*tag= a 214..1410
 FT W09507983-A.
 PN 23-MAR-1995.
 PD 13-SEP-1984; U10358.
 PR 13-SEP-1993; US-120601.
 PA (INDV) UNIV INDIANA FOUND.
 PI Yu L;
 DR WPI; 95-131351/17.
 DR P-PSDB; R71964.
 PT New nucleic acid encoding new human mu opioid receptor - and
 PT related vectors, transformed cells, antibodies etc., useful in
 PT diagnosis, treatment and drug screening.
 PS Disclosure: Page 190-194; 266pp; English.
 CC A 365 bp fragment of the mouse delta opioid receptor was used to
 CC screen a rat brain cDNA library under low stringency conditions.
 CC One positive clone included the sequence given in Q89222, encoding a
 CC mu opioid receptor, MOR-1 (R71964). MOR-1 was stably expressed in
 CC transfected CHO cells.

Query Match 20.6%; Score 291; DB 10; Length 1821;
 Best Local Similarity 70.8%; Pred. No. 8,82e-192;
 Matches 597; Conservative 0; Mismatches 234; Indels 12; Gaps 8;

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Db 181 catcacgcgcctactgcgcgtgtgtgcgaatgtgggtcttcgggcaacgtgtcgtcat 240
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QY 368 CATCACGCCGCTGCTACTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 427
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Db 241 gtttggcatcgtcgcgttacccaatgtgaagacgcgcaccaatcatcatcattc 300
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 428 GTTTGTCATTCATCCGATACACGAGATGAAGACCCCAACCAATCATCATTTTAACCT 487
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Db 301 ggccttgctatgtgcgtgcgcacagagcgtgccttcgcagagcgcgaagtattat 360
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QY 488 GGCCTTTGGAGATGCTTTGTTACTACCACTATGCCCTTTCAGAGTGTCTGTACTTGAT 547
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Db 361 gaaacgtgtgcgtttgtgcagagcgtgtgcacagcgtgtccttcattgtactacaa 420
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QY 548 GAATCTTGCGCTTTTGGAGATGTGTATGCAAGATGTTCATTTCCATGTACTACAA 607
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 421 catgttcacatagcatcttcacccatcaatgatgatgagcgtgtgacacgtatctgtctg 480
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 608 CATGTTCACCAATATTCACCTTGACCATGATGATGTGTGTGTGTGTGTGTGTGTGT 667
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Db 481 catcctgtcaaacgccttgcgttccgcacaccagccaaagccaaagctgtatataatg 540
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 668 CCACCTGTGGAAGCTTTGGACTTCCGAACACCTTTGAAAGCAAGATCATPAACATCTG 727
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 541 catctgtgctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 600
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 728 CATTTGGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 787
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Db 601 ccggagatgtgtgagtggt-at-gcatgtcc---agttcccaagtcacagctgtgtactg 654
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QY 788 CAGGAGAGATGTGAGATGTGATGATGATGATGATGATGATGATGATGATGATGAT 847
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Db 655 g-gaca-ctgtg-accagaatctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 711
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QY 848 GTGGGATCTCTTCATGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 907
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Db 712 catcaagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 771
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QY 908 CATCATGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 967
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Db 772 ttccaaaggaagagcagcagcgtgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 831
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QY 968 CTCGCCAGAGAGAGACCGAATCTCCGCCGCAATCCCAAGACTGCTGATGATGATGAT 1027
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Db 832 cgccttcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 891
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QY 1028 AGCTTCATCATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1085
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Db 892 calcaatcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 951
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QY 1086 -ACGACCTCCCAAGAGACAGCTGACCTCCCTCCCAAGCTTATTTCTGATTTGCTTTGGGTTA 1144
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 952 cgcacaacagcagcctcaaccccggttctctacagccttcctcgtgagcagaactcaagcgcg 1011
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QY 1145 TACCAACAGAGAGCTGAATCCTGTTCTATGCTTTTGGATGAAGAAACTTCAAGCGGTG 1204
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Db 1012 ctt 1014
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1205 TTT 1207
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OS Mus musculus.
 FH Key Location/Qualifiers
 FT CDS 12..1130
 FT /*tag= a
 FT /product= mouse delta opioid receptor
 FN W09428132-A.
 PD 08-DEC-1994.
 PT 20-MAY-1994; U05747.
 PR 20-MAY-1993; US-066296.
 PR 30-JUL-1993; US-100694.
 PR 05-NOV-1993; US-147592.
 PA (ARCH-) ARCH DEV CORP.
 PI Bell GI, Reisine T, Yasuda K;
 DR WPI: 95-022804/03.
 DR P-PSDB; R67670.
 PT Polynucleotides and peptides derived from opioid receptor
 PI polypeptides - for use in therapeutic compositions and in
 PT screening assays for useful drug substances.
 PS Claim 6; Page 215-221; 300pp; English.
 CC The nucleotide sequence of the novel mouse delta opioid receptor gene
 CC MOR1. The gene was isolated from a mouse brain cDNA library using a
 CC fragment (amplified from the cDNA library with primers Q75925-30) as a
 CC probe. The primers are based on the conserved sequences present in the
 CC second and third transmembrane domains of somatostatin (SRIF) receptor
 CC subtypes SSRI, SSRI2 and SSRI3. The 1.3 kb EcoRI-SacI fragment from the
 CC mouse delta opioid receptor clone, lambda msl-2, was subcloned into the
 CC CMV promoter-based expression vector pCMV-6c. The resultant construct
 CC pCMV-msl-2 was transfected into COS-1 cells for protein production. The
 CC gene encoding the opioid receptor can be used to produce complete,
 CC truncated or chimeric opioid receptor proteins. The opioid receptors
 CC thus produced are useful for the development of novel assays designed to
 CC select or improve substances, capable of interacting with the opioid
 CC receptor proteins, for use in diagnosis, drug design and therapeutic
 CC applications.
 SQ Sequence 2272 BP; 485 A; 665 C; 472 T;

Query Match 20.6%; Score 291; DB 13; Length 2272;
 Best Local Similarity 70.8%; Pred. No. 8,82e-192;
 Matches 597; Conservative 0; Mismatches 234; Indels 12; Gaps 8;

```

Db 164 catcacgcgcctactgcgcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtcat 223
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 368 CATCACGCCGCTGCTACTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 427
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 224 gtttggcatcgtcgcgttacccaatgtgaagacgcgcaccaatcatcatcattcatt 283
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 428 GTTTGTCATTCATCCGATACACGAGATGAAGACCCCAACCAATCATCATTTTAACCT 487
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Db 284 ggccttgctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 343
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 488 GCGTTTGGAGATGCTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 547
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 344 ggaacgtgtgcgtttgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 403
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 548 GAATCTTGCGCTTTTGGAGATGTGTATGCAAGATGTTCATTTCCATGTACTACAA 607
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 404 catgttcacatagcatcttcacccatcaatgatgatgagcgtgtgacacgttactgtctg 463
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 608 CATGTTCACCAATATTCACCTTGACCATGATGATGATGATGATGATGATGATGATGAT 667
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 464 ccactcgtcaaacgccttgcgttccgcgaacagcgaacagcgaacagcgtatcaataatg 523
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 668 CCACCTGTGGAAGCTTTGAGACTTCGGAACACTTTGAAAGCAAGATCATCAACTCTG 727
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 524 catctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 583
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 728 CATTTGGCTCCTCCGACATCTGTTGTATATACGAGATGATGATGATGATGATGATGAT 787
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 584 ccggagatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 637
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 788 CAGGAGAGATGTGAGATCTATTAATGCTCTTGGCAATTTCCATGATGATTAATTTCTG 847
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 638 g-gaca-ctgtg-accagaatctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtcat 694
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```



```

QY      848 GTGGGATCTTCATGAAATGCTGTCTTCGCTTTCCTTGTGATCCAGTCTCAT 907
Db      695 catcaaggtgtctatgagcctatgctatgagccctgcagcgtgtctgtctcgg 754
QY      908 CATCATGTCTCTCTACACCTGATGATCTGTGCTGAGAGATGCTCCGCTCTGCTG 967
Db      755 tccaagaagaagaccgacgctgcgcacatcaagcgcagtgctgtgtgtgtgtg 814
QY      968 CTCGCGAGAGAGAGACCAATCTCCGCGCATACCAAGCTGTGCTGTGATGATTGC 1027
Db      815 ggcctctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtg 874
QY      1028 AATCTTCATCATCTGTGTGAGACCCCATTCACATCTTATCTGCTGCTGCTG 1085
Db      875 catcaatgcgagcgcacccctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtg 934
QY      1086 -AGCATCTTCCACAGACAGCTGCTCCACGCTATTTCTGTATTTGCTGCTGCTG 1144
Db      935 cgcacacagcagcctcaaacccggtctctcaagccttcctgcagcagcagcagcagc 994
QY      1145 TACCAACAGACAGACCTGATTCCTGCTCTATGCTCTTCTGTGATGAAACTTCAAGCGGTG 1204
Db      995 cct 997
QY      1205 TTT 1207

```

```

RESULT 11
ID      Q89226 standard; cDNA; 1610 BP.
AC      Q89226;
DT      20-OCT-1995 (first entry)
DE      Human mu opioid receptor cDNA.
KW      Mu opioid receptor; MOR; gene therapy; diagnostic; ss.
OS      Homo sapiens.
FH      Key
FT      CDS      Location/Qualifiers
           /tag= a
           PN      WO9507983-A.
           PD      23-MAR-1995.
           PE      13-SEP-1994; U10358.
           PR      13-SEP-1993; US-120601.
           PA      (INDV ) UNIV INDIANA FOUND.
           PI      YU L;
           DR      WPI: 95-131351/17.
           PT      New nucleic acid encoding new human mu opioid receptor - and
           PT      related vectors, transformed cells, antibodies etc., useful in
           PS      Claim 5; Page 208-210; 266pp; English.
           CC      A cDNA library constructed from human caudate nucleus mRNA was
           CC      screened with rat mu opioid receptor cDNA under conditions of
           CC      low stringency. One positive clone included the sequence given in
           CC      Q89226, encoding a mu opioid receptor MOR (R71964). The cDNA
           CC      is used for prodn. of recombinant MOR, in gene therapy, etc.
           SQ      Sequence 1610 BP; 384 A; 467 C; 359 G; 400 T;

```

```

Query Match      20.5%; Score 289; DB 14; Length 1610;
Best Local Similarity 70.0%; Pred. No. 2,84e-190;
Matches 601; Conservative 0; Mismatches 246; Indels 11; Gaps 10;

```

```

Db      455 atcatgccccctcatcatcatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtg 514
QY      369 ATCACCCTGTCTTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 428
Db      515 tatgtgtgtgtcatgatacacaagatgaagactccacaacatctcatcttcaacgt 574
QY      429 TTGTGATCATTCGATACAGAGATGAAGACCCCAACCAACTCTCATATTTAACCTG 488
Db      575 ggcctgcagatgctcttagacacagcagcagcctgtccagagtggtgaattcaatg 634
QY      489 GCTTTGGCAGATGCTTTGTTGTTACTACCATATGACCTTTTACAGATGCTGTCTACTGATG 548

```

```

Db      635 ggaacatgcatcttgggaaccatctcttgcagaagatgatcatcatattactataac 694
QY      549 AATTTTGGCTTTTGGAGATGTGCTATGCAAGATTTGATTTCCATTGACATACAAAC 608
Db      695 atgttaccagatatccaacctcgcacacatgatatgtgtgatcatcatcagctgtgc 754
QY      609 ATGTTTACAGCATATTCACCTTGACATGATGAGATGAGACCGCTACATTTCTGTGTCG 668
Db      755 caccctgtcaagccttcatcttctgtctactcccgcaatgccaataatcatatgtctgc 814
QY      669 CACCGTGTAAAGCTTTGGACTTCCGAACACCTTTGAAAGCAAAATCTCAACATCTGC 728
Db      815 aactgtatctctctctccagcattgtctctctgtatgaatgtcatgtacaaacaataac 874
QY      729 ATTGGCTCTGGACATCATCTGTGTGTATATAGGGAATAGTCTTGAGGACCAAAAGTC 788
Db      875 aggcaggt-tccatag-atgta--cac-taacatctc-tcatccaacctgtactgg 928
QY      789 AAGGAGATGTGAGATGATGAAAGCTCCCTGCAATTCCTGATGATGAAATATTCCTGG 848
Db      929 -gaaac-ctgc-tgaagatctgttttcatcttcctgcctcatattatccagtgctatc 985
QY      849 TGGGATCTCTTCATGAATCTGTCTTCTGCTCTTGTGCTTGTGATCCAGTCTGCTATC 908
Db      986 attaccgtgtctatgactgactgatalctctgtgcctcaagagtgctccgatgctctctgc 1045
QY      909 ATCATTTGCTGTACACCCCTGATGATCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 968
Db      1046 tccaaagaagaagcaggaacatcttcgaagatcaacagatgtgtgtgtgtgtgtgtgt 1105
QY      969 TCCGAGAGAGAGACCGAAATCTCCGCGCATACCAAGCTGTGCTGTGATGATGATGCA 1028
Db      1106 gtgttcatctgtctgtgaaccccatcaatcttaacgtcatcatcaataagccttggttaca 1165
QY      1029 GTCCTTCATCATCTGTGTGACCCCATTTACATCTTATCTGAGGAGCTGTGGAAGC 1088
Db      1166 atccagagaactac-gttccagactgttctgtgcaactctgcattgtctcaggttaac 1224
QY      1089 ACCCTCCACACAGACAGCTGCCCTCTCCAGCTAT-ATTTCGTATTCCTTGGGTTATC 1147
Db      1225 aaacagctgctcaacccagctcttatgtcaattctgtgataaactcaaacagatgctt 1284
QY      1148 CACACGACGCTGATCTGTCTGTCTGTGCTGTGATGAAACTTCAAGCGGTGTT 1207
Db      1285 cagagagttctgtatccc 1302
QY      1208 TAGGCACTTCTGCTTCCC 1225

```

```

RESULT 12
ID      Q93102 standard; cDNA; 2160 BP.
AC      Q93102;
DT      11-DEC-1995 (first entry)
DE      Human mu opiate receptor cDNA.
KW      Mu opiate receptor; hMOR; opiate agonist; opiate antagonist;
KW      drug abuse; analgesic; ds.
OS      Homo sapiens.
FH      Key
FT      CDS      Location/Qualifiers
           /tag= a
           PN      WO9520667-A1.
           PD      03-AUG-1995.
           PE      30-JAN-1995; U01144.
           PR      28-JAN-1994; US-188275.
           PA      (USSH ) US DEPT HEALTH & HUMAN SERVICES.
           PA      (USSH ) US SEC DEPT HEALTH.
           PI      Johnson PS, Persico AM, Jnl G, Wang J;
           PI      WPI: 95-275452/36.
           DR      P-PSDB: R76780.
           PT      New DNA encoding human mu opiate receptor - used esp. for screening
           PT      cpds. for activity as opiate agonists or antagonists
           PS      Claim 4; Page 24-25; 49pp; English.
           CC      hMOR cDNA was obtd. from a human cerebral cortical cDNA library

```




(TM)

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Merch_m n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Mon Apr 20 23:47:36 1998; Maspar time 728.47 Seconds

Tabular output not generated. 1156.083 Million cell updates/sec

Title: >US-08-292-694A-11
Description: (1-1000) from US08292694A.seq

Perfect Score: 994
N.A. Sequence: 1 AAGAGCAAAATCAGTATAC.....CCAGTATGACTGTCGTGGA 1000

Comp: TTCTTCGTTTGTGTCATTAG.....GGTCATCTGATCAGACACCT

Scoring table: TABLE default

Gap 6

Match STD : DBase 0; Query 0

Searched: 1126798 segs, 421067984 bases x 2

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database:

embl-est

1:em_est1 2:em_est2 3:em_est3 4:em_est4 5:em_est5

6:em_est6 7:em_est8 8:em_gss

Database:

genbank-est

9:gb_est1 10:gb_est11 9:gb_est12 9:gb_est13 9:gb_est14

14:gb_est15 15:gb_est16 16:gb_est17 17:gb_est18 18:gb_est19

19:gb_est20 20:gb_est21 21:gb_gss 22:gb_est23 23:gb_est24

Statistics: Mean 11.137; Variance 2.017; scale 5.520

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	163	16.4	183	10	YJ04b04.r1 Homo sapien	3.10e-289
2	137	15.8	153	10	Yh62c10.r1 Homo sapien	1.85e-231
3	40	4.0	433	10	YJ04b04.s1 Homo sapien	3.82e-21
4	35	3.5	345	13	H. sapiens partial cDN	1.22e-22
5	35	3.5	386	11	YM65c04.r1 Homo sapien	1.22e-22
6	34	3.4	181	19	AA039537	5.34e-21
7	34	3.4	377	18	AA236709	5.34e-21
8	34	3.4	484	10	W79255	3.26e-16
9	31	3.1	442	15	R77881	3.26e-16
10	31	3.1	1664	20	G28514	1.14e-14
11	30	3.0	304	18	AA227933	1.14e-14
12	30	3.0	320	10	R81133	1.14e-14
13	30	3.0	351	19	AA330028	1.14e-14
14	30	3.0	363	19	HSPD07459	1.14e-14
15	30	3.0	370	23	R1C51541A	1.14e-14

16	30	3.0	384	9	T90564	YJ40101.s1 Homo sapien	1.14e-14
17	30	3.0	390	23	HDMBC4896	similar to HMG-1.	1.14e-14
18	30	3.0	402	23	HDMGSC01731	Human HL60 3/directed	1.14e-14
19	30	3.0	422	15	AA101746	z880d11.r1 Stratagene	1.14e-14
20	30	3.0	422	10	R34185	yH84C06.r1 Homo sapien	1.14e-14
21	30	3.0	431	23	AA467444	yT05904.r1 Knowles Sol	1.14e-14
22	30	3.0	431	23	W07682	z166e12.s1 Stratagene	1.14e-14
23	30	3.0	451	15	AA045606	z166e12.s1 Stratagene	1.14e-14
24	30	3.0	451	15	AA13213	mm25h03.s1 Beddington	1.14e-14
25	30	3.0	455	12	N26596	yx93h03.s1 Homo sapien	1.14e-14
26	30	3.0	476	12	N38849	y743h05.s1 Homo sapien	1.14e-14
27	30	3.0	572	14	W97542	mf98g08.r1 Soares mous	1.14e-14
28	30	3.0	580	19	AA054783	zk68804.r1 Soares preg	1.14e-14
29	30	3.0	588	16	AA196344	z956b01.r1 Stratagene	1.14e-14
30	30	3.0	628	17	AA120232	mp85b01.r1 Soares 2NB	1.14e-14
31	29	2.9	339	13	HS18A052	H. sapiens partial cDN	3.74e-13
32	29	2.9	404	11	H14901	y126a04.r1 Homo sapien	3.74e-13
33	29	2.9	416	11	H44713	yp24d06.r1 Homo sapien	3.74e-13
34	29	2.9	521	16	AA196802	zq08g11.r1 Homo sapien	3.74e-13
35	29	2.9	791	13	W28236	44a1 Human retina cDNA	3.74e-13
36	28	2.8	203	19	AA360842	SEB70092.T-cell lympho	1.14e-11
37	28	2.8	249	11	H29103	ym31f07.r1 Homo sapien	1.14e-11
38	28	2.8	261	18	AA331167	z5T35211 Embryo, 8 wee	1.14e-11
39	28	2.8	266	17	AA217211	cs90874.f seg.F Human fe	1.14e-11
40	28	2.8	274	13	HSC27C022	H. sapiens partial cDN	1.14e-11
41	28	2.8	385	15	AA083771	zn39f12.s1 Stratagene	1.14e-11
42	28	2.8	547	18	AA275567	vc16g04.r1 Barstead xp	1.14e-11
43	27	2.7	200	14	N88386	K3212F Fetal heart, 1a	3.24e-10
44	27	2.7	492	21	B50064	CIT978SK-2206.TV CIT97	3.24e-10
45	27	2.7	614	13	W26028	1994 Human retina cDNA	3.24e-10

ALIGNMENTS

RESULT 1
LOCUS R81583 183 bp mRNA EST 12-JUN-1995
DEFINITION YJ04b04.r1 Homo sapiens cDNA clone 147727 5' similar to gb:U25119
MO-TYPE OPIOID RECEPTOR (HUMAN);
ACCESSION R81583
NID 9858186
KEYWORDS SOURCE

human clone-147727 library-Soares placenta Nb2HP vector-PT73D
(Pharmacia) with a modified polylinker host-DH10B (ampicillin
resistant) primer-M13R1 Rsite1-Not I Rsite2-Eco RI Female Placenta
obtained at birth (full term). 1st strand cDNA was primed with a
Not I - oligo(dT) primer 15'
AACTGGAGATTCGGCGCGCAGCAATTTTCTTTTCTTTT 3', double-stranded
cDNA was ligated into Eco RI adaptors (Pharmacia), digested with Not
I and cloned into the Not I and Eco RI sites of the modified pT73
vector. Library went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaldo.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 183)

REFERENCE

Hillier,L., Clark,N., Dubouche,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsous,U., Rifkin,L., Romling,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and
Wilson,R.
The WashU-Merck EST Project
Unpublished (1995)

TITLE

JOURNAL

COMMENT

Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
High quality sequence starts: 1

High quality sequence stops: 1
 Source: IMAGE Consortium, LNLN
 This clone is available royalty-free through LNLN; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Trace considered overall poor quality.

FEATURES
 source
 1.183
 /organism="Homo sapiens"
 /clone="147727"

BASE COUNT 31 a 56 c 40 g 46 t 10 others
 ORIGIN

Query Match 16.4%; Score 163; DB 10; Length 183;
 Best Local Similarity 90.7%; Pred. No. 3,10e-289;
 Matches 166; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

Db 1 CATCTTCCTTCGAGACCCCTGTCATCATCATGCTACACCCCTNATGATCT 60
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 QY 536 CATCTTCCTTCGAGACCCCTGTCATCATCATGCTACACCCCTNATGATCT 595
 |||||
 Db 61 GCGTCTCAAGAGCCTGCGGCTTCCTGCTCCGAGAGAAAGATCGACCTCGTAG 120
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 QY 596 GCGTCTCAAGAGCCTGCGGCTTCCTGCTCCGAGAGAAAGATNNCAACCTCGTAG 655
 |||||
 Db 121 GATCAGCAGACGCTGCTGAGTAGTGGGAGAGATTCGTCGCTGAGACCTCCATTC 180
 |||||
 QY 656 GATCAGCAGACGCTGCTGAGTAGTGGGAGAGATTCGTCGCTGAGACCTCCATTC 715
 |||||
 Db 181 CAT 183
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 QY 716 CAT 718

RESULT 2
 LOCUS R31984 153 bp mRNA EST 28-APR-1995
 DEFINITION yb62c10.r1 Homo sapiens cDNA clone 134322 5' similar to gb:125119
 MU-TYPE OTOTOID RECEPTOR (HUMAN);
 R31984
 ACCESSION
 NID 9787827
 KEYWORDS
 SOURCE

human clone=134322 library=Soares placenta Nb2HP vector=PT73D
 (Pharmacia) with a modified polylinker host=DH10B (ampicillin
 resistant) primer=M13Rpi RstI=Not I RstI=2-Eco RI Female Placenta
 obtained at birth (full term). 1st strand cDNA was primed with a
 Not I - oligo(dT) primer [5' -
 AACTGAGAGATTTCGCGCGCAGAGATTTTCTTTTCTTTT 3'], double-stranded
 cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not
 I and cloned into the Not I and Eco RI sites of the modified pT73
 vector. Library went through one round of normalization. Library
 constructed by Bento Soares and M.Fatima Bonaldo.

ORGANISM
 Homo sapiens
 Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
 Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE
 1 (bases 1 to 153)
 AUTHORS
 Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
 Holman,M., Hiltman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
 Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
 Trevasakis,E., Waterston,R., Williamson,A., Wohlmann,P. and
 Wilson,R.

TITLE
 JOURNAL
 COMMENT
 The WashU-Merck EST Project
 Unpublished (1995)

Contact: Wilson RK
 WashU-Merck EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@wustl.edu
 High quality sequence stops: 120
 Source: IMAGE Consortium, LNLN
 This clone is available royalty-free through LNLN; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.

FEATURES
 source
 1.153
 /organism="Homo sapiens"
 /clone="134322"

BASE COUNT 25 a 49 c 37 g 42 t
 ORIGIN

Query Match 13.8%; Score 137; DB 10; Length 153;
 Best Local Similarity 97.2%; Pred. No. 1.85e-231;
 Matches 137; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 1 GCGTTCATCTTTCCTTCGTGAGACCTGTCATCATCATGCTGCTACACCCCTGA 60
 |||||
 QY 529 GCGTTCATCTTTCCTTCGTGAGACCTGTCATCATCATGCTGCTACACCCCTGA 588
 |||||
 Db 61 TGATCTCGGCTCAGAGCGCTCGGCTCTTTCGCTCCGAGAGAAAGATCGCAAC 120
 |||||
 QY 589 TGATCTCGGCTCAGAGCGCTCGGCTCTTTCGCTCCGAGAGAAAGATNNCAAC 648
 |||||
 Db 121 TGCGTAGATCAGCAGACTGG 141
 |||||
 QY 649 TGCGTAGATCAGCAGACTGG 669

RESULT 3
 LOCUS R81332 433 bp mRNA EST 12-JUN-1995
 DEFINITION y104b04.s1 Homo sapiens cDNA clone 147727 3'.
 ACCESSION
 NID R81332
 KEYWORDS
 SOURCE

human clone=147727 library=Soares placenta Nb2HP vector=PT73D
 (Pharmacia) with a modified polylinker host=DH10B (ampicillin
 resistant) primer=Promega -2ln13 RstI=Not I RstI=2-Eco RI Female
 placenta obtained at birth (full term). 1st strand cDNA was primed
 with a Not I - oligo(dT) primer [5' -
 AACTGAGAGATTTCGCGCGCAGAGATTTTCTTTTCTTTT 3'], double-stranded
 cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not
 I and cloned into the Not I and Eco RI sites of the modified pT73
 vector. Library went through one round of normalization. Library
 constructed by Bento Soares and M.Fatima Bonaldo.

ORGANISM
 Homo sapiens
 Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
 Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
 Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;
 Eutheria; Archonta; Primates; Catarrhini; Homiidae; Homo.

REFERENCE
 1 (bases 1 to 433)
 AUTHORS
 Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
 Holman,M., Hiltman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
 Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
 Trevasakis,E., Waterston,R., Williamson,A., Wohlmann,P. and
 Wilson,R.

TITLE
 JOURNAL
 COMMENT
 The WashU-Merck EST Project
 Unpublished (1995)

Contact: Wilson RK
 WashU-Merck EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
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 Email: est@wustl.edu
 High quality sequence stops: 241
 Source: IMAGE Consortium, LNLN
 This clone is available royalty-free through LNLN; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.

FEATURES
 source
 1.433
 /organism="Homo sapiens"
 /clone="147727"

BASE COUNT 102 a 97 c 100 g 114 t 20 others
 ORIGIN

Query Match 4.0%; Score 40; DB 10; Length 433;

[illegible]

DEFINITION	NCBI12493 Retina II Homo sapiens cDNA 5' end similar to guanine nucleotide-binding protein coupled receptor A23b.					
ACCESSION	A2296709					
NID	k1949271					
KEYWORDS	EST.					
SOURCE	human.					
ORGANISM	Homo sapiens					
	Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.					
REFERENCE	1.(bases 1 to 377)					
AUTHORS	Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Faldut,R.A., White,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., Bult,C., Sutton,G., Blake,J.A., Brandon,R.C., Man-vel,C., Clifton,R.A., Cline,T.R., Cotton,M.D., Barle-Hughes,J., Fine,L.D., Fitzgerald,U.M., Fitzhugh,W.M., Fritchman,J.L., Geoghegan,N.S., Glodzer,A., Gnehm,C.L., Hanna,M.C., Heblum,E., Hinkle,P.S., Jr., Kelley,T.M., Kelley,J.C., Liu,H.-I., Marnaros,S.M., Merrick,J.M., Moreno-Palmarques,R.F., McDonald,L.A., Nguyen,D.T., Pellegrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Uterback,T.R., Weldman,J.F., Li,Y., Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J., Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A., He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meisner,P.S., Olsen,H., Raymond,L., Wel,y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillion,P.J., Rannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.					
TITLE	Initial assessment of human gene diversity and expression pattern based upon 83 million nucleotides of cDNA sequence					
JOURNAL MEDLINE	Nature 377 (6547 Suppl), 3-174 (1995)					
COMMENT	96026280 Other_ESTS: THC177269 Contact: Kerlavage, AR Bioinformatics The Institute for Genomic Research 9712 Medical Center Drive, Rockville, MD 20850 USA Tel.: 3018699056 Fax: 3018699423 Email: arkerlav@tigr.org For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/cdb/hgi/hgi.html) Seq primer: M13 Reverse. Location/Qualifiers 1..377 /organism="Homo sapiens" /note="Organ: retina; Vector: phuescript SK-, Site_1: ECORI; Site_2: XhoI" /db_xref="ATCC (Inhost):118592" /db_xref="taxon:9606" /clone_id="Retina II" /sex="mixed" /dev_stage="adult" <1..377 BASE COUNT 78 a 90 c 89 g 116 t 4 others ORIGIN rRNA Query Match 3.4%; score 34; DB 18; Length 377; Best Local Similarity 77.6%; Pred.No. 5,34e-21; Matches 45; Conservative 0; Mismatches 13; Indels 0; Gaps 0;					
Db	103	GAGTGGCGGTGTTGGTGCTGTNTTTNTGTCGTGCCTGGACTCCATTACCATTTT	160			
OY	664	GAGGTGCTCTGTGGTGGTGGCACTGTCGCGTCTGCTGGACTCCCATTCACATTAAT	721			
RESULT	8	R77831	484 bp	mRNA	EST	07-JUN-1995
LOCUS						
DEFINITION	U17705.x1 Homo sapiens cDNA clone 145305 5' similar to SP-BHL1_HUMAN P32302 BURKITT'S LYMPHOMA RECEPTOR ; .					
ACCESSION	R77831					
NID	g852991					



(TM)

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Mesrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu Apr 16 13:40:06 1998; MasPar time 8.55 Seconds

Tabular output not generated. 479,455 Million cell updates/sec

Title: >US-08-292-694A-12

Description: (1-295) from US08292694A.pep

Perfect Score: 2229

Sequence: 1 YTKMKATNTIYFNLALDA.....NTVQDPATLRIDGMKRPV 295

Scoring table: PAM 150

Gap 11

Searched: 111726 segs, 13889129 residues

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database:

a-geneseg30

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23

Statistics: Mean 33.578; Variance 146.821; scale 0.226

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	2223	99.7	295 12	R67672	Human kappa opioid re	4,45e-199
2	2192	98.3	380 17	R88722	Human kappa opioid re	4,42e-196
3	2136	95.8	380 12	R67669	Mouse kappa opioid re	1,15e-190
4	2132	95.6	380 13	R72591	Mammalian kappa opioi	2,79e-190
5	2132	95.6	380 13	R76783	Rat kappa opiate rece	2,79e-190
6	1522	68.3	356 11	R65188	Murine mu-subtype opi	1,81e-131
7	1522	68.3	398 13	R76781	Rat mu opiate receptor	1,81e-131
8	1522	68.3	400 13	R71966	Human mu opioid recep	1,81e-131
9	1520	68.2	398 13	R71964	Rat mu opioid recep	2,82e-131
10	1452	65.1	400 13	R76780	Human mu opiate rece	2,82e-131
11	1448	65.0	372 13	R76782	Rat delta opiate rece	9,62e-125
12	1448	65.0	372 9	R48629	Sequence of murine de	2,33e-124
13	1448	65.0	372 12	R67670	Mouse delta opioid re	2,33e-124
14	1348	60.5	371 10	R66503	Murine delta opioid r	9,17e-115
15	1345	60.3	367 13	R71968	Rat opioid receptor	2,77e-114
16	1343	60.3	367 13	R67671	Mouse opioid receptor	2,77e-114
17	1336	59.9	367 13	R76638	Rat opiorph receptor	1,30e-113
18	1066	47.8	367 13	R74298	Mouse kappa-3 opioid	8,46e-88
19	830	37.2	391 7	R39259	Human somatostatin re	2,19e-65
20	830	37.2	391 7	R39260	Murine somatostatin r	2,19e-65

21	785	35.2	369 7	R39262	Murine somatostatin r	3,91e-61
22	780	35.0	369 7	R39261	Human somatostatin re	1,16e-60
23	780	35.0	369 18	R97269	Human somatostatin re	1,16e-60
24	767	34.4	369 5	R27504	Pituitary somatostati	1,95e-59
25	736	33.0	333 13	R72885	Epsilon opioid recept	1,62e-56
26	727	32.6	322 15	R48754	Rat RGH G-protein cou	1,14e-55
27	727	32.6	322 19	W02726	Rat RGH G-protein c	1,14e-55
28	683	30.6	418 7	R39263	Human somatostatin re	1,56e-51
29	661	29.7	328 13	R72984	Epsilon opioid recept	1,80e-49
30	658	29.5	242 22	W10017	G-protein coupled rec	3,43e-49
31	589	26.9	428 7	R39264	Murine somatostatin r	1,12e-43
32	586	26.3	241 22	W10016	G-protein coupled rec	1,19e-42
33	545	24.5	349 14	R79443	Galanin receptor	1,19e-38
34	545	24.5	349 17	R95070	Human galanin recepto	1,19e-38
35	518	23.2	348 17	R91329	Mouse pancreas G-prot	3,77e-36
36	518	23.2	348 17	R95069	Mouse pancreas beta-c	3,77e-36
37	510	22.9	402 17	R98358	Somatostatin-like rec	2,07e-35
38	496	22.3	355 10	R52749	C-C chemokine recepto	4,07e-34
39	496	22.3	355 23	W25751	Human MIP-1alpha/RAN	1,45e-33
40	490	22.0	363 12	R66934	Mouse A12 receptor	8,18e-32
41	471	21.1	355 18	W03376	CC-chemokine receptor	8,18e-32
42	471	21.1	355 22	W10100	Human C-C chemokine r	8,18e-32
43	467	21.0	325 15	R48730	G-protein coupled bo	1,91e-31
44	468	21.0	335 23	W27124	Human chemokine recep	1,54e-31
45	468	21.0	335 18	W03377	CC-chemokine receptor	1,54e-31

ALIGNMENTS

RESULT 1
ID R67672 standard; Protein: 295 AA.
AC R67672;

DE 18-AUG-1995 (first entry)
DE Human kappa opioid receptor partial protein.

KW Mouse; kappa; delta; mu; opioid receptor; brain; primer; PCR; amplify;
KW Transmembrane domain; somatostatin; receptor; human; expression vector;
KW truncate; chimeric; assay; probe.

OS Homo sapiens.

FT Key Location/Qualifiers

FT MISC-difference 169

FT /label= Any amino acid

FT MISC-difference 181

FT /label= Any amino acid

FT MISC-difference 265

FT /label= Any amino acid

FT MISC-difference 269

FT /label= Any amino acid

PN W09428132-A.

PD 08-DEC-1994.

PE 20-MAY-1994; U05747.

PR 20-MAY-1993; US-066296.

PR 30-JUL-1993; US-100694.

PR 05-NOV-1993; US-147592.

PA (ARCH-) ARCH DEV CORP.

PI Bell GI, Ralsine T, Yasuda K;

DR WPI; 95-022804/03.

DR N-PSDB; 075931.

PT Polynucleotides and peptides derived from opioid receptor

PT polypeptides for use in therapeutic compositions and in

PT screening assays for useful drug substances.

PS Claim 12; Page 236-239; 300pp; English.

CC The partial amino acid sequence of the novel human kappa opioid receptor.

CC The corresponding gene was isolated from a human brain hippocampus cDNA

CC library using a probe from the mouse kappa opioid receptor gene (075926).

CC The gene is missing the N-terminal sequence. The C-terminal sequence is

CC very similar to the mouse kappa opioid receptor sequence. Of the

CC C-terminal 293 amino acids, 281 residues are identical and 6 residues

CC have conservative substitutions. The gene encoding the human opioid

CC receptor can be placed in a suitable expression vector for production of

CC the protein in a cell. The opioid receptors thus produced are useful for

CC the development of novel assays designed to select or improve substances,

CC capable of interacting with the opioid receptor proteins, for use in

CC diagnosis, drug design and therapeutic applications.

SQ Sequence 295 AA:
 Query Match 99.7%; Score 2223; DB 12; Length 295;
 Best Local Similarity 99.7%; Pred. No. 4,45e-199;
 Matches 294; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Db 1 ytkmktatlyifnlnaladalyttmfpfgstvylnmswpgfdgkckivisidymnfstl 60
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 QY 1 ytkmktatlyifnlnaladalyttmfpfgstvylnmswpgfdgkckivisidymnfstl 60
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 61 fcltmmsvdrlylavchpvykaldfrtpkakiiniciwllssvgsiaalyggtkxregvd 120
 QY 61 fcltmmsvdrlylavchpvykaldfrtpkakiiniciwllssvgsiaalyggtkxregvd 120
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 QY 121 vleccqgfdpdddykwdlrmkicvffafvpyllivcytlmllrkxvrlsgrskd 180
 Db 181 xnlrtitrlvlyvavfvcwptpnhifllvealgssthsaalssyyfcialgytnssjn 240
 181 xnlrtitrlvlyvavfvcwptpnhifllvealgssthsaalssyyfcialgytnssjn 240
 QY 181 xnlrtitrlvlyvavfvcwptpnhifllvealgssthsaalssyyfcialgytnssjn 240
 Db 241 pilyaflidenfkrcfdcfcpikmmerxstsvrntvqdpaylreidgmunkpv 295
 241 pilyaflidenfkrcfdcfcpikmmerxstsvrntvqdpaylreidgmunkpv 295
 QY 241 pilyaflidenfkrcfdcfcpikmmerxstsvrntvqdpaylreidgmunkpv 295
 RESULT 2
 ID R88722 standard; Protein; 380 AA.
 AC R88722;
 DE 04-SEP-1996 (first entry)
 DT Human kappa opioid receptor.
 KM Human; kappa opioid receptor; psychiatric disorder; cardiovascular;
 KW neurology; diagnosis.
 OS Homo sapiens.
 PN W09601898-A1.
 PD 25-JAN-1996.
 PE 07-JUL-1995; F00912.
 PR 11-JUL-1994; FR-008531.
 PA (UYST-) UNIT PASTEUR STRASBOURG LOUIS.
 PI Kieffer B, Simonin F;
 DR N-PSDB; J12550.
 DR N-PSDB; J12550.
 PT New nucleic acid encoding the human Kappa opioid receptor - useful
 PT in diagnosis and therapy, and for isolating receptor ligands and
 PT modulators
 PS Claim 7; Page 13-15; 30pp; French.
 CC The sequence coding for the human kappa opioid receptor was
 CC obtained from two overlapping cDNA fragments isolated from a
 CC human placental cDNA library. The fragments were amplified from
 CC the library using PCR primers based on the sequence of human
 CC genomic clones which hybridised with a murine delta receptor cDNA
 CC probe. Nucleotide probes derived from the kappa opioid receptor
 CC coding sequence are useful for diagnosis of neurological, cardio-
 CC vascular and psychiatric disorders associated with opioid
 CC receptors. The receptor can be used for identifying e.g. agonists
 CC of its activity for potential use as analgesics.
 SQ Sequence 380 AA.
 Query Match 98.3%; Score 2192; DB 17; Length 380;
 Best Local Similarity 97.6%; Pred. No. 4,42e-196;
 Matches 288; Conservative 1; Mismatches 5; Indels 1; Gaps 1;
 Db 87 ytkmktatlyifnlnaladalyttmfpfgstvylnmswpgfdgkckivisidymnfstl 146
 87 ytkmktatlyifnlnaladalyttmfpfgstvylnmswpgfdgkckivisidymnfstl 146
 QY 1 ytkmktatlyifnlnaladalyttmfpfgstvylnmswpgfdgkckivisidymnfstl 60
 Db 147 fcltmmsvdrlylavchpvykaldfrtpkakiiniciwllssvgsiaalyggtkxregvd 206
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 QY 61 fcltmmsvdrlylavchpvykaldfrtpkakiiniciwllssvgsiaalyggtkxregvd 120
 61 fcltmmsvdrlylavchpvykaldfrtpkakiiniciwllssvgsiaalyggtkxregvd 120
 Db 207 vlecsqgfdpdddykwdlrmkicvffafvpyllivcytlmllrkxvrlsgrskd 266
 207 vlecsqgfdpdddykwdlrmkicvffafvpyllivcytlmllrkxvrlsgrskd 266
 QY 181 xnlrtitrlvlyvavfvcwptpnhifllvealgssthsaalssyyfcialgytnssjn 240
 181 xnlrtitrlvlyvavfvcwptpnhifllvealgssthsaalssyyfcialgytnssjn 240

QY 121 vleccqgfdpdddykwdlrmkicvffafvpyllivcytlmllrkxvrlsgrskd 180
 Db 267 xnlrtitrlvlyvavfvcwptpnhifllvealgssthsaalssyyfcialgytnssjn 326
 267 xnlrtitrlvlyvavfvcwptpnhifllvealgssthsaalssyyfcialgytnssjn 326
 QY 181 xnlrtitrlvlyvavfvcwptpnhifllvealgssthsaalssyyfcialgytnssjn 240
 181 xnlrtitrlvlyvavfvcwptpnhifllvealgssthsaalssyyfcialgytnssjn 240
 QY 241 pilyaflidenfkrcfdcfcpikmmerxstsvrntvqdpaylreidgmunkpv 295
 241 pilyaflidenfkrcfdcfcpikmmerxstsvrntvqdpaylreidgmunkpv 295
 RESULT 3
 ID R67669 standard; Protein; 380 AA.
 AC R67669;
 DE 17-AUG-1995 (first entry)
 DT Mouse kappa opioid receptor MOR1.
 KM Mouse; kappa; delta; mu; opioid receptor; brain; primer; PCR; amplify;
 KW transmembrane domain; somatostatin; receptor; human; expression vector;
 KW truncate; chimeraic; assay; probe.
 OS Mus musculus.
 PN W09428132-A.
 PD 08-DEC-1994.
 PE 20-MAY-1994; U05747.
 PR 20-MAY-1993; US-066286.
 PR 30-JUL-1993; US-100684.
 PR 05-NOV-1993; US-147582.
 PA (ARCH-) ARCH DEV CORP.
 PI Bell GI, Relsine T, Yasuda K;
 DR WPI; 95-022804/03.
 DR N-PSDB; Q75925.
 PT Polynucleotides and peptides derived from opioid receptor
 PT screening assays for use in therapeutic compositions and in
 PT screening assays for use in therapeutic compositions and in
 PS Claim 8; Page 207-211; 300pp; English.
 CC The amino acid sequence of the novel mouse kappa opioid receptor MOR1.
 CC The corresponding gene was isolated from a mouse brain cDNA library using
 CC a fragment (amplified from the cDNA library with primers Q75929-30) as a
 CC probe. The primers are based on the conserved sequences present in the
 CC second and third transmembrane domains of somatostatin (SSTR) receptor
 CC subtypes SSTR1, SSTR2 and SSTR3. The 1.2 kb PstI fragment from the mouse
 CC kappa opioid receptor clone, lambda msl-1, was subcloned into the CMV
 CC promoter-based expression vector pCMV-6b. The resultant construct
 CC pCMV-msl-1 was transfected into COS-1 cells for protein production. The
 CC gene encoding the opioid receptor can be used to produce complete,
 CC truncated or chimeric opioid receptor proteins. The opioid receptors
 CC thus produced are useful for the development of novel assays designed to
 CC select or improve substances, capable of interacting with the opioid
 CC receptor proteins, for use in diagnosis, drug design and therapeutic
 CC applications.
 SQ Sequence 380 AA.
 Query Match 95.8%; Score 2136; DB 12; Length 380;
 Best Local Similarity 92.9%; Pred. No. 1,15e-190;
 Matches 274; Conservative 13; Mismatches 7; Indels 1; Gaps 1;
 Db 87 ytkmktatlyifnlnaladalyttmfpfgstvylnmswpgfdgkckivisidymnfstl 146
 87 ytkmktatlyifnlnaladalyttmfpfgstvylnmswpgfdgkckivisidymnfstl 146
 QY 1 ytkmktatlyifnlnaladalyttmfpfgstvylnmswpgfdgkckivisidymnfstl 60
 Db 147 fcltmmsvdrlylavchpvykaldfrtpkakiiniciwllssvgsiaalyggtkxregvd 206
 147 fcltmmsvdrlylavchpvykaldfrtpkakiiniciwllssvgsiaalyggtkxregvd 206
 QY 61 fcltmmsvdrlylavchpvykaldfrtpkakiiniciwllssvgsiaalyggtkxregvd 120
 61 fcltmmsvdrlylavchpvykaldfrtpkakiiniciwllssvgsiaalyggtkxregvd 120
 Db 207 vlecsqgfdpdddykwdlrmkicvffafvpyllivcytlmllrkxvrlsgrskd 266
 207 vlecsqgfdpdddykwdlrmkicvffafvpyllivcytlmllrkxvrlsgrskd 266
 QY 121 vleccqgfdpdddykwdlrmkicvffafvpyllivcytlmllrkxvrlsgrskd 180
 121 vleccqgfdpdddykwdlrmkicvffafvpyllivcytlmllrkxvrlsgrskd 180
 Db 267 xnlrtitrlvlyvavfvcwptpnhifllvealgssthsaalssyyfcialgytnssjn 326
 267 xnlrtitrlvlyvavfvcwptpnhifllvealgssthsaalssyyfcialgytnssjn 326
 QY 181 xnlrtitrlvlyvavfvcwptpnhifllvealgssthsaalssyyfcialgytnssjn 240
 181 xnlrtitrlvlyvavfvcwptpnhifllvealgssthsaalssyyfcialgytnssjn 240
 Db 327 pilyaflidenfkrcfdcfcpikmmerxstsvrntvqdpaylreidgmunkpv 380
 327 pilyaflidenfkrcfdcfcpikmmerxstsvrntvqdpaylreidgmunkpv 380

QY 241 PIIYAFIDENKRCRDFCFPLKMKMERKSTSRVNTVODPAYLRIDGMNKPV 295

RESULT 4
ID R72591 standard; Protein; 380 AA.
AC R72591;
DE 01-DEC-1995 (first entry)
DE Mammalian kappa opioid receptor protein.
KW Mammalian kappa opioid receptor; mouse delta opioid receptor; analgesic;
OS amplification; primer: rat; probe: E.coli; RT-PCR; hypnotic compound; ds.
PI Rattus rattus.
FH Key
FT CDS Location/Qualifiers
FT 111..1253
FT /*tag= a
FT /product= kappa opioid receptor
FT 007070191-8.
PD 14-MAR-1995.
PR 30-JUL-1993: 190261.
PR 09-JUL-1993: JP-170591.
PA (TAKE) TAKEDA CHEM IND LTD.
DR WPI: 95-144857/13.
DR N-PSDB; Q86725.
PI Kappa opioid receptor protein and cells expressing it - useful
PI for the screening of compounds for analgesic and hypnotic
PI properties
PS Claim 2: Page 9-10; 15pp; Japanese.
CC The amino acid sequence of the novel mammalian kappa opioid receptor.
CC The gene was isolated by amplifying a fragment from rat brain mRNA by
CC reverse transcriptase-PCR (RT-PCR) using primers Q86726-7 derived from
CC the mouse delta-opioid receptor gene. This fragment was cloned into the
CC plasmid pCMT1 to produce pR1. The plasmid pR1 was used to probe a rat
CC brain DNA library in lambda ZAPIT to obtain a clone of the rat kappa
CC opioid receptor gene, designated pROR2. This clone was introduced into
CC E.coli JM109 for production of the receptor protein. The receptor protein
CC is useful for screening of analgesic and hypnotic compounds including
CC peptides and proteins.
SQ Sequence 380 AA.

Query Match 95.6%; Score 2132; DB 13; Length 380;
Best Local Similarity 92.5%; Pred. No. 2,79e-190;
Matches 273; Conservative 13; Mismatches 8; Indels 1; Gaps 1;

DB 87 ytkmktatniyifnlaadalyttmpfgsavylnmswpgfvdckivisidymftsi 146
QY 1 YTKMKTATNIYIFNLAADALVTTMPFGSVLYLNMSWPGVDCKIVISIDYNNFTSI 60
DB 147 fltmsvdrlylavchpvrkaldftrplkaklnic:wllassvgsaivlggtkxredvd 206
QY 61 FLTMSVDRLYAVCHPVRKALDFTRPLKAKLNIC:WLLSSVGSIAIVLGGTKXREDVD 120
DB 207 viecslgfdddeyswdlfmkicovfafavpvlilivcyltmilrpkavrllsgrkd 266
QY 121 VIECCLGPFDDDYRSDWMDLMKICVFIFAFVYPLIIVCTTLMILRKXVRLISSGREND 160
DB 267 nrlrlltkllyvvavfllcwprhifllvealgsstshstavlssyyfclalqyltnsln 326
QY 181 NXLRRTRRLVAVVAVFVWCWPIHIFLIVELAGSTSHSTAALSSYYFCIALGYTNSLN 240
DB 327 pvllyafldenfkrcfdcfpikmmerqstsrvtntvdpasmrdvggm-rkpv 380
QY 241 PIIYAFIDENKRCRDFCFPLKMKMERKSTSRVNTVODPAYLRIDGMNKPV 295

RESULT 5
ID R76783 standard; Protein; 380 AA.
AC R76783;
DE 11-DEC-1995 (first entry)
DE Rat kappa opiate receptor.
KW Kappa opiate receptor; mu opiate receptor; hMOR; opiate agonist;
OS opiate antagonist; drug abuse; analgesic.
PI Rattus sp.
PN W09520657-A1.
PD 03-AUG-1995.

PF 30-JAN-1995; U01144.
PR 28-JAN-1994; US-189275.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA (USSH) US SEC DEPT HEALTH.
PI Johnson PS, Persico AM, Uhl G, Wang J;
DR WPI: 95-275452/36.
FT New DNA encoding human mu opiate receptor - used esp. for screening
FT opds. for activity as opiate agonists or antagonists
PS Disclosure; Page 29-30; 49pp; English.
CC hMOR cDNA was obtd. from a human cerebral cortical cDNA library
CC screened with fragments of a rat mu opiate receptor. The encoded
CC protein showed homology to rat mu, delta and kappa opiate
CC receptors (R/6781-83).
SQ Sequence 380 AA.

Query Match 95.6%; Score 2132; DB 13; Length 380;
Best Local Similarity 92.5%; Pred. No. 2,79e-190;
Matches 273; Conservative 13; Mismatches 8; Indels 1; Gaps 1;

DB 87 ytkmktatniyifnlaadalyttmpfgsavylnmswpgfvdckivisidymftsi 146
QY 1 YTKMKTATNIYIFNLAADALVTTMPFGSVLYLNMSWPGVDCKIVISIDYNNFTSI 60
DB 147 fltmsvdrlylavchpvrkaldftrplkaklnic:wllassvgsaivlggtkxredvd 206
QY 61 FLTMSVDRLYAVCHPVRKALDFTRPLKAKLNIC:WLLSSVGSIAIVLGGTKXREDVD 120
DB 207 viecslgfdddeyswdlfmkicovfafavpvlilivcyltmilrpkavrllsgrkd 266
QY 121 VIECCLGPFDDDYRSDWMDLMKICVFIFAFVYPLIIVCTTLMILRKXVRLISSGREND 180
DB 267 nrlrlltkllyvvavfllcwprhifllvealgsstshstavlssyyfclalqyltnsln 326
QY 181 NXLRRTRRLVAVVAVFVWCWPIHIFLIVELAGSTSHSTAALSSYYFCIALGYTNSLN 240
DB 327 pvllyafldenfkrcfdcfpikmmerqstsrvtntvdpasmrdvggm-rkpv 380
QY 241 PIIYAFIDENKRCRDFCFPLKMKMERKSTSRVNTVODPAYLRIDGMNKPV 295

RESULT 6
ID R65188 standard; Protein; 356 AA.
AC R65188;
DE 19-APR-1995 (first entry)
DE Murine mu-subtype opioid receptor.
KW Mu-subtype opioid receptor; MSOR; drug addiction.
OS Rattus rattus.
FH Key
FT Modified_site 10..12
FT /note= "putative N-linked glycosylation site"
FT Modified_site 230
FT /note= "threonine residue especially favourable
FT for protein kinase A phosphorylation"
FT 25..48
FT Region "hydrophobic membrane spanning region"
FT /note= "hydrophobic membrane spanning region"
FT 58..78
FT Region "hydrophobic membrane spanning region"
FT /note= "hydrophobic membrane spanning region"
FT 96..118
FT Region "hydrophobic membrane spanning region"
FT /note= "hydrophobic membrane spanning region"
FT 139..166
FT Region "hydrophobic membrane spanning region"
FT /note= "hydrophobic membrane spanning region"
FT 187..212
FT Region "hydrophobic membrane spanning region"
FT /note= "hydrophobic membrane spanning region"
FT 236..257
FT Region "hydrophobic membrane spanning region"
FT /note= "hydrophobic membrane spanning region"
FT 274..294
FT Region "hydrophobic membrane spanning region"
FT /note= "hydrophobic membrane spanning region"
PN EP-612845-A.
PD 31-AUG-1994.
PR 09-FEB-1994; 101968.
PR 26-FEB-1993; US-026140.
PA (AMCY) AMERICAN CYNAMID CO.
PI Corbett M, Eppler CM, Shieh H, Zysk JR;

DR WPI: 94-265963/73.
 DR N-PSDB: Q79199.
 PT Pure mu-type opioid receptor protein - and nucleic acid coding
 PT for 1t
 PS Clamr 2: Fig 9, 39pp: English.
 CC R65188 is the rat mu-subtype opioid receptor protein purified
 CC from rat brain membranes, with bicitinyl-b-endorphin (R65666)
 CC as its ligand. It is encoded by the nucleotide sequence Q79199
 CC which was synthesised using Q71022 and Q71023 as PCR primers.
 CC R65188 is useful for identifying the receptor subtypes, for
 CC screening new opioid ligands, and for studying mechanisms of
 CC opioid action, e.g. drug addiction.
 SQ Sequence 356 AA;

Query Match 68.3%; Score 1522; DB 11; Length 356;
 Best Local Similarity 66.1%; Pred. No. 1,81e-131;
 Matches 191; Conservative 45; Mismatches 49; Indels 4; Gaps 4;

Db 54 ytkmktatniyifnialadalatslpfgsvnylmgtwpfgtlckivisidyymftsi 113
 |||||||
 QY 1 YTKMKTATNIYIFNLALADALVTTMPFQSTVYLMNSWPGDVLCKIVISIDYNNFTSI 60
 |||||||
 Db 114 fclctmsvdrlyavchpvrkaldftrprnakivncwmllssaiqlpvmfmatkkyrg-s 172
 |||||||
 QY 61 FLLTMSVDRYIAVCHPVRKALDFTRPLKAKIINICIMLLSSVGSIAIYLGTGKVEDVD 120
 |||||||
 Db 173 -ldcrltfshpkr-ywenllkicvffafimpyllltvcygmllrlksvmlsgskexd 230
 |||||||
 QY 121 VIECCIQFPDDDSWMDLMAKICVFIFAFVPLIIVCTIMLRLKXVRLSSGREMD 180
 |||||||
 Db 231 nrlrltmwlvvavfivcwprphiyvllkalittpetftqvswhfclagytmscln 290
 |||||||
 QY 181 XNLRRTIRLVVAVFVVCWPIHIFILVEALGSHSTALSSYFCIALGYTSSSLN 240
 |||||||
 Db 291 pvllyalidenfkrctfrcfcpstlegnqstvrqntrephstantvd 339
 |||||||
 QY 241 PILYALIDENFKRCFRDPCFPLKMXERXSTSVR-NTVQDPAYLEID 288
 |||||||

RESULT 7
 ID R76781 standard; Protein: 398 AA.
 AC R76781;
 DT 11-DEC-1995 (first entry)
 DE Rat mu opiate receptor.
 KW Mu opiate receptor; hMOR; opiate agonist; opiate antagonist;
 KM drug abuse; analgesic.
 OS Rattus sp.
 PN W09520667-A1.
 PD 03-AUG-1995.
 PR 30-JAN-1995; U01144.
 PR 28-JAN-1994; US-188275.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PA (USSH) US SEC DEPT HEALTH.
 PI Johnson PS, Persico AM, Ohl G, Wang J;
 PI WPI: 95-275452/36.
 PT New DNA encoding human mu opiate receptor - used esp. for screening
 PT cpds. for activity as opiate agonists or antagonists
 PS Disclosure: Page 26-28, 49pp: English.
 CC hMOR cDNA was obt. from a human cerebral cortical cDNA library
 CC screened with fragments of a rat mu opiate receptor. The encoded
 CC protein showed homology to rat mu, delta and kappa opiate
 CC receptors (R76781-83).
 SQ Sequence 398 AA;

Query Match 68.3%; Score 1522; DB 13; Length 398;
 Best Local Similarity 66.1%; Pred. No. 1,81e-131;
 Matches 191; Conservative 45; Mismatches 49; Indels 4; Gaps 4;

Db 96 ytkmktatniyifnialadalatslpfgsvnylmgtwpfgtlckivisidyymftsi 155
 |||||||
 QY 1 YTKMKTATNIYIFNLALADALVTTMPFQSTVYLMNSWPGDVLCKIVISIDYNNFTSI 60
 |||||||
 Db 156 fclctmsvdrlyavchpvrkaldftrprnakivncwmllssaiqlpvmfmatkkyrg-s 214
 |||||||

QY 61 FLLTMSVDRYIAVCHPVRKALDFTRPLKAKIINICIMLLSSVGSIAIYLGTGKVEDVD 120
 |||||||
 Db 215 -ldcrltfshpkr-ywenllkicvffafimpyllltvcygmllrlksvmlsgskexd 272
 |||||||
 QY 121 VIECCIQFPDDDSWMDLMAKICVFIFAFVPLIIVCTIMLRLKXVRLSSGREMD 180
 |||||||
 Db 273 nrlrltmwlvvavfivcwprphiyvllkalittpetftqvswhfclagytmscln 332
 |||||||
 QY 181 XNLRRTIRLVVAVFVVCWPIHIFILVEALGSHSTALSSYFCIALGYTSSSLN 240
 |||||||
 Db 333 pvllyalidenfkrctfrcfcpstlegnqstvrqntrephstantvd 381
 |||||||
 QY 241 PILYALIDENFKRCFRDPCFPLKMXERXSTSVR-NTVQDPAYLEID 288
 |||||||

RESULT 8
 ID R71964 standard; Protein: 400 AA.
 AC R71964;
 DT 20-OCT-1995 (first entry)
 DE Human mu opioid receptor.
 KW Mu opioid receptor; MOR; gene therapy; diagnostic.
 OS Homo sapiens.
 PN W09507983-A.
 PD 23-MAR-1995.
 PR 13-SEP-1994; U10358.
 PR 13-SEP-1993; US-120601.
 PA (INDV) UNITV INDIANA FOUND.
 PA Yu L;
 DR WPI: 95-131351/17.
 DR N-PSDB: Q89226.
 PT New nucleic acid encoding new human mu opioid receptor - and
 PT related vectors, transformed cells, antibodies etc., useful in
 PT diagnosis, treatment and drug screening.
 PS Clamr 4; Page 211-214; 266pp: English.
 CC A cDNA library constructed from human caudate nucleus mRNA was
 CC screened with rat mu opioid receptor cDNA under conditions of
 CC low stringency. One positive clone included the sequence given in
 CC 089226, encoding a mu opioid receptor MOR (R71964). The cDNA
 CC is used for prodn. of recombinant MOR, in gene therapy, etc.
 SQ Sequence 400 AA;

Query Match 68.3%; Score 1522; DB 13; Length 400;
 Best Local Similarity 67.1%; Pred. No. 1,81e-131;
 Matches 188; Conservative 43; Mismatches 46; Indels 3; Gaps 3;

Db 98 ytkmktatniyifnialadalatslpfgsvnylmgtwpfgtlckivisidyymftsi 157
 |||||||
 QY 1 YTKMKTATNIYIFNLALADALVTTMPFQSTVYLMNSWPGDVLCKIVISIDYNNFTSI 60
 |||||||
 Db 158 fclctmsvdrlyavchpvrkaldftrprnakivncwmllssaiqlpvmfmatkkyrg-s 216
 |||||||
 QY 61 FLLTMSVDRYIAVCHPVRKALDFTRPLKAKIINICIMLLSSVGSIAIYLGTGKVEDVD 120
 |||||||
 Db 217 -ldcrltfshpkr-ywenllkicvffafimpyllltvcygmllrlksvmlsgskexd 274
 |||||||
 QY 121 VIECCIQFPDDDSWMDLMAKICVFIFAFVPLIIVCTIMLRLKXVRLSSGREMD 180
 |||||||
 Db 275 nrlrltmwlvvavfivcwprphiyvllkalittpetftqvswhfclagytmscln 334
 |||||||
 QY 181 XNLRRTIRLVVAVFVVCWPIHIFILVEALGSHSTALSSYFCIALGYTSSSLN 240
 |||||||
 Db 335 pvllyalidenfkrctfrcfcpstlegnqstvrqntrephstantvd 374
 |||||||
 QY 241 PILYALIDENFKRCFRDPCFPLKMXERXSTSVRNTVQD 280
 |||||||

RESULT 9
 ID R71964 standard; Protein: 398 AA.
 AC R71964;
 DT 20-OCT-1995 (first entry)
 DE Rat mu opioid receptor.
 KW Mu opioid receptor; MOR-1; gene therapy; diagnostic.

CC hMOR cDNA was ctd. from a human cerebral cortical cDNA library
 CC screened with fragments of a rat mu opiate receptor. The encoded
 CC protein showed homology to rat mu, delta and kappa opiate
 CC receptors (R76761-83).
 CC Sequence 372 AA;

Query Match 65.1%; Score 1452; DB 13; Length 372;
 Best Local Similarity 68.8%; Pred. No. 9,62e-125;

Matches 179; Conservative 44; Mismatches 33; Indels 4; Gaps 4;

DB 77 ytklktatnlyifnlaladalatstlpqfsakylmetwpgfellokavlsidyymfcsi 136
 QY 1 YTKMKTATNITFIENALADALVTTMTPOSTVYLNMSWPFQDVLOCKYISIDYVMFCSI 60
 DB 137 ftllmsvdyriavchpckaldftfpakaklinicivtlaagvqyplmnavtqprda- 195
 QY 61 FTLLMSVDRIAVCHPKALDFRPLAKAKIINICWILSSVGSALVLTGTRKREVD 120
 DB 196 vv-cltqfppsw-ywdtvlkvcvflafavpdlitvcyglmllrsvrljsgsked 253
 QY 121 VIECLOPPDDDYSWMDLFMKICVIFFAFVPLVILITVCTIMIRLKKXVRLSSREKD 180
 DB 254 rslritltmvlvvgafvvcapilhiyvtlvdinrtpdlvaalhlcalayanssl 313
 QY 181 XNLRITRLVAVVAVFVWCWTPPIHIFILVEALGSTSHSTA-ALSSYFCIALGYTNSL 239
 DB 314 npvlyafidenfkrfqlc 333
 QY 240 NPLIYAFIDENFKRCFRDQC 259

RESULT 12

ID R48629 standard; Protein; 372 AA.

AC R48629; 15-SEP-1994 (first entry)
 DE Sequence of murine delta opiod receptor deduced from the
 DE DOR-1 cDNA clone.
 KW Opioid receptor; morphine; opiate.
 OS Mus musculus.
 FH Key Location/Qualifiers
 FT Region 46..75
 FT /label= putative membrane spanning region
 FT Region 85..102
 FT /label= see above
 FT Region 125..144
 FT /label= see above
 FT Region 168..189
 FT /label= see above
 FT Region 215..238
 FT /label= see above
 FT Region 262..284
 FT /label= see above
 FT Region 295..308
 FT /label= see above
 PN W09404552-A.
 PD 03-MAR-1994.
 PE 13-AUG-1993; US-922900.
 PR 13-AUG-1993; US-922900.
 PA (REGC.) UNIV CALIFORNIA.
 PI Edwards RH, Evans CJ, Kaufman D, Keith DE;
 DR WPI: 94-083099/10.
 DR N-PSDB: 056700.
 PT DNA encoding opioid receptors and antibodies against this
 PT receptor - used to express and locate these receptors, and screen
 PT cpls. for opiod (ant)agonist activity
 PS Claim 10; Fig 5; 7abp; English.
 CC A cDNA library was constructed using mRNA isolated from the NG109-15
 CC cell line. A single clone, named the DOR-1 clone was isolated.
 CC Comparisons with known sequences in GenBank showed highest homology
 CC between DOR-1 and the G-protein-coupled somatostatin receptor. Other
 CC features of the DOR-1 clone AA sequence deduced from the cDNA
 CC sequence include 3 consensus glycosylation sites at residues 18 and
 CC 33 (predicted to be in the extracellular N-terminal domain), and at

CC residue 310 (close to the C-terminus and predicted to be
 CC intracellular). Phosphokinase C consensus sites are present within
 CC predicted intracellular domains, at residues 242,255, 344 & 352.
 CC Seven putative membrane-spanning regions were identified. The DOR-1
 CC clone produces a delta receptor with a predicted mol. wt. of 40,558
 CC kaltions prior to post-translational modifications.
 CC Sequence 372 AA;

Query Match 65.0%; Score 1448; DB 9; Length 372;
 Best Local Similarity 68.8%; Pred. No. 2.33e-124;

Matches 179; Conservative 44; Mismatches 33; Indels 4; Gaps 4;

DB 77 ytklktatnlyifnlaladalatstlpqfsakylmetwpgfellokavlsidyymfcsi 136
 QY 1 YTKMKTATNITFIENALADALVTTMTPOSTVYLNMSWPFQDVLOCKYISIDYVMFCSI 60
 DB 137 ftllmsvdyriavchpckaldftfpakaklinicivtlaagvqyplmnavtqprda- 195
 QY 61 FTLLMSVDRIAVCHPKALDFRPLAKAKIINICWILSSVGSALVLTGTRKREVD 120
 DB 196 vv-cltqfppsw-ywdtvlkvcvflafavpdlitvcyglmllrsvrljsgsked 253
 QY 121 VIECLOPPDDDYSWMDLFMKICVIFFAFVPLVILITVCTIMIRLKKXVRLSSREKD 180
 DB 254 rslritltmvlvvgafvvcapilhiyvtlvdinrtpdlvaalhlcalayanssl 313
 QY 181 XNLRITRLVAVVAVFVWCWTPPIHIFILVEALGSTSHSTA-ALSSYFCIALGYTNSL 239
 DB 314 npvlyafidenfkrfqlc 333
 QY 240 NPLIYAFIDENFKRCFRDQC 259

RESULT 13

ID R67670 standard; Protein; 372 AA.

AC R67670; 17-AUG-1995 (first entry)
 DE Mouse delta opiod receptor MORDI.
 DE Mouse; kappa; delta; mu; opiod receptor; brain; primer; PCR; amplify;
 KW transmembrane domain; somatostatin; receptor; human; expression vector;
 KW truncate; chimaeric; assay; probe.
 OS Mus musculus.
 PN W09428132-A.
 PD 08-DEC-1994.
 PE 20-MAY-1994; 005747.
 PR 20-MAY-1993; US-066296.
 PR 30-JUL-1993; US-100694.
 PR 05-NOV-1993; US-147592.
 PA (ARCH-) ARCH DEV CORP.
 PI Bell GI, Reisine T, Yasuda K;
 DR WPI: 95-022804/03.
 DR N-PSDB: Q75927
 PI Polynucleotides and peptides derived from opiod receptor
 PI polypeptides - for use in therapeutic compositions and in
 PI screening assays for useful drug substances.
 PS Claim 5; Page 215-221; 300pp; English.
 CC The amino acid sequence of the novel mouse delta opiod receptor MORDI.
 CC The corresponding gene was isolated from a mouse brain cDNA library using
 CC a fragment (amplified from the cDNA library with primers Q75929-30) as a
 CC probe. The primers are based on the conserved sequences present in the
 CC second and third transmembrane domains of somatostatin (SSTR) receptor
 CC subtypes SSTR1, SSTR2 and SSTR3. The 1.3 kb EcoRI-SacI fragment from the
 CC mouse delta opiod receptor clone, lambda ds1-2, was subcloned into the
 CC CMV promoter-based expression vector pCMV-6c. The resultant construct
 CC pCMV-msl-2 was transfected into COS-1 cells for protein production. The
 CC gene encoding the opiod receptor can be used to produce complete,
 CC truncated or chimaeric opiod receptor proteins. The opiod receptors
 CC thus produced are useful for the development of novel assays designed to
 CC select or improve substances, capable of interacting with the opiod
 CC receptor proteins, for use in diagnosis, drug design and therapeutic
 CC applications.
 CC Sequence 372 AA;

Query Match 65.0%; Score 1448; DB 12; Length 372;
 Best Local Similarity 68.8%; Pred No. 2,33e-124;
 Matches 179; Conservative 44; Mismatches 35; Indels 4; Gaps 4;

Db 77 ytklktatniyifnalaadalstlfpfsakylmetwfpfgellokavlsidyymfsl 136
 1 YTKMKTATNIYIFNLAADALVTITMPFQSTYILNMSWFGVGLKVIYSIDYYNNFTSI 60

Db 137 ftlntmsvdyryavchpvcakldfrtpakaklincicwlaagvgyvimmavtqprda- 195
 61 FTLEWMSVDRYAVCHPVCALDFRTPAKAKIINICIMWLLSSVGSIAIVLGSTKVEDVD 120

Db 196 vv-cmlgfpspsw-ywdvtvk:covflfafvvpvllitvcygmllrlsvrllsgsked 253
 121 VIECLQFPDDYSWMDLFMKICVFIFAFVLPVLLIIVCYTLMILRLKXVRLSSREXD 180

Db 254 rslrlrtmvlvvygafvvcwagphifvylvcladlnrrdpjlvaaahlcialgyanssl 313
 181 XNLRRTITRLVLYVAVFVVCWPIHIFITLVEALGSTSHSTA-ALSSYFCLALGTNSSL 239

Db 314 npvlyafldenfkrcfrcqlc 333
 240 NPILYAFLDENFKRCFRDQC 259

RESULT 14
 ID R66503 standard; Protein; 371 AA.
 AC R66503;

DE 19-VAN-1995 (first entry)
 DE Murine delta opioid receptor.
 KM delta opioid: enkephalin; receptor; mouse; murine; analgesic; pain;
 KW drug addiction; neurological disorder; psychiatric; disorder;
 KM cardiovascular disorder.
 OS Mus musculus.
 PN FR2697850-A.
 PD 13-MAY-1994.
 PF 10-NOV-1992; 013525.
 PR 10-NOV-1992; FR-013526.
 RA (USTR-) UNITV PASTEROR STRASBOURG LOUIS.
 PI Kieffer B;
 DR WPI; 94-178255/22.
 DR N-PSDB; 066556.
 PT New nucleic acid encoding opioid receptor - and related
 PT polypeptide, antisense nucleic acid, probes; recombinant cells
 PT and ligands, useful in diagnosis and treatment of e.g.
 PS Claim 8; Page 19-20; 29pp; French.
 CC A cDNA bank constructed from hybridoma NG109-15, was used to
 CC transfect COS-1 cells. The cells were tested for ability to bind
 CC tritium-labelled Tyr-D-Thr-Gly-Phe-Leu-Thr, in the presence or
 CC absence of the opioid antagonist naloxone. Clone K56 was isolated
 CC from a positive colony and found to contain a 2218bp insert. This
 CC cDNA encodes a delta opioid (enkephalin) receptor with apparent
 CC dissociation constant 1.4nM and Bmax 3.9-6.4 pmole/mg protein.
 SQ Sequence 371 AA;

Query Match 60.5%; Score 1348; DB 10; Length 371;
 Best Local Similarity 66.9%; Pred. No. 9,17e-115;
 Matches 174; Conservative 45; Mismatches 36; Indels 5; Gaps 5;

Db 77 ytklktatniyifnalaadalstlfpfsakylmetwfpfgellokavlsidyymfsl 136
 1 YTKMKTATNIYIFNLAADALVTITMPFQSTYILNMSWFGVGLKVIYSIDYYNNFTSI 60

Db 137 ftlntmsvdyryavchpvcakldfrtpakaklincicwlaagvgyvimmavtqprda- 195
 61 FTLEWMSVDRYAVCHPVCALDFRTPAKAKIINICIMWLLSSVGSIAIVLGSTKVEDVD 120

Db 196 wycas-ssvvg-1vl-dtvtkiovfifafvvpvllitvcygmllrlsvrllsgsked 252
 121 VIECLQFPDDYSWMDLFMKICVFIFAFVLPVLLIIVCYTLMILRLKXVRLSSREXD 180

Db 254 rslrlrtmvlvvygafvvcwagphifvylvcladlnrrdpjlvaaahlcialgyanssl 312

Db 181 XNLRRTITRLVLYVAVFVVCWPIHIFITLVEALGSTSHSTA-ALSSYFCLALGTNSSL 239
 240 NPILYAFLDENFKRCFRDQC 259

RESULT 15
 ID R71968 standard; Protein; 367 AA.
 AC R71968;

DE 20-OCT-1995 (first entry)
 DE Rat opioid receptor.
 KM Opioid receptor; gene therapy; diagnostic.
 OS Rattus sp.
 FN W09507983-A.
 PD 23-MAR-1995.
 PF 13-SEP-1994; U10358.
 PR 13-SEP-1993; US-120501.
 RA (INDV) UNITV INDIANA FOUND.
 PI Yu L;
 DR WPI; 95-13351/17.
 DR N-PSDB; 089233.
 PT New nucleic acid encoding new human mu opioid receptor - and
 PT related vectors, transformed cells, antibodies etc., useful in
 PT diagnosis, treatment and drug screening.
 PS Example 9; Page 218-222; 266pp; English.
 CC The cDNA given in 089233 was isolated from a rat brain library by
 CC low stringency hybridization with rat mu opioid receptor cDNA
 CC (089222). The clone encoded a 367-amino acid protein (71968)
 CC that showed high homology with mu, kappa and delta opioid receptors
 CC but lacked affinity for their ligands, suggesting it to be
 CC a novel member of the opioid receptor family.
 SQ Sequence 367 AA;

Query Match 60.3%; Score 1345; DB 13; Length 367;
 Best Local Similarity 62.1%; Pred. No. 1,78e-114;
 Matches 174; Conservative 46; Mismatches 55; Indels 5; Gaps 5;

Db 77 tkmktatniyifnalaadalstlfpfgtdlllgfwfgnalcktyaadyymfstrf 136
 2 YTKMKTATNIYIFNLAADALVTITMPFQSTYILNMSWFGVDVLCIVSIDYYNNFTSIF 61

Db 137 tltmsvdyryavchpvcakldfrtpakaklincicwlaagvgyvimmavtqprda- 194
 62 FTLEWMSVDRYAVCHPVCALDFRTPAKAKIINICIMWLLSSVGSIAIVLGSTKVEDVD 121

Db 195 leclveipapqdy-wgyrfa-iciflflfpvllsvcsimtrllrgvrlsgsrek 252
 122 IECCQFPD-DYSWMDLFMKICVFIFAFVLPVLLIIVCYTLMILRLKXVRLSSREXD 180

Db 253 nrlrlrtmvlvvygafvvcwagphifvylvcladlnrrdpjlvaaahlcialgyanssl 312
 181 XNLRRTITRLVLYVAVFVVCWPIHIFITLVEALGSTSHSTAALSSYFCLALGTNSSL 240

Db 313 pilyafldenfkacrfkocaaslhrmvgdsrvsjakd 352
 241 PITYAFLDENFKRCFRDQCPLKMMEXSTSRVANTYOD 280

Search completed: Thu Apr 16 13:41:27 1998
 Job time : 81 secs.

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 W O R L D
 (TM)

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MSrch_PP protein - protein database search, using Smith-Waterman algorithm
 Run on: Thu Apr 16 13:38:52 1998; MasPar time 16.01 Seconds
 Tabular output not generated. 789,710 Million cell updates/sec

Title: >US-08-292-694A-12
 Description: (1-295) from US08292694A.pep
 Perfect Score: 2229
 Sequence: 1 YTKKRTAINIYFNIALADALADLVTTMPEFQSYLANSWEPGVLKIVISIDYNNFTSI 295

Scoring table: PAM 150
 Gap 11

Searched: 195121 seqs, 42852602 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: pirs5
 1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 38.996; Variance 175.140; scale 0.223

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	2192	98.3	380	2	157005	4,746-191
2	2192	98.3	380	2	JC2338	4,746-191
3	2157	96.8	380	2	A55259	1,016-187
4	2135	95.8	310	2	MESPQIRRG	1,016-185
5	2132	95.6	380	2	JC6143	2,436-185
6	2114	94.8	380	2	JC2434	1,256-183
7	1524	68.4	398	2	A57510	1,156-127
8	1522	68.3	400	2	I56553	1,786-127
9	1520	68.2	392	2	S65693	2,746-127
10	1520	68.2	398	2	I56517	2,746-127
11	1505	67.5	398	2	I56504	7,186-126
12	1458	65.4	372	2	I38657	1,976-121
13	1452	65.1	372	2	S34592	7,276-121
14	1448	65.0	372	2	B48227	1,736-120
15	1345	60.3	367	2	I56520	8,996-111
16	1343	60.3	367	2	JC2421	1,396-110
17	1342	60.2	367	2	I49022	1,726-110
18	1331	59.7	370	2	S43087	1,876-109
19	830	37.2	391	2	C41795	1,416-62
20	830	37.2	391	2	A41795	1,416-62
21	822	36.9	394	2	A39297	1,416-62
22	820	36.9	384	2	A47249	7,796-62
23	816	36.6	388	2	JN0605	2,806-61

RESULT ID	1	STANDARD	PRT	380 AA	ALIGNMENTS
XX	157005				
XX	xxxxxx				
DT	01-JAN-1900				
XX	TOIG of: 157005	check: 8302	from: 1	to: 380	
DE	TOIG of: 157005	check: 8302	from: 1	to: 380	
XX	TOIG of: 157005	check: 8302	from: 1	to: 380	
CC	>P1:157005				
CC	Oploid receptor kappa-1 - human				
CC	C:Species: Homo sapiens (man)				
CC	C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #ext_change 29-Aug-1997				
CC	C:Accession: 157005				
CC	R:Zhu, J.; Chen, C.; Xue, J.				
CC	Life Sci. 56, 201-207, 1995				
CC	A:Title: Cloning of a human kappa oploid receptor from the brain.				
CC	A:Reference number: 157005				
CC	A:Accession: 157005				
CC	A:Status: preliminary; translated from GB/EMBL/DBJ				
CC	A:Molecule type: mRNA				
CC	A:Residues: 1-380 <RES>				
CC	A:Cross-references: GB:I37362; NID:g722617; PID:g722618				
CC	C:Genetics:				
CC	A:Gene: GDB:OPRL; KOR				
CC	A:Cross-references: GDB:132651; OMIM:165196				
CC	A:Map position: 8q11.2-8q11.2				
CC	SEQUENCE 380 AA; 42645 MW; 802905 CN;				
QQ	Query Match	98.3%	Score 2192;	DB 2;	Length 380;
QQ	Best local similarity	97.6%	Pred. No. 4,746-191;		
QQ	Matches 288;	Conservative 1;	Mismatches 5;	Indels 1;	Gaps 1;

DB	87	YTKKRTAINIYFNIALADALADLVTTMPEFQSYLANSWEPGVLKIVISIDYNNFTSI	146
QY	1	YTKKRTAINIYFNIALADALADLVTTMPEFQSYLANSWEPGVLKIVISIDYNNFTSI	60
DB	147	FTITMNSVDRIYVAVCHPRVADLDFRTPLKAKIINICIMWLLSSVGSIAIVLGGIKRVEDVD	206
QY	61	FTITMNSVDRIYVAVCHPRVADLDFRTPLKAKIINICIMWLLSSVGSIAIVLGGIKRVEDVD	120
DB	207	VIECCLOFPDDDDYSDWDLFKICIVFIFAFYIPVLIIVYCIIMILKSVRLSSGREND	266
QY	121	VIECCLOFPDDDDYSDWDLFKICIVFIFAFYIPVLIIVYCIIMILKSVRLSSGREND	180


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Db      327  PLIVAFLEENFRCDCEFPILKMKEROSTSRVNTVODPAVLPIDGM-NKPV 380
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Qy      241  PLIVAFLEENFRCDCEFPILKMKERKXSTRVNTVODPAVLEIDGMNKPV 295
          |||||

RESULT 3
ID      A55259          STANDARD;          PRT;          380 AA.
XX
AC      xxxxxx
XX
XX      01-JAN-1900
XX
DE      TOIG of: a55259  check: 7081 from: 1 to: 380.
XX
XX      TOIG of: a55259  check: 7081 from: 1 to: 380
CC
CC      >P1:A55259
CC      kappa opioid receptor - guinea pig
CC      M/alternate names: dynorphin receptor
CC      C/species: Cavia porcellus (guinea pig)
CC      C/date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 10-Sep-1997
CC      C/accession: A55259
CC      R/xie, G.; Meng, F.; Mansour, A.; Thompson, R.C.; Hovesten, M.T.; Goldstein, A
CC      proc. Natl. Acad. Sci. U.S.A. 91, 3779-3783, 1994
CC      A/title: Primary structure and functional expression of a guinea pig kappa opioid
CC      A/reference number: A55259
CC      A/accession: A55259
CC      A/status: Preliminary
CC      A/molecule type: mRNA
CC      A/residues: 1-380 <XIR>
CC      A/cross-references: GB:U04092; NID:g476106; PID:g476107
CC      C/keywords: transmembrane protein
SQ      SEQUENCE 380 AA: 42736 MW; 800736 CN;
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Query Match	95.8%;	Score 2157;	DB 2;	length 380;
Best Local Similarity	94.6%;	Pred. No. 1,01e-187;		
Matches 279;	Conservative	10;	Mismatches 5;	Indels 1;
				Gaps 1;
Db	87	YTKMKTATNIITFNLALADALVTTTMEPQSTVYILMNSWPFGDVLCKIYISIDYYNMTTSI	146	
QY	1	YTKMKTATNIITFNLALADALVTTTMEPQSTVYILMNSWPFGDVLCKIYISIDYYNMTTSI	60	
Db	147	FTLTMASVDRIIANVCHPVKALDEPRTPLAKITINICIMWLSSSVGISAITIGGTVRREDVD	206	
QY	61	FTLTMASVDRIIANVCHPVKALDEPRTPLAKITINICIMWLSSSVGISAITIGGTVRREDVD	120	
Db	207	IIIESIOEPDDDDYNNMPLDMKICVFVFAFVIVLLIIVCYITMLIRLKSVALSGSSEKD	266	
QY	121	VIECOLQEPDDDDYNNMPLDMKICVFIFAFVIVLLIIVCYITMLIRLKSVALSGSSEKD	180	
Db	267	ENLRIRITLVYVAVNAVEILICWTPIHIFILVEALGSTSHSTALSSYFCIALGXTNSLN	326	
QY	181	XNLRRITELVYVAVNAVEPVWCPTIHIFILVEALGSTSHSTALSSYFCIALGXTNSLN	240	
Db	327	PILAFIDLENKRCFDFPCFPIKRMEROSTSRVKNVYODPAIKRVNDGV-NKCV	380	
QY	241	PILAFIDLENKRCFDFPCFPIKRMERKXSTSRVKNVODPAIKRVNDGVNMNKEY	295	

Db 17 YTKMTATNIIYIFNLALADALVTTTTPQSAVYLMNSWPFQGVLCIKIVISIDYNNFTSI 76
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QY 1 YTKMTATNIIYIFNLALADALVTTTTPQSAVYLMNSWPFQGVLCIKIVISIDYNNFTSI 60
|||||
Db 77 FLLTMASVDRIYAVCHPVPKALDFRPLKAKIINICIMILASSVGISAIVLGSTKREVD 136
|||||
QY 61 FLLTMASVDRIYAVCHPVPKALDFRPLKAKIINICIMILASSVGISAIVLGSTKREVD 120
|||||
Db 137 VIECSLOEPDDERYSWMDLPMKICVFAFVAPVLLITVYCYTMTIRLKSVRLLSGSREXD 196
|||||
QY 121 VIECSLOEPDDERYSWMDLPMKICVFAFVAPVLLITVYCYTMTIRLKSVRLLSGSREXD 180
|||||
Db 197 RNLRRTIKLVVAVAFIICWTPPIHFIILVEALGSTSHSTAALSSYFCIALGYTNSLN 256
|||||
QY 181 XNLRRTIKLVVAVAFIICWTPPIHFIILVEALGSTSHSTAALSSYFCIALGYTNSLN 240
|||||
Db 257 PVLVAFIDENFRKCRDFCFPIKMEROSTNRVNTVODPASMVDGSM-NKPV 310
|||||
QY 241 PVLVAFIDENFRKCRDFCFPIKMEROSTNRVNTVODPASMVDGSM-NKPV 295
|||||

RESULT 5
ID S36143 STANDARD; PRT; 380 AA.
XX xxxxxx
AC xxxxxx
DT 01-JAN-1900
XX
DE A/Accession: S36143.
XX
XX A/Accession: S36143
CC A/Status: preliminary
CC A/Molecule type: mRNA
CC A/Residues: 1-380 <NLS>
CC R/Chem. Y.; Mestek A.; Liu, J.; Yu, L.
CC Biochem. J. 295, 625-628, 1993
CC A/Title: Molecular cloning of a rat kappa opioid receptor reveals sequence similar
CC A/Reference number: S38825
CC A/Accession: S38825
CC A/Status: preliminary
CC A/Molecule type: mRNA
CC A/Residues: 1-380 <CHE>
CC A/Cross-references: GB:L22001; NID:G409236; PID:G409337
CC R/Name. M.; Toya, T.; Katao, Y.; Maekawa, K.; Nakamura, S.; Onogi, T.; Kaneko, S
CC FEBS Lett. 329, 291-295, 1993
CC A/Title: Cloning and expression of a cDNA for the rat kappa-opioid receptor.
CC A/Reference number: S36102
CC A/Accession: S36102
CC A/Molecule type: mRNA
CC A/Residues: 1-41, 1, 43-380 <MIN>
CC R/Ref. S.; Zhu, J.; Chen, C.; Chen, Y.W.; Dertel, J.K.; Ashby, B.; Liu-Chen, L.Y.
CC Biochem. J. 295, 628-633, 1993
CC A/Title: Molecular cloning and expression of a rat kappa opioid receptor.
CC A/Reference number: S39015
CC A/Accession: S39015
CC A/Molecule type: mRNA
CC A/Residues: 1-344, 1, 346-380 <LTS>
CC R/Meng, F.; Xie, G.
CC Proc. Natl. Acad. Sci. U.S.A. 90, 9954-9958, 1993
CC A/Title: Cloning and pharmacological characterization of a rat kappa opioid recept
CC A/Reference number: A48789; M01D:94052210
CC A/Accession: A48789
CC A/Status: preliminary; translated from GB/EMBL/DDJ
CC A/Molecule type: mRNA
CC A/Residues: 1-380 <RES>
CC A/Cross-references: EMBL:U00442; NID:G403486; PID:G403487
CC C/Keywords: G protein-coupled receptor; transmembrane protein
SQ SEQUENCE 380 AA; 42688 MW; 808499 CN;

Query Match 95.6%; Score 2132; DB 2; Length 380;
Best Local Similarity 92.5%; Pred. No. 2,43e-185;
Matches 273; Conservative 13; Mismatches 8; Indels 1; Gaps 1;

Db 87 YTKMTATNIIYIFNLALADALVTTTTPQSAVYLMNSWPFQGVLCIKIVISIDYNNFTSI 146
|||||
QY 1 YTKMTATNIIYIFNLALADALVTTTTPQSAVYLMNSWPFQGVLCIKIVISIDYNNFTSI 60
|||||
Db 147 FLLTMASVDRIYAVCHPVPKALDFRPLKAKIINICIMILASSVGISAIVLGSTKREVD 206
|||||
QY 61 FLLTMASVDRIYAVCHPVPKALDFRPLKAKIINICIMILASSVGISAIVLGSTKREVD 120
|||||
Db 207 VIECSLOEPDDERYSWMDLPMKICVFAFVAPVLLITVYCYTMTIRLKSVRLLSGSREXD 266
|||||
QY 121 VIECSLOEPDDERYSWMDLPMKICVFAFVAPVLLITVYCYTMTIRLKSVRLLSGSREXD 180
|||||
Db 267 RNLRRTIKLVVAVAFIICWTPPIHFIILVEALGSTSHSTAALSSYFCIALGYTNSLN 326
|||||
QY 181 XNLRRTIKLVVAVAFIICWTPPIHFIILVEALGSTSHSTAALSSYFCIALGYTNSLN 240
|||||
Db 327 PVLVAFIDENFRKCRDFCFPIKMEROSTNRVNTVODPASMVDGSM-NKPV 380
|||||
QY 241 PVLVAFIDENFRKCRDFCFPIKMEROSTNRVNTVODPASMVDGSM-NKPV 295
|||||

RESULT 6
ID JC2434 STANDARD; PRT; 380 AA.
XX xxxxxx
AC xxxxxx
DT 01-JAN-1900
XX
DE A/Accession: JC2434.
XX
XX A/Accession: JC2434
CC A/Molecule type: mRNA
CC A/Residues: 1-380 <NLS>
CC A/Cross-references: DDBJ:D31663
CC C/Genetics:
CC A/Map position: 1A2-3
CC A/Introns: 86/2; 204/1
CC C/Keywords: Receptor
SQ SEQUENCE 380 AA; 42630 MW; 803251 CN;

Query Match 94.8%; Score 2114; DB 2; Length 380;
Best Local Similarity 92.5%; Pred. No. 1.25e-183;
Matches 273; Conservative 13; Mismatches 8; Indels 1; Gaps 1;

Db 87 YTKMTATNIIYIFNLALADALVTTTTPQSAVYLMNSWPFQGVLCIKIVISIDYNNFTSI 146
|||||
QY 1 YTKMTATNIIYIFNLALADALVTTTTPQSAVYLMNSWPFQGVLCIKIVISIDYNNFTSI 60
|||||
Db 147 FLLTMASVDRIYAVCHPVPKALDFRPLKAKIINICIMILASSVGISAIVLGSTKREVD 206
|||||
QY 61 FLLTMASVDRIYAVCHPVPKALDFRPLKAKIINICIMILASSVGISAIVLGSTKREVD 120
|||||
Db 207 VIECSLOEPDDERYSWMDLPMKICVFAFVAPVLLITVYCYTMTIRLKSVRLLSGSREXD 266
|||||
QY 121 VIECSLOEPDDERYSWMDLPMKICVFAFVAPVLLITVYCYTMTIRLKSVRLLSGSREXD 180
|||||
Db 267 RNLRRTIKLVVAVAFIICWTPPIHFIILVEALGSTSHSTAALSSYFCIALGYTNSLN 326
|||||
QY 181 XNLRRTIKLVVAVAFIICWTPPIHFIILVEALGSTSHSTAALSSYFCIALGYTNSLN 240
|||||
Db 327 PVLVAFIDENFRKCRDFCFPIKMEROSTNRVNTVODPASMVDGSM-NKPV 380
|||||
QY 241 PVLVAFIDENFRKCRDFCFPIKMEROSTNRVNTVODPASMVDGSM-NKPV 295
|||||


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DE A:Status: nucleic acid sequence not shown; translation not shown.
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CC A:Status: nucleic acid sequence not shown; translation not shown
CC A:Molecule type: mRNA
CC A:Residues: 1-398 <ROS>
CC A:Cross-references: EMBL:U26915; NID:g1055230; PID:g1055231
CC A:Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1
CC C:Genetics:
CC A:Gene: MOR-1
CC A:Introns: 95/2; 213/1; 386/3
CC C:Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; trans
SEQUENCE 398 AA; 44421 MW; 862989 CN;

Query Match 68.4%; Score 1524; DB 2; Length 398;
Best Local Similarity 65.7%; Pred. No. 1.15e-127;
Matches 190; Conservative 47; Mismatches 48; Indels 4; Gaps 4;

Db 96 YTKMTATNITVFNLADALATSTLPFQSVNYIMGTWPFNGTLCKIVISIDYNNFTSI 155
|||
1 YTKMTATNITVFNLADALATSTLPFQSVNYIMGTWPFNGTLCKIVISIDYNNFTSI 60
|||
Db 156 FLLCMASVDRIYAVCHPYKALDFRTPRNKAIYVNCWILSSAIGLPVEMATTKYRQG-S 214
|||
61 FLLCMASVDRIYAVCHPYKALDFRTPRNKAIYVNCWILSSAIGLPVEMATTKYRQGD 120
|||
Db 215 -IDCITLTSHPFW-YWENLTKICVFIFAFIMPVLLITCYGIMILRLKSVRLSGSKED 272
|||
121 VEECLIQPDDYSWMDLFMKICVFIFAFIPVLLITCYGIMILRLKSVRLSGSKED 180
|||
Db 273 RNLRRTITRVLYVAVFVWCWPIHIIYVIRKALITIPETFEQVSWHCIALGTNSCIN 332
|||
181 XNLRRTITRVLYVAVFVWCWPIHIIYVIRKALITIPETFEQVSWHCIALGTNSCIN 240
|||
Db 333 PYLYAFDENEFKRCFRFCIPTSNIEQNSRIRONTREHSTIANVVD 381
|||
241 PYLYAFDENEFKRCFRFCIPTSNIEQNSRIRONTREHSTIANVVD 288
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RESULT 3 STANDARD; PRT; 400 AA.
ID I56553
AC xxxxxx
DT 01-JAN-1900
DE A:Accession: I56553.
XX
CC A:Accession: I56553
CC A:Status: nucleic acid sequence not shown; translated from GB/EMBL/DBJ
CC A:Molecule type: mRNA
CC A:Residues: 1-400 <RES>
CC A:Cross-references: GB:J28301; NID:g459831; PID:g459832
CC R:Wang, J.B.; Johnson, P.S.; Persico, A.M.; Hawkins, A.L.; Griffin, C.A.; Uhl, G.F
submitted to GenBank, August 1994
CC A:Reference number: A38991
CC A:Accession: A38991
CC A:Status: translated from GB/EMBL/DBJ
CC A:Residues: 1-50, 'N', '52-233, 'V', '235-400 <MAN>
CC A:Cross-references: GB:J25119; PID:g452073
CC R:Wang, J.B.; Johnson, P.S.; Persico, A.M.; Hawkins, A.L.; Griffin, C.A.; Uhl, G.F
EMBL Lett. 338, 217-222, 1994
CC A:Title: Human mu opiate receptor. cDNA and genomic clones, pharmacologic characte
CC A:Reference number: S41075
CC A:Accession: S41075
CC A:Status: nucleic acid sequence not shown
CC A:Molecule type: mRNA
CC A:Residues: 1-50, 'N', '52-400 <MA>
CC R:Bare, L.A.; Manson, E.; Yang, D.
CC EMBL Lett. 354, 213-216, 1994
CC A:Title: Expression of two variants of the human mu opioid receptor mRNA in SK-N-S
CC A:Reference number: S51215
CC A:Accession: S51215

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CC A:Status: preliminary
CC A:Molecule type: mRNA
CC A:Residues: 387-400 <BAR>
CC C:Genetics:
CC A:Gene: GDB:OPRML
CC A:Cross-references: GDB:137216; OMIM:600018
CC A:Map position: 6q24-q25
CC C:Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein
CC F:73-96/Domain: transmembrane #status predicted <TM1>
CC F:107-132/Domain: transmembrane #status predicted <TM2>
CC F:144-165/Domain: transmembrane #status predicted <TM3>
CC F:188-208/Domain: transmembrane #status predicted <TM4>
CC F:236-257/Domain: transmembrane #status predicted <TM5>
CC F:283-304/Domain: transmembrane #status predicted <TM6>
CC F:323-342/Domain: transmembrane #status predicted <TM7>
CC F:9,12,33,40,48/Binding site: carbohydrate (Asn) (covalent) #status predicted
SEQUENCE 400 AA; 44779 MW; 873826 CN;

Query Match 68.3%; Score 1522; DB 2; Length 400;
Best Local Similarity 67.1%; Pred. No. 1.78e-127;
Matches 188; Conservative 43; Mismatches 46; Indels 3; Gaps 3;

Db 98 YTKMTATNITVFNLADALATSTLPFQSVNYIMGTWPFNGTLCKIVISIDYNNFTSI 157
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1 YTKMTATNITVFNLADALATSTLPFQSVNYIMGTWPFNGTLCKIVISIDYNNFTSI 60
|||
Db 158 FLLCMASVDRIYAVCHPYKALDFRTPRNKAIYVNCWILSSAIGLPVEMATTKYRQG-S 216
|||
61 FLLCMASVDRIYAVCHPYKALDFRTPRNKAIYVNCWILSSAIGLPVEMATTKYRQGD 120
|||
Db 217 -IDCITLTSHPFW-YWENLTKICVFIFAFIMPVLLITCYGIMILRLKSVRLSGSKED 274
|||
121 VEECLIQPDDYSWMDLFMKICVFIFAFIPVLLITCYGIMILRLKSVRLSGSKED 180
|||
Db 275 RNLRRTITRVLYVAVFVWCWPIHIIYVIRKALITIPETFEQVSWHCIALGTNSCIN 334
|||
181 XNLRRTITRVLYVAVFVWCWPIHIIYVIRKALITIPETFEQVSWHCIALGTNSCIN 240
|||
Db 335 PYLYAFDENEFKRCFRFCIPTSNIEQNSRIRONTREHSTIANVVD 374
|||
241 PYLYAFDENEFKRCFRFCIPTSNIEQNSRIRONTREHSTIANVVD 280
|||

RESULT 9 STANDARD; PRT; 392 AA.
ID S65693
AC xxxxxx
DT 01-JAN-1900
DE TOIG of: S65693 check: 6977 from: 1 to: 392.
XX
CC TOIG of: S65693 check: 6977 from: 1 to: 392
CC
CC >P1:565693
CC Opioid receptor mu variant MOR1A - human
CC C:Species: Homo sapiens (man)
CC C:Date: 12-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 10-Sep-1997
CC C:Accession: S65693; S51216
CC R:Bare, L.A.; Manson, E.; Yang, D.
submitted to the EMBL Data Library, July 1994
CC A:Description: Expression of two variants of the human mu opioid receptor mRNA
CC A:Reference number: S65693
CC A:Accession: S65693
CC A:Molecule type: mRNA
CC A:Residues: 1-392 <BAR>
CC A:Cross-references: EMBL:U2569; NID:g607911; PID:g607912
CC R:Bare, L.A.; Manson, E.; Yang, D.
CC EMBL Lett. 354, 213-216, 1994
CC A:Title: Expression of two variants of the human mu opioid receptor mRNA in SK-
CC A:Reference number: S51216
CC A:Accession: S51216
CC A:Molecule type: mRNA

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CC A:Residues: 387-392 <RAW>
CC SEQUENCE 392 AA; 43939 MW; 850481 CN;
Query Match 68.2%; Score 1520; DB 2; Length 392;
Best Local Similarity 67.1%; Pred. No. 2,74e-127;
Matches 188; Conservative 43; Mismatches 46; Indels 3; Gaps 3;
Db 98 YTKKATATNITFIENLADALATSTLPQSVNYLMGTPEFTILCKIYISIDYNNMFTSI 157
1 YTKKATATNITFIENLADALATSTLPQSVNYLMGTPEFTILCKIYISIDYNNMFTSI 60
158 FTLCMSVDRTIACVHPKALDFRTPRNAKIIVNCWILSSAIGLPMVAFMTKYRQC-S 216
61 FTLCMSVDRTIACVHPKALDFRTPRNAKIIVNCWILSSAIGLPMVAFMTKYRQC-S 120
217 -IDCLTFRSHPTW-YWENMLKCVFIKVFIFAFIMFVLIITVCYGMILRLKSVRLSGSKREKD 274
121 VIECLOPFPDDYSWMDLFKXICVFIKVFIFAFIVLIIIVCYITMLIRLXVRLSSRKED 180
275 RNLRRITKVLVAVVAVFIVCWTPPIHIVYIKALVITPITQTQVSMHRCIALGYNSCIN 334
181 XNLRRITLVLVAVVAVFIVCWTPPIHIVYIKALVITPITQTQVSMHRCIALGYNSCIN 240
335 PYLVAFIDENKRCRRCRCPPISSNIEQNSRIVQNTREID 374
241 PILVAFIDENKRCRRCRCPPISSNIEQNSRIVQNTREID 280
RESULT 10
ID I56517 STANDARD; PRT; 398 AA.
XX xxxxxx
DT 01-JAN-1900
XX
DE TOIG of: I56517 check: 8374 from: 1 to: 398.
XX
CC TOIG of: I56517 check: 8374 from: 1 to: 398
CC
CC >P1:I56517
CC mu-opioid receptor - rat
CC C:Species: Rattus norvegicus (Norway rat)
CC C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 13-Mar-1997
CC C:Accession: I56517; I57951; A49680; I52314; S34593; A48799; I58154
CC R:Butzow, J.R.; Zhang, G.; Bouvier, C.; Saez, C.; Ronnekleiv, O.K.; Kelly, M.J.; G
CC J. Neurochem. 64, 14-24, 1995
CC A:Title: Characterization and distribution of a cloned rat mu-opioid receptor.
CC A:Reference number: I56517; MUID:95096825
CC A:Accession: I56517
CC A:Status: preliminary; translated from GB/EMBL/DBJ
CC A:Molecule type: mRNA
CC A:Residues: 1-398 <RES>
CC A:Cross-references: EMBL:J02083; NID:g403573; PID:g403574
CC R:Chen, Y.; Mestek, A.; Liu, J.; Hurley, J.A.; Yu, L.
CC Mol. Pharmacol. 44, 8-12, 1993
CC A:Title: Molecular cloning and functional expression of a mu-opioid receptor from
CC A:Reference number: I57951; MUID:93341493
CC A:Accession: I57951
CC A:Status: preliminary; translated from GB/EMBL/DBJ
CC A:Molecule type: mRNA
CC A:Residues: 1-398 <RES>
CC A:Cross-references: GB:LI3069; NID:g348250; PID:g348251
CC R:Leppier, C.M.; Hulmes, J.D.; Wang, J.B.; Johnson, B.; Corbett, M.; Luthin, D.R.;
CC J. Biol. Chem. 268, 26447-26451, 1993
CC A:Title: Purification and partial amino acid sequence of a mu opioid receptor from
CC A:Reference number: A49680; MUID:94075533
CC A:Accession: A49680
CC A:Status: preliminary
CC A:Molecule type: protein
CC A:Residues: 272-291 <BBP>
CC A:Experimental source: brain membranes
CC A:Note: sequence extracted from NCBI backbone (NCBIP:140841)
CC R:Seidl, M.; Roy, S.; Ramakrishnan, S.; Elde, R.; Ich, H.H.

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CC Biochem. Biophys. Res. Commun. 209, 563-574, 1995
CC A:Title: Complementary DNA cloning of a mu-opioid receptor from rat peritoneal
CC A:Reference number: I52314; MUID:95251654
CC A:Accession: I52314
CC A:Status: preliminary
CC A:Molecule type: mRNA
CC A:Residues: 101-340 <SED>
CC A:Cross-references: GB:S77863; NID:g9980526
CC R:Fukuda, K.; Kato, S.; Mori, K.; Nishi, M.; Takeshima, H.
CC FEBS Lett. 327, 311-314, 1993
CC A:Title: Primary structures and expression from cDNAs of rat opioid receptor de
CC A:Reference number: S34592
CC A:Accession: S34593
CC A:Molecule type: mRNA
CC A:Residues: 1-244, 'V', 246-398 <FRK>
CC R:Wang, J.
CC Proc. Natl. Acad. Sci. U.S.A. 90, 10230-10234, 1993
CC A:Title: Mu opiate receptor: cDNA cloning and expression.
CC A:Reference number: A48799; MUID:94052137
CC A:Accession: A48799
CC A:Status: preliminary; translated from GB/EMBL/DBJ
CC A:Molecule type: mRNA
CC A:Residues: 1-244, 'V', 246-398 <RAW>
CC A:Residues: 1-244, 'V', 246-398 <RAW>
CC A:Cross-references: GB:U20684; NID:g409149; PID:g409150
CC R:Thompson, R.C.; Mansour, A.; Akil, H.; Watson, S.J.
CC Neuron 11, 903-913, 1993
CC A:Title: Cloning and pharmacological characterization of a rat mu opioid recept
CC A:Reference number: I58154; MUID:94059560
CC A:Accession: I58154
CC A:Status: preliminary; translated from GB/EMBL/DBJ
CC A:Molecule type: mRNA
CC A:Residues: 1-244, 'V', 246-398 <THO>
CC A:Cross-references: GB:L22455; NID:g437671; PID:g437672
CC C:Keywords: G protein-coupled receptor; transmembrane protein
CC A:Gene: MOR1
CC C:Keywords: G protein-coupled receptor; transmembrane protein
CC SEQUENCE 398 AA; 44508 MW; 870781 CN;
Query Match 68.2%; Score 1520; DB 2; Length 398;
Best Local Similarity 65.7%; Pred. No. 2,74e-127;
Matches 190; Conservative 46; Mismatches 49; Indels 4; Gaps 4;
Db 96 YTKKATATNITFIENLADALATSTLPQSVNYLMGTPEFTILCKIYISIDYNNMFTSI 155
1 YTKKATATNITFIENLADALATSTLPQSVNYLMGTPEFTILCKIYISIDYNNMFTSI 60
156 FTLCMSVDRTIACVHPKALDFRTPRNAKIIVNCWILSSAIGLPMVAFMTKYRQC-S 214
61 FTLCMSVDRTIACVHPKALDFRTPRNAKIIVNCWILSSAIGLPMVAFMTKYRQC-S 120
215 -IDCLTFRSHPTW-YWENMLKCVFIKVFIFAFIMFVLIITVCYGMILRLKSVRLSGSKREKD 272
121 VIECLOPFPDDYSWMDLFKXICVFIKVFIFAFIVLIIIVCYITMLIRLXVRLSSRKED 180
275 RNLRRITKVLVAVVAVFIVCWTPPIHIVYIKALVITPITQTQVSMHRCIALGYNSCIN 332
181 XNLRRITLVLVAVVAVFIVCWTPPIHIVYIKALVITPITQTQVSMHRCIALGYNSCIN 240
335 PYLVAFIDENKRCRRCRCPPISSNIEQNSRIVQNTREID 381
241 PILVAFIDENKRCRRCRCPPISSNIEQNSRIVQNTREID 288
RESULT 11
ID I56504 STANDARD; PRT; 398 AA.
XX xxxxxx
XX
DT 01-JAN-1900
XX
DE TOIG of: I56504 check: 8604 from: 1 to: 398.

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RESULT 14
ID B48227 STANDARD: PRT; 372 AA.
AC xxxxxx
XX
XX 01-JAN-1900
DE TOIG of: b48227 check: 3372 from: 1 to: 372.
XX
XX TOIG of: b48227 check: 3372 from: 1 to: 372
CC
CC >P1:B48227
CC delta opioid receptor 1 - mouse
CC C:Species: Mus musculus (house mouse)
CC C:Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 10-Sep-1997
CC C:Accession: B48227; S37807; A48685; S36745
CC R:Yasuda, K.; Raynor, K.; Kong, H.; Breder, C.D.; Takeda, J.; Reisine, T.; Bell, G
CC Proc. Natl. Acad. Sci. U.S.A. 90, 6736-6740, 1993
CC A:Title: Cloning and functional comparison of kappa and delta opioid receptors fro
CC A:Reference number: A48227
CC A:Accession: B48227
CC A:Status: preliminary
CC A:Molecule type: mRNA
CC A:Residues: 1-372 <XAS>
CC A:Cross-references: GB:LI1064; NID:9348246; PID:9348247
CC R:Kieffer, B.L.; Befort, K.; Gaveriaux-Ruff, C.; Hirth, C.G.
CC submitted to the EMBL Data Library, February 1993
CC A:Reference number: S37807
CC A:Accession: S37807
CC A:Status: preliminary
CC A:Molecule type: mRNA
CC A:Residues: 1-372 <KIE>
CC A:Cross-references: EMBL:506322; NID:9192942; PID:9192943
CC R:Bodega, T.; Chin, H.; Jung, H.H.; Kozak, C.A.; Klee, W.A.
CC Proc. Natl. Acad. Sci. U.S.A. 90, 9305-9309, 1993
CC A:Title: Regional expression and chromosomal localization of the delta opiate rece
CC A:Reference number: A48685; MID:94022364
CC A:Accession: A48685
CC A:Status: preliminary
CC A:Molecule type: mRNA
CC A:Residues: 8-372 <BZD>
CC A:Experimental source: NG108-15 hybrid cells
CC A:Note: sequence extracted from NCB1 backbone (NCBIN:138618, NCBIR:138619)
CC R:Kieffer, B.L.; Befort, K.; Gaveriaux-Ruff, C.; Hirth, C.G.
CC Proc. Natl. Acad. Sci. U.S.A. 89, 12048-12052, 1992
CC A:Title: The delta-opioid receptor: isolation of a cDNA by expression cloning and
CC A:Reference number: S36745
CC A:Accession: S36745
CC A:Molecule type: mRNA
CC A:Residues: 1-189, N', 191, GMVQ', 207-208, 'ACSSSPVQLV', 210-372 <KIW>
CC A:Cross-references: EMBL:L06322
CC C:Keywords: brain; G protein-coupled receptor; glycoprotein; phosphoprotein; trans
SQ SEQUENCE 372 AA; 40561 MW; 727422 CN;

Query Match 65.0%; Score 1448; DB 2; Length 372;
Best Local Similarity 68.8%; Pred. No. 1.73e-120;
Matches 179; Conservative 44; Mismatches 33; Indels 4; Gaps 4;

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DB 314 NEVIAFLDENKRCRQLC 333
OY 240 NPIIVAFDENKRCRQFDFC 259

RESULT 15
ID I56520 STANDARD: PRT; 367 AA.
AC xxxxxx
XX
XX 01-JAN-1900
DE A:Accession: I52654.
XX
XX A:Accession: I52654
CC A:Status: preliminary; translated from GB/EMBL/DBJ
CC A:Molecule type: mRNA
CC A:Residues: 1-367 <RE2>
CC A:Cross-references: GB:LI29419; NID:9510718; PID:9510719
CC C:Keywords: G protein-coupled receptor; transmembrane protein
SQ SEQUENCE 367 AA; 40523 MW; 720655 CN;

Query Match 60.3%; Score 1345; DB 2; Length 367;
Best Local Similarity 62.1%; Pred. No. 8.99e-111;
Matches 174; Conservative 46; Mismatches 55; Indels 5; Gaps 5;

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Search completed: Thu Apr 16 13:39:47 1998
Job time : 55 secs.

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(TM)

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Msrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Thu Apr 16 13:38:02 1998; Msrch time 8.87 Seconds
Tabular output not generated. 833.772 Million cell updates/sec

Title: >US-08-292-694A-12
Description: (1-295) from US08292694A.pep
Perfect Score: 2229
Sequence: 1 YTKMKATATNIYIFNLALADA.....NTVDPAYLREIDGMNRPV 295

Scoring table: PAM 150
Gap 11

Searched: 69112 seqs, 25083644 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot35
1:swiss1

Statistics: Mean 48.402; Variance 96.886; scale 0.500

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	2192	98.3	380	1	OPRK_HUMAN KAPPA-TYPE OPIOID RECE	0.00e+00
2	2157	96.8	380	1	OPRK_CAVPO KAPPA-TYPE OPIOID RECE	0.00e+00
3	2136	95.8	380	1	OPRK_MOUSE KAPPA-TYPE OPIOID RECE	0.00e+00
4	2132	95.6	380	1	OPRK_RAT KAPPA-TYPE OPIOID RECE	0.00e+00
5	1524	68.4	388	1	OPRK_MOUSE MU-TYPE OPIOID RECEPTO	2.16e-282
6	1522	68.3	358	1	OPRK_RAT MU-TYPE OPIOID RECEPTO	2.16e-282
7	1520	68.2	400	1	OPRM_HUMAN MU-TYPE OPIOID RECEPTO	1.50e-281
8	1518	68.1	401	1	OPRM_PIG MU-TYPE OPIOID RECEPTO	3.96e-281
9	1458	65.4	372	1	DELTA-TYPE OPIOID RECE	1.62e-288
10	1452	65.1	372	1	OPRD_HUMAN DELTA-TYPE OPIOID RECE	2.95e-287
11	1448	65.0	372	1	OPRD_MOUSE DELTA-TYPE OPIOID RECE	2.04e-286
12	1345	60.3	367	1	OPRX_RAT NOCICEPTIN RECEPTOR (O	8.24e-245
13	1343	60.3	367	1	OPRX_MOUSE NOCICEPTIN RECEPTOR (O	2.16e-244
14	1331	59.7	370	1	OPRX_HUMAN NOCICEPTIN RECEPTOR (O	7.05e-242
15	1327	59.5	370	1	OPRX_PIG NOCICEPTIN RECEPTOR (O	4.85e-241
16	1319	59.2	370	1	OPRX_CAVPO NOCICEPTIN RECEPTOR (O	2.30e-239
17	1240	55.6	228	1	OPRD_PIG DELTA-TYPE OPIOID RECE	7.59e-223
18	830	37.2	381	1	SSRL_RAT SOMATOSTATIN RECEPTOR	6.35e-128
19	830	37.2	391	1	SSRL_HUMAN SOMATOSTATIN RECEPTOR	6.35e-128
20	830	37.2	391	1	SSRL_MOUSE SOMATOSTATIN RECEPTOR	6.35e-128
21	822	36.9	384	1	SSR4_RAT SOMATOSTATIN RECEPTOR	2.76e-136
22	816	36.6	388	1	SSR4_HUMAN SOMATOSTATIN RECEPTOR	4.67e-135
23	810	36.3	384	1	SSR4_MOUSE SOMATOSTATIN RECEPTOR	7.89e-134

24	789	35.4	368	1	SSR2_BOVIN SOMATOSTATIN RECEPTOR	1.55e-129
25	789	35.4	369	1	SSR2_PIG SOMATOSTATIN RECEPTOR	1.55e-129
26	788	35.4	369	1	SSR2_RAT SOMATOSTATIN RECEPTOR	2.48e-129
27	785	35.2	369	1	SSR2_MOUSE SOMATOSTATIN RECEPTOR	1.02e-128
28	780	35.0	369	1	SSR2_HUMAN SOMATOSTATIN RECEPTOR	1.06e-127
29	736	33.0	333	1	SPR8_HUMAN PROBABLE G PROTEIN-COU	9.79e-119
30	689	30.9	363	1	SSR5_MOUSE SOMATOSTATIN RECEPTOR	3.36e-109
31	683	30.6	418	1	SSR3_HUMAN SOMATOSTATIN RECEPTOR	5.49e-108
32	676	30.3	363	1	SSR5_HUMAN SOMATOSTATIN RECEPTOR	1.43e-106
33	668	30.0	363	1	SSR5_RAT SOMATOSTATIN RECEPTOR	5.91e-105
34	661	29.7	328	1	SPR7_HUMAN PROBABLE G PROTEIN-COU	1.53e-103
35	601	27.0	428	1	SSR3_RAT SOMATOSTATIN RECEPTOR	1.77e-91
36	592	26.9	428	1	SSR3_MOUSE SOMATOSTATIN RECEPTOR	4.45e-91
37	545	24.5	349	1	GALR_HUMAN GALANIN RECEPTOR (GAL1	2.61e-80
38	525	23.6	346	1	GALR_RAT GALANIN RECEPTOR (GAL1	2.41e-76
39	510	22.9	402	1	GPRL_HUMAN PROBABLE G PROTEIN-COU	2.21e-73
40	496	22.3	355	1	CKRL_HUMAN C-C CHEMOKINE RECEPTOR	1.27e-70
41	496	22.3	359	1	AG2R_CANPA TYPE-1 ANGIOTENSIN II	1.27e-70
42	490	22.0	363	1	AG22_MOUSE TYPE-2 ANGIOTENSIN II	1.92e-68
43	488	21.9	363	1	AG22_HUMAN TYPE-1A ANGIOTENSIN II	4.75e-68
44	486	21.8	359	1	AG2R_HUMAN TYPE-2 ANGIOTENSIN II	1.17e-68
45	486	21.8	363	1	AG22_RAT TYPE-2 ANGIOTENSIN II	1.17e-68

ALIGNMENTS

RESULT ID	1	OPRK_HUMAN	STANDARD:	PRT:	380 AA.
AC	P41145:				
AD	01-FEB-1995 (REL. 31, CREATED)				
DE	01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)				
DI	01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)				
DE	KAPPA-TYPE OPIOID RECEPTOR (KOR-1).				
GN	OPRK1 OR OPRK.				
OS	HOMO SAPIENS (HUMAN).				
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA;				
OC	EUTHERIA; PRIMATES.				
OC	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=PLACENTA;				
RX	MEDLINE: 94338360.				
RA	MANSION E., BARE L.A., YANG D.;				
RL	BIOCHEM. BIOPHYS. RES. COMMON. 202:1431-1437(1994).				
RL	[2]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=PLACENTA;				
RX	MEDLINE: 95350200.				
RA	SIMONIN F., GAVERIAUS-RUPF C., BEFORT K., LANNES B., MICHELETTI G.,				
RL	WATTEL M.-G., CHARON G., BLOCH B., KIEFFER B.;				
RL	PROC. NATL. ACAD. SCI. U.S.A. 92:7006-7010(1995).				
RL	[3]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=BRAIN;				
RX	MEDLINE: 95174504.				
RA	ZHU J., CHEN C., XUE J.C., KUNAPUTTI S., DERTIEL J.K., LIU-CHEN L.-Y.;				
RL	LIFE SCI. 56:201-207(1995).				
CC	-1- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM				
CC	ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. RECEPTOR				
CC	FOR DENDROPHINS. MAY PLAY A ROLE IN AROUSAL AND REGULATION OF				
CC	AUTONOMIC AND NEUROENDOCRINE FUNCTIONS.				
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.				
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.				
DR	EMBL: U11053; G532060; -				
DR	EMBL: U17298; G596070; -				
DR	EMBL: L37362; G722618; -				
DR	PIR: J02338; J02338.				
DR	MIN: 165196; -				
DR	PROSITE: PS00237; G.PROTEIN.RECEPTOR. 1.				
KW	G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;				
KW	PHOSPHORYLATION; LIPIDPROTEIN; PALMITATE.				
FT	DOMAIN 1 58				
FT	TRANSMEM 59 85				
FT	DOMAIN 1 (POTENTIAL)				
FT	CYTOPLASMIC (POTENTIAL).				


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FT TRANSMEM 96 117 2 (POTENTIAL).
FT DOMAIN 132 132 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 138 154 3 (POTENTIAL).
FT TRANSMEM 155 173 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 174 196 4 (POTENTIAL).
FT TRANSMEM 197 222 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 223 247 5 (POTENTIAL).
FT TRANSMEM 248 275 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 276 299 6 (POTENTIAL).
FT TRANSMEM 300 311 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 312 333 7 (POTENTIAL).
FT DOMAIN 334 380 CYTOPLASMIC (POTENTIAL).
FT DISULFID 131 210 BY SIMILARITY.
FT LIPID 345 345 PALMITATE (POTENTIAL).
FT CARBOHYD 25 25 POTENTIAL.
FT CONFLICT 39 39 E -> D (IN REF. 2 AND 3).
SQ SEQUENCE 380 AA: 42659 MW; 1980629E CRC32;

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Query Match 98.3%; Score 2192; DB 1; Length 380;
 Best Local Similarity 97.6%; Pred. No. 0.00e+00;
 Matches 288; Conservative 1; Mismatches 5; Indels 1; Gaps 1;

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Db 87 YTKMTATNIYIFNLADALVTTMPFQSTVYLMNSWFGVLCIKIVSIDYNNKFTSI 146
1 YTKMTATNIYIFNLADALVTTMPFQSTVYLMNSWFGVLCIKIVSIDYNNKFTSI 60
147 FLLTMSVDRYAVCHPKALDFRPLKAKIINICIMWISSVGSATVLSGSKYREVD 206
61 FLLTMSVDRYAVCHPKALDFRPLKAKIINICIMWISSVGSATVLSGSKYREVD 120
207 VTECSLOFPDDYSWMDLFMKICVFVFAVLPVLIIVCYTMIIRKSVRLSSREXD 266
121 VTECSLOFPDDYSWMDLFMKICVFVFAVLPVLIIVCYTMIIRKSVRLSSREXD 180
267 RNLKRITRLVLYVAVFYVCWTPHIFILVEALGSTSHSTAALSYTCIALGYTNSSLN 326
181 XNLKRITRLVLYVAVFYVCWTPHIFILVEALGSTSHSTAALSYTCIALGYTNSSLN 240
327 PLTYAFLEENFKRCRDFCFPLKMKMERKSTSRVNTVQDPAYLREIDGMANKPV 380
241 PLTYAFLEENFKRCRDFCFPLKMKMERKSTSRVNTVQDPAYLREIDGMANKPV 295

```

RESULT 2 STANDARD; PRT: 380 AA.

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ID OPK CAVPO AC P41144;
AC P41144;
DT 01-FEB-1995 (REL. 31, CREATED)
DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE KAPPA-TYPE OPIOID RECEPTOR (KOR-1).
GN OPRK1.
OS CAVIA PORCELLUS (GUINEA PIG).
OC EUDARTOIA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
CC [1]
CC SEQUENCE FROM N.A.
CC STRAIN-HARTLEY; TISSUE-BRAIN;
CC MEDLINE; 94224825.
RA XIE G.X., MENG F., MANSOUR A., THOMPSON R.C., HOVERSTEN M.T.,
RA GOLDSTEIN A., WATSON S.J., AKIL H.;
CC PROC. NATL. ACAD. SCI. U.S.A. 91:3779-3783(1994).
CC -1- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM
CC ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. RECEPTOR
CC FOR DYNORPHINS. MAY PLAY A ROLE IN AROUSAL AND REGULATION OF
CC AUTONOMIC AND NEUROENDOCRINE FUNCTIONS.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC EMBL: U04092; G476107; -.
DR GCRDB: GCR 0991; -.
DR PROSITE: PS00237; G-PROTEIN_RECEPTOR; 1.
DR G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
KW PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.

```

```

FT DOMAIN 1 58 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 59 85 1 (POTENTIAL).
FT TRANSMEM 86 95 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 96 117 2 (POTENTIAL).
FT TRANSMEM 118 132 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 133 154 3 (POTENTIAL).
FT TRANSMEM 155 173 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 174 196 4 (POTENTIAL).
FT TRANSMEM 197 222 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 223 247 5 (POTENTIAL).
FT TRANSMEM 248 275 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 276 299 6 (POTENTIAL).
FT TRANSMEM 300 311 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 312 333 7 (POTENTIAL).
FT DOMAIN 334 380 CYTOPLASMIC (POTENTIAL).
FT DISULFID 131 210 BY SIMILARITY.
FT LIPID 345 345 PALMITATE (POTENTIAL).
FT CARBOHYD 25 25 POTENTIAL.
SQ SEQUENCE 380 AA: 42736 MW; F9F34C4C CRC32;

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Query Match 96.8%; Score 2157; DB 1; Length 380;
 Best Local Similarity 94.6%; Pred. No. 0.00e+00;
 Matches 279; Conservative 10; Mismatches 5; Indels 1; Gaps 1;

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Db 87 YTKMTATNIYIFNLADALVTTMPFQSTVYLMNSWFGVLCIKIVSIDYNNKFTSI 146
1 YTKMTATNIYIFNLADALVTTMPFQSTVYLMNSWFGVLCIKIVSIDYNNKFTSI 60
147 FLLTMSVDRYAVCHPKALDFRPLKAKIINICIMWISSVGSATVLSGSKYREVD 206
61 FLLTMSVDRYAVCHPKALDFRPLKAKIINICIMWISSVGSATVLSGSKYREVD 120
207 IIECSLOFPDDYSWMDLFMKICVFVFAVLPVLIIVCYTMIIRKSVRLSSREXD 266
121 VTECSLOFPDDYSWMDLFMKICVFVFAVLPVLIIVCYTMIIRKSVRLSSREXD 180
267 RNLKRITRLVLYVAVFYVCWTPHIFILVEALGSTSHSTAALSYTCIALGYTNSSLN 326
181 XNLKRITRLVLYVAVFYVCWTPHIFILVEALGSTSHSTAALSYTCIALGYTNSSLN 240
327 PLTYAFLEENFKRCRDFCFPLKMKMERKSTSRVNTVQDPAYLREIDGMANKPV 380
241 PLTYAFLEENFKRCRDFCFPLKMKMERKSTSRVNTVQDPAYLREIDGMANKPV 295

```

RESULT 3 STANDARD; PRT: 380 AA.

```

ID OPK MOUSE AC P33534;
AC P33534;
DT 01-FEB-1994 (REL. 28, CREATED)
DT 01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE KAPPA-TYPE OPIOID RECEPTOR (KOR-1) (MSL-1).
GN OPRK1.
OS MUS MUSCULUS (MOUSE).
OC EUDARTOIA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
CC [1]
CC SEQUENCE FROM N.A.
CC TISSUE-BRAIN;
CC MEDLINE; 93342064.
RA YASUDA K., RAYNOR K., KONG H., BREDER C.D., TAKEDA J., REISINE T.,
RA BELL G.T.;
CC PROC. NATL. ACAD. SCI. U.S.A. 90:6736-6740(1993).
CC [2]
CC SEQUENCE FROM N.A.
CC MEDLINE; 95100967.
RA NISHI M., TAKESHIMA H., MORI M., NAKAGAWARA K.I., TAKEUCHI T.,
RA BIOCHEM. BIOPHYS. RES. COMMUN. 205:1353-1357(1994).
CC [3]
CC SEQUENCE FROM N.A.
CC MEDLINE; 95251663.
RA LIT H.C., LU S., AUGUSTIN L.B., FELSHEIM R.F., CHEN H.C.,

```


RA LOH H.H., WEI L.N.:
 RA BIOCHEM. BIOPHYS. RES. COMMUN. 209:639-647(1995).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 96084989.
 RA BELKOWSKI S.M., ZHU T., LIU-CHEN L.Y., EISENSTEIN T.K.,
 RA ADLER M.W., ROGERS T.J.,
 RL J. NEUROLIMMUNOL. 62:113-117(1995).
 CC -1- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM
 CC ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. RECEPTOR
 CC FOR DYNORPHINS. MAY PLAY A ROLE IN AROUSAL AND REGULATION OF
 CC AUTONOMIC AND NEUROENDOCRINE FUNCTIONS.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: BRAIN (NEOCORTEX, HIPPOCAMPUS, AMYGDALA,
 CC MEDIAL HYPOTHALAMUS, LOCUS CERULEUS, AND PARABRACHIAL
 CC NUCLEUS).
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DR EMBL; L11065; G348249; -.
 DR EMBL; D31665; G80876; -.
 DR EMBL; D31663; G80876; JOINED.
 DR EMBL; D31664; G80876; JOINED.
 DR EMBL; S77872; G998532; -.
 DR EMBL; S77868; G998532; JOINED.
 DR EMBL; S77869; G998532; JOINED.
 DR EMBL; S81111; E257489; -.
 DR PIR; A48227; A48227.
 DR GCRDB; GCR_0635; -.
 DR MGD; MGI:97439; OPRL.
 DR PROSITE; PS00237; G.PROTEIN.RECEPTOR.1.
 KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
 KW PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.
 FT DOMAIN 1 58
 FT TRANSMEM 59 85
 FT DOMAIN 86 95
 FT TRANSMEM 96 117
 FT DOMAIN 118 132
 FT TRANSMEM 133 154
 FT DOMAIN 155 173
 FT TRANSMEM 174 196
 FT DOMAIN 197 222
 FT TRANSMEM 223 247
 FT DOMAIN 248 275
 FT TRANSMEM 276 299
 FT DOMAIN 300 311
 FT TRANSMEM 312 333
 FT DOMAIN 334 380
 FT DISULFID 131 210
 FT LIPID 345 345
 FT CARBOHYD 25 25
 FT CARBOHYD 39 39
 FT CONFLICT 211 211
 FT CONFLICT 231 231
 SQ SEQUENCE 380 AA; 42652 MW; C6F33212 CRC32;
 Query Match 95.8%; Score 2136; DB 1; Length 380;
 Best Local Similarity 92.9%; Pred. No. 0.00e-00;
 Matches 274; Conservative 13; Mismatches 7; Indels 1; Gaps 1;

DB 327 PVLYAFIDENKRCFDFCPPIKRMEROSTNRVNTVQDPASRVDGGM-NKCV 380
 QY 241 PLVAFIDENKRCFDFCPPIKRMEROSTNRVNTVQDPASRVDGGM-NKCV 295
 RESULT 4
 ID OPRL_RAT STANDARD; PRT; 380 AA.
 AC P34975;
 DI 01-FEB-1994 (REL. 28, CREATED)
 DI 01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
 DI 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
 DE KAPPA-TYPE OPIOID RECEPTOR (XOR-1).
 GN OPRL1 OR KOR-D.
 OS RATTUS NORVEGICUS (RAT).
 OC EURKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN;
 RX MEDLINE; 94059008.
 RA CHEN Y., MESTER A., LIU J., YU L.,
 RL BIOCHEM. J. 295:625-628(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 93374033.
 RA MINAMI M., TOYA T., KATAO Y., MAEKAWA K., NAKAMURA S., ONOGI T.,
 RA KANEKO S., SATOH M.,
 RL FEBS LETT. 329:291-295(1993).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SPRAGUE-DAWLEY; TISSUE-BRAIN;
 RX MEDLINE; 94059009.
 RA LI S., ZHU J., CHEN C., CHEN Y.-W., DERIEL J.K., ASHEY B.,
 RL BIOCHEM. J. 295:629-633(1993).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SPRAGUE-DAWLEY; TISSUE-BRAIN;
 RX MEDLINE; 94052210.
 RA MENG F., XIE G.-X., THOMPSON R.C., MANSOUR A., GOLDSTEIN A.,
 RA WATSON S.J., AKIL H.,
 RL PROC. NATL. ACAD. SCI. U.S.A. 90:9954-9958(1993).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN-WISTAR; TISSUE-BRAIN;
 RX MEDLINE; 93360575.
 RA NISHT M., TAKESHIMA H., FUKUDA K., KATO S., MORI K.,
 RL FEBS LETT. 330:77-80(1993).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SPRAGUE-DAWLEY;
 RX MEDLINE; 95204422.
 RA YAKOVLEV A.G., KROEGER K.E., FADEN A.I.,
 RL J. BIOL. CHEM. 270:6421-6424(1995).
 CC -1- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM
 CC ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. RECEPTOR
 CC FOR DYNORPHINS. MAY PLAY A ROLE IN AROUSAL AND REGULATION OF
 CC AUTONOMIC AND NEUROENDOCRINE FUNCTIONS.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DR EMBL; L22001; G409237; -.
 DR EMBL; D16829; G404116; -.
 DR EMBL; L22536; G425189; -.
 DR EMBL; U00442; G403487; -.
 DR EMBL; D16534; G415310; -.
 DR EMBL; U17995; G727260; -.
 DR EMBL; U17993; G727260; JOINED.
 DR EMBL; U17994; G727260; JOINED.
 DR PIR; S36143; S36143.
 DR PIR; S38825; S38825.
 DR GCRDB; GCR_0636; -.
 DR GCRDB; GCR_0724; -.

DR GCRDB; GCR 0790; -
 DR GCRDB; GCR 0804; -
 DR PROSITE; PS00237; G-PROTEIN RECEPTOR; 1.
 KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
 KW PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.
 FT DOMAIN 1 58
 FT TRANSMEM 59 85
 FT DOMAIN 86 95
 FT TRANSMEM 96 117
 FT DOMAIN 118 132
 FT TRANSMEM 133 154
 FT DOMAIN 155 173
 FT TRANSMEM 174 196
 FT DOMAIN 197 222
 FT TRANSMEM 223 247
 FT DOMAIN 248 275
 FT TRANSMEM 276 299
 FT DOMAIN 300 311
 FT TRANSMEM 312 333
 FT DOMAIN 334 380
 FT DISULFID 131 210
 FT LIPID 345 345
 FT CARBOHYD 25 25
 FT CARBOHYD 39 39
 FT CONFLICT 42 42
 FT CONFLICT 345 345
 FT CONFLICT 345 345
 SQ SEQUENCE 380 AA; 42688 MW; EB58A46 CRC32;

Query Match 95.6%; Score 2132; DB 1; Length 380;
 Best Local Similarity 92.5%; Pred. No. 0.00e+00;
 Matches 273; Conservative 13; Mismatches 8; Indels 1; Gaps 1;

Db 87 YTKMTATNTYIFNLADALATVTTPQSNAYLMSNPFQVLYCKIYISIDYIMFTSI 146
 QY 1 YTKMTATNTYIFNLADALATVTTPQSNAYLMSNPFQVLYCKIYISIDYIMFTSI 60
 Db 147 FLLTMSYDRIYAVCHPKALDFRTPKAKINICIMVLASVGSIAVYLGSTKREVD 206
 QY 61 FLLTMSYDRIYAVCHPKALDFRTPKAKINICIMVLASVGSIAVYLGSTKREVD 120
 Db 207 VIECSLOPPDEYSKWDLFMKICVFNAPVPLIIIVCYLMLRLKSVLLSSRREK 266
 QY 121 VIECSLOPPDEYSKWDLFMKICVFNAPVPLIIIVCYLMLRLKSVLLSSRREK 180
 Db 267 RNLRRITLVVAVVAVFVLCWTPPIHIFLIVELGSHSTALSSYFICIALGTNNSSIN 326
 QY 181 RNLRRITLVVAVVAVFVLCWTPPIHIFLIVELGSHSTALSSYFICIALGTNNSSIN 240
 Db 327 PVLXAFIDENFKRCFRCFPIKMEROSTNRVNTVQDPASMDVQGM-NKPY 380
 QY 241 PVLXAFIDENFKRCFRCFPIKMEROSTNRVNTVQDPASMDVQGM-NKPY 295

RESULT 5
 ID OPRM_MOUSE STANDARD; PRG 398 AA.
 AC P42866; 060768;
 DT 01-NOV-1995 (REL. 32, CREATED)
 DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
 DE 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
 DE MU-TYPE OPTOID RECEPTOR (MOR-1).
 GN OPRM1 OR OPRM OR MOR.
 OS MUS MUSCULUS (MORSE).
 OC EUKAROTA; METAEOA;
 OC EUTHERIA; ROSENTIA.
 OC CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=LIVER;
 RX MEDLINE; 94377496.
 RA MIN B.H., AUGUSTIN L.B., ELSHEIM R.F., FUCHS J.A., LOH H.H.;
 RL PROC. NATL. ACAD. SCI. U.S.A. 91:9081-9085(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BRAIN;

RX MEDLINE; 95377399.
 RA ROSSI G.C., PAN Y.X., BROWN G.P., PASTERNAK G.W.;
 RL FEBS LETT. 369:192-196(1995).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BAB/C; TISSUE=BRAIN;
 RX MEDLINE; 95318184.
 RA KAUFMAN D.L., KEITH D.E., ANTON B., TIAN J., MANGENDZO K.,
 RA NEWMAN D., TRAN T., LEE D.S., WEN C., XIA Y., LUSIS A.J.,
 RA EVANS C.J.;
 RL J. BIOL. CHEM. 270:15877-15883(1995).
 CC -I- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM
 CC ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. RECEPTOR
 CC FOR BETA-ENDOPHIN.
 CC -I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -I- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DR EMBL; U10561; G565069; -;
 DR EMBL; U10558; G565069; JOINED.
 DR EMBL; U10559; G565069; JOINED.
 DR EMBL; U10560; G565069; JOINED.
 DR EMBL; U26915; G1055231; -;
 DR EMBL; U19380; G885865; -;
 DR MGD; MGI:97441; OPRM.
 DR PROSITE; PS00237; G-PROTEIN RECEPTOR; 1.
 KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
 KW PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.
 FT DOMAIN 1 64
 FT TRANSMEM 65 94
 FT DOMAIN 95 103
 FT TRANSMEM 104 121
 FT DOMAIN 122 143
 FT TRANSMEM 144 163
 FT DOMAIN 164 193
 FT TRANSMEM 194 209
 FT DOMAIN 210 234
 FT TRANSMEM 235 257
 FT DOMAIN 258 280
 FT TRANSMEM 281 303
 FT DOMAIN 304 311
 FT TRANSMEM 312 328
 FT DOMAIN 329 398
 FT DISULFID 140 217
 FT LIPID 351 351
 FT CARBOHYD 9 9
 FT CARBOHYD 31 31
 FT CARBOHYD 38 38
 FT CARBOHYD 46 46
 FT CONFLICT 22 22
 SQ SEQUENCE 398 AA; 44421 MW; C0211489 CRC32;

Query Match 68.4%; Score 1524; DB 1; Length 398;
 Best Local Similarity 65.7%; Pred. No. 2.16e-282;
 Matches 190; Conservative 47; Mismatches 48; Indels 4; Gaps 4;

Db 96 YTKMTATNTYIFNLADALATVTTPQSNAYLMSNPFQVLYCKIYISIDYIMFTSI 155
 QY 1 YTKMTATNTYIFNLADALATVTTPQSNAYLMSNPFQVLYCKIYISIDYIMFTSI 60
 Db 156 FLLTMSYDRIYAVCHPKALDFRTPKAKINICIMVLASVGSIAVYLGSTKREVD 272
 QY 121 VIECSLOPPDEYSKWDLFMKICVFNAPVPLIIIVCYLMLRLKSVLLSSRREK 180
 Db 273 RNLRRITLVVAVVAVFVLCWTPPIHIFLIVELGSHSTALSSYFICIALGTNNSSIN 332
 QY 181 RNLRRITLVVAVVAVFVLCWTPPIHIFLIVELGSHSTALSSYFICIALGTNNSSIN 240
 Db 333 PVLXAFIDENFKRCFRCFPIKMEROSTNRVNTVQDPASMDVQGM-NKPY 381
 QY 241 PVLXAFIDENFKRCFRCFPIKMEROSTNRVNTVQDPASMDVQGM-NKPY 288

RESULT 6
ID OPERA RAT STANDARD: PRT: 398 AA.
AC P3535; 064064; 062846;
DI 01-FEB-1994 (REL. 28, CREATED)
DT 01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
DE MU-TYPE OP2OID RECEPTOR (MOR-1) (OP2OID RECEPTOR B) (MORI).
OS EUPHORIA; RODENTIA.
OC EUPHORIA; RODENTIA.
RA EUPHORIA; RODENTIA.
RX MEDLINE; 93351652.
BA FUKUDA K., KATO S., MORI K., NISHI M., TAKESHIMA H.;
RE FEBS LETT. 327:311-314(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RX MEDLINE; 94052137.
BA WANG J.-B., IKAI Y., EPLER M.C., GREGOR P., SPIYAK C., UHL G.R.;
RE PROC. NATL. ACAD. SCI. U.S.A. 90:10230-10234(1993).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RX MEDLINE; 93341493.
BA CHEN Y., WESTER A., LIU J., HURLEY J.A., YU L.;
RE MOL. PHARMACOL. 44:8-12(1993).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN-SPRAGUE-DAWLEY; TISSUE-BRAIN;
BA BUNZOW J.R., GRANDY D.K., KELLY M.;
RE SUBMITTED (SEP-1993) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN-SPRAGUE-DAWLEY; TISSUE-OLFACTORY BULB;
RX MEDLINE; 94059560.
BA THOMPSON R.C., MANSOUR A., AKIL H., WATSON S.J.;
RE NEURON 11:903-913(1993).
RN [6]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RX MEDLINE; 94246380.
BA ZASTAWNY R.L., GEORGE S.R., NGUYEN T., CHENG R., TSATSOS J.,
BA BRINES-URBINA R., O'DOWD B.F.;
RE J. NEUROCHEM. 62:2099-2105(1994).
RN [7]
RP SEQUENCE OF 356-391 FROM N.A.
RX MEDLINE; 95172221.
BA ZIMPRICH A., SIMON T., HOLTM V.;
RE FEBS LETT. 359:142-146(1995).
RN [8]
RP ION CURRENTS INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM
CC -I- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM
CC FOR BETA-ENDORPHIN.
CC -I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -I- TISSUE SPECIFICITY: BRAIN. IS EXPRESSED IN THE CEREBRAL CORTEX,
CC CAUDATE PUTAMEN, NUCLEUS ACCUMBENS, SEPTAL NUCLEI, THALAMUS,
CC HIPPOCAMPUS, AND HABENULA. NOT DETECTED IN CEREBELLUM.
CC -I- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; D16349; G391867; -
DR EMBL; L20684; G409150; -
DR EMBL; L13069; G348251; -
DR EMBL; D02083; G403574; -
DR EMBL; L22455; G437672; -
DR EMBL; U35424; G1017732; -
DR EMBL; S75569; G861432; -
DR PIR; S34593; S34593.
DR GCRDB; GCR_0633; -
DR GCRDB; GCR_0637; -
DR GCRDB; GCR_0639; -

DR GCRDB; GCR_0640; -
DR GCRDB; GCR_0644; -
DR POSITIVE; PS00237; G-PROTEIN RECEPTOR. 1.
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
KW PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.
FT DOMAIN 1 64 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 94 1 (POTENTIAL).
FT DOMAIN 95 103 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 104 121 2 (POTENTIAL).
FT DOMAIN 122 143 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 144 163 3 (POTENTIAL).
FT DOMAIN 164 193 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 194 209 4 (POTENTIAL).
FT DOMAIN 210 234 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 235 257 5 (POTENTIAL).
FT DOMAIN 258 280 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 281 303 6 (POTENTIAL).
FT DOMAIN 304 311 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 312 328 7 (POTENTIAL).
FT DOMAIN 329 398 CYTOPLASMIC (POTENTIAL).
FT DISULFID 140 217 BY SIMILARITY.
FT LIPID 351 351 PALMITATE (POTENTIAL).
FT CARBOHYD 9 POTENTIAL.
FT CARBOHYD 31 31 POTENTIAL.
FT CARBOHYD 38 38 POTENTIAL.
FT CARBOHYD 46 46 POTENTIAL.
FT CARBOHYD 53 53 POTENTIAL.
FT CONFLICT 237 237 F -> G (IN REF. 6).
FT CONFLICT 245 245 V -> I (IN REF. 3 AND 4).
FT CONFLICT 387 391 LENSE -> KYLF (IN REF. 7).
SQ SEQUENCE 398 AA; 44494 MW; 2C21013D CRC32;

Query Match 68.3%; Score 1522; DB 1; Length 398;
Best Local Similarity 66.1%; Pred. No. 5,70e-282;
Matches 191; Conservative 45; Mismatches 49; Incls 4; Gaps 4;

DB 96 YTKMTAINIYFNALADALASTIPDSVNTLMTGTPGTLICKIYISIDYNNFTSI 155
1 YTKMTAINIYFNALADALASTIPDSVNTLMTGTPGTLICKIYISIDYNNFTSI 60
DB 156 FTLCITSVRYIANGCPVPAALDERTPRNAKIYVNCWIISSALGLPYVMATKTYNG-S 214
61 FTLCITSVRYIANGCPVPAALDERTPRNAKIYVNCWIISSALGLPYVMATKTYNG-S 120
DB 215 -IDCTTFSPHW-XWENLTKICVFPAFIMPVLIITVCYGMILRLKRVKMSGSKEND 272
121 VIECCQFPDDDXSWMDLTKICVFPAFIVPILIIIVITLILKRVKLSGSKEND 180
DB 273 RNLRTIRVLYVAVFIVCWTPIHLYVILKALITIPETPQVSWHFCIALGYNSCLN 332
181 XNLRITRVLVAVFIVCWTPIHLYVILKALITIPETPQVSWHFCIALGYNSCLN 240
DB 333 PVLYALDENFKRCPEPCIPTSSTIEQONSSTRVKNTEHSTANTVD 381
241 PVLYALDENFKRCPEPCIPTSSTIEQONSSTRVKNTEHSTANTVD 288
RESULT 7
ID OPERA HUMAN STANDARD: PRT: 400 AA.
AC P35372;
DI 01-JUN-1994 (REL. 29, CREATED)
DT 01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
DE MU-TYPE OP2OID RECEPTOR (MOR-1).
OS HOMO SAPIENS (HUMAN).
OC EUPHORIA; RODENTIA.
OC EUPHORIA; RODENTIA.
RA EUPHORIA; RODENTIA.
RX MEDLINE; 94139928.
BA WANG J.-B., JOHNSON P.S., PERSICO A.M., HAWKINS A.L., GRITFIN C.A.,


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RA UHL G.R.;
RL FEBS LETT. 338:217-222(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RA WESER A. JR., HURLEY J.E., BYE L.S., CAMPBELL A., TIAN M.,
  CHEN Y., YU L.;
RL SUBMITTED (XXX-1994) TO EMBL/GENBANK/DDJ DATA BANKS.
CC -1- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM
  ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. RECEPTOR
  FOR BETA-ENDORPHIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; L25119; G452073; -
DR EMBL; L29301; G459832; -
DR GCRDB; GCR 0885; -
DR GCRDB; GCR 0966; -
DR MIN; 600018; -
DR PROSITE; PS00237; G-PROTEIN-RECEPTOR; 1.
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
  PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.
FT DOMAIN 1 66
FT TRASMEX 67 96
FT TRASMEX 97 105
FT TRASMEX 106 123
FT TRASMEX 124 145
FT TRASMEX 146 165
FT TRASMEX 166 195
FT TRASMEX 196 211
FT TRASMEX 212 236
FT TRASMEX 237 259
FT TRASMEX 260 282
FT TRASMEX 283 305
FT TRASMEX 306 313
FT TRASMEX 314 330
FT TRASMEX 331 400
FT DISULFID 142 219
FT LIPID 353 353
FT CARBOHYD 9 9
FT CARBOHYD 12 12
FT CARBOHYD 33 33
FT CARBOHYD 40 40
FT CARBOHYD 48 48
FT CARBOHYD 51 51
FT CONFLICT 234
FT CONFLICT 234
SQ SEQUENCE 400 AA; 44764 MW; 3F40D610 CRC32;

Query Match 68.2%; Score 1520; DB 1; Length 400;
Best Local Similarity 67.1%; Pred. No. 1,50e-281;
Matches 188; Conservative 43; Mismatches 46; Indels 3; Gaps 3;

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ID OPRM.PTG STANDARD; PRT; 401 AA.
AC 095247;
AD 01-NOV-1997 (REL. 35, CREATED)
AD 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
AD 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE MU-TYPE OPIOID RECEPTOR (MOR-1).
GN OPRM1.
OS SUS SCROFA (PTG).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; ARTIODACTYLA.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-CEREBRAL CORTEX;
RA PAMPUCH M.P., OSTINSKI M.A., BROWN D.R., MURTAUGH M.P.;
RL SUBMITTED (NOV-1995) TO EMBL/GENBANK/DDJ DATA BANKS.
CC -1- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM
  ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. RECEPTOR
  FOR BETA-ENDORPHIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; L38645; G1553057; -
DR PROSITE; PS00237; G-PROTEIN-RECEPTOR; 1.
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
  PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.
FT DOMAIN 1 67
FT TRASMEX 68 97
FT TRASMEX 98 106
FT TRASMEX 107 124
FT TRASMEX 125 146
FT TRASMEX 147 166
FT TRASMEX 167 196
FT TRASMEX 197 212
FT TRASMEX 213 237
FT TRASMEX 238 260
FT TRASMEX 261 283
FT TRASMEX 284 306
FT TRASMEX 307 314
FT TRASMEX 315 331
FT TRASMEX 332 401
FT DISULFID 143 220
FT LIPID 354 354
FT CARBOHYD 9 9
FT CARBOHYD 12 12
FT CARBOHYD 34 34
FT CARBOHYD 41 41
FT CARBOHYD 49 49
SQ SEQUENCE 401 AA; 45098 MW; 6786FD94 CRC32;

Query Match 68.1%; Score 1518; DB 1; Length 401;
Best Local Similarity 67.1%; Pred. No. 3,96e-281;
Matches 188; Conservative 43; Mismatches 46; Indels 3; Gaps 3;

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RESULT 9
ID OPD_HUMAN STANDARD: PRT; 372 AA.
AC P41143;
DI 01-FEB-1995 (REL. 31, CREATED)
DI 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
DI 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE DELTA-TYPE OPIOID RECEPTOR (DOR-1).
GN OPRI1 OR OPRI.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=CEREBRAL CORTEX, AND STRIATUM;
RX MEDLINE; 94260835.
RA KNAPE R.J., MALATYNSKA E., FANG L., LI X., BABIN E., NGUYEN M.,
RA SANTORO G., VARGA E.V., HRUBY V.J., ROESKE W.R., YAMAMURA H.I.;
RL LIFE SCI. 54:463-469(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 95107267.
RA SIMONIN F., BEFORT K., GAVERIAUX-RUFF C., MATTHES H., NAPPREY V.,
RA LANNES B., MICHELETTI G., KIEFFER B.;
RL MOL. PHARMACOL. 46:1015-1021(1994).
CC -1- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM
CC ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. HIGHLY
CC STEREOSELCTIVE. RECEPTOR FOR ENKEPHALINS.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
DR EMBL; 007882; G497314; -.
DR EMBL; 010504; E162517; -.
DR MIM; 165195; -.
DR PROSITE; PS00237; G-PROTEIN RECEPTOR; 1.
KM G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
KM PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.
FT DOMAIN 1 45
FT TRANSMEM 46 75
FT DOMAIN 76 84
FT TRANSMEM 85 102
FT DOMAIN 103 124
FT TRANSMEM 125 144
FT DOMAIN 145 174
FT TRANSMEM 175 190
FT DOMAIN 191 215
FT TRANSMEM 216 238
FT DOMAIN 239 261
FT TRANSMEM 262 284
FT DOMAIN 285 293
FT TRANSMEM 294 310
FT DOMAIN 311 372
FT CARBOHYD 18 33
FT CARBOHYD 33 33
FT DISULFID 121 198
FT LIPID 333 333
FT CONFLICT 27 27
FT CONFLICT 40 41
FT CONFLICT 348 348
FT CONFLICT 370 370
SQ SEQUENCE 372 AA; 40450 MW; CFE92985 CRC32;

Query Match 65.4%; Score 1456; DB 1; Length 372;
Best Local Similarity 69.2%; Pred. No. 1.62e-268;
Matches 180; Conservative 43; Mismatches 33; Indels 4; Gaps 4;

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RESULT 10
ID OPD_RAT STANDARD: PRT; 372 AA.
AC P33533;
DI 01-FEB-1994 (REL. 28, CREATED)
DI 01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
DI 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE DELTA-TYPE OPIOID RECEPTOR (DOR-1) (OPIOID RECEPTOR A).
GN OPRI1 OR MOR-A.
OS RATTUS NORVEGICUS (RAT).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE; 93351652.
RA FUKUDA K., KATO S., MORI K., NISHI M., TAKESHIMA H.;
RL FEBS LETT. 327:311-314(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=BRAIN;
RX MEDLINE; 94322412.
RA ABOOD M.E., NOEL M.A., FARNSWORTH J.S., TAO Q.;
RL J. NEUROSCI. RES. 37:714-719(1994).
CC -1- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM
CC ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. HIGHLY
CC STEREOSELCTIVE. RECEPTOR FOR ENKEPHALINS.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
DR EMBL; D16348; G391865; -.
DR EMBL; 000475; G514211; -.
DR PIR; S34592; S34592.
DR GCRDB; GCR_0638; -.
DR GCRDB; GCR_0805; -.
DR PROSITE; PS00237; G-PROTEIN RECEPTOR; 1.
KM G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
KM PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.
FT DOMAIN 1 45
FT TRANSMEM 46 75
FT DOMAIN 76 84
FT TRANSMEM 85 102
FT DOMAIN 103 124
FT TRANSMEM 125 144
FT TRANSMEM 145 174
FT TRANSMEM 175 190
FT DOMAIN 191 215
FT TRANSMEM 216 238
FT DOMAIN 239 261
FT TRANSMEM 262 284
FT DOMAIN 285 293
FT TRANSMEM 294 310
FT DOMAIN 311 372
FT CARBOHYD 18 33
FT CARBOHYD 33 33
FT DISULFID 121 198
FT LIPID 333 333
SQ SEQUENCE 372 AA; 40449 MW; 59F5EE50 CRC32;

Query Match 65.1%; Score 1452; DB 1; Length 372;
Best Local Similarity 68.8%; Pred. No. 2.95e-267;
Matches 179; Conservative 44; Mismatches 33; Indels 4; Gaps 4;

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ID	OPRD	MOUSE	STANDARD	PRT	372 AA.
AC	P32300				
DT	01-OCT-1993	(REL. 27, CREATED)			
DT	01-OCT-1993	(REL. 27, LAST SEQUENCE UPDATE)			
DT	01-NOV-1997	(REL. 35, LAST ANNOTATION UPDATE)			
DE	DELTA-TYPE OPIOID RECEPTOR (DOR-1) (K56) (MSL-2).				
GN	OPRD1				
OS	MUS MUSCULUS (MOUSE).				
OC	EDAROTLA; METAOC; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;				
OC	EDHERITA; RODENTIA.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE: 93101664.				
RA	KIEFERER B.L., BEFORT K., GAVERIAUX-ROUF C., HIRSH C.G.;				
RL	PROC. NATL. ACAD. SCI. U.S.A. 89:12048-12052(1992).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE: 93110361.				
RA	EVANS C.J., KEITH D.E. JR., MORRISON H., MAGENDO K., EDWARDS R.H.;				
RL	SCIENCE 258:1952-1955(1992).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=BRAIN;				
RX	MEDLINE: 93342064.				
RA	YASUDA K., RAYNOR K., KONG H., BREDER C.D., TAKEDA J., REISINE T.;				
RL	BEUL G.I.;				
RA	PROC. NATL. ACAD. SCI. U.S.A. 90:6736-6740(1993).				
RN	[4]				
RP	SEQUENCE FROM N.A.				
RA	KEITH D.E. JR., ANTON B., EVANS C.J.;				
RL	PROC. WEST. PHARMACOL. SOC. 36:299-306(1993).				
RN	[5]				
RP	SEQUENCE OF 8-372 FROM N.A.				
RX	MEDLINE: 94022364.				
RA	BZEGRA T., CHIN H., KIM K., JUNG H.H., KOZAK C.A., KLEE W.A.;				
RL	PROC. NATL. ACAD. SCI. U.S.A. 90:9305-9309(1993).				
RN	[6]				
RP	3D-STRUCTURE MODELING.				
RX	MEDLINE: 97001837.				
RA	AKOITA I., LOEW G.H.;				
RL	PROTEIN ENG. 9:573-583(1996).				
CC	-1- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM				
CC	ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. HIGHLY				
CC	STEREOSSELECTIVE. RECEPTOR FOR ENKEPHALIN.				
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.				
CC	-1- TISSUE SPECIFICITY: BRAIN, WITH HIGH CONCENTRATIONS IN THE BASAL				
CC	GANGLIA AND LIMBIC REGIONS				
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.				
DR	EMBL: L06322; G19243; -;				
DR	EMBL: L07271; -; NOT_ANNOTATED_CDS.				
DR	EMBL: L10164; G348247; -;				

DR	EMBL; S65335; G443226; -;
DR	EMBL; S66181; G435782; -;
DR	PIR; S37807; S37807.
DR	PIR; B48227; B48227.
DR	GCRDB; GCR_02292; -.
DR	GCRDB; GCR_L0493; -.
DR	GCRDB; GCR_O634; -.
DR	GCRDB; GCR_O642; -.
DR	MGI; MGI:97438; OPERD.
DR	PROSITE; PS00237; G_PROTEIN_RECEPTOR. 1.
KW	PHOSPHOYLATION; LIPOPROTEIN; PALMITATE.
KW	PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.
KV	DOMAIN 1 45
FT	DOMAIN 1 45
FT	TRANSMEM 46 75
FT	DOMAIN 76 84
FT	TRANSMEM 85 102
FT	DOMAIN 103 124
FT	TRANSMEM 125 144
FT	DOMAIN 145 174
FT	TRANSMEM 175 190
FT	DOMAIN 191 215
FT	TRANSMEM 216 238
FT	DOMAIN 239 261
FT	TRANSMEM 262 284
FT	DOMAIN 285 293
FT	TRANSMEM 294 310
FT	DOMAIN 311 372
FT	CARBOHYD 18 18
FT	CARBOHYD 33 33
FT	DISULFID 121 198
FT	LIPID 333 333
Q	SEQUENCE 372 AA; 40561 MW; 51022F5 CRC32;

Query Match	65.0%;	Score 1448;	DB 1;	Length 372;
Best Local Similarity	68.8%;	Fred. No. 2,04e-266;		
Matches 179;	Conservative	44;	Mismatches 33;	Indels 4;
				Gaps 4;
Db	77	YTKTKTANITVFNPLADALATSLPQPSKAYLMEFPELLCKXVLSTIDYNNMTSI	136	
QY	1	YTKKATANNITLFLNALADALVITIMPEQSTVYLMNSWPFSDVLCIKYISIDYNNFTSI	60	
Db	137	FTLTMASVDRILAVCHPKALDEFTPKAKKLINICIMWLASGVCPIDVMAVTPORDGA	195	
QY	61	FTLTMASVDRILAVCHPKALDEFTPKAKKLINICIMWLSSVGSALVYLGITVREVD	120	
Db	196	VV-CMLQPPSPW-YMDPTVKICVFLDAFVVPILITTCYIGIMTLTRSRVLLSGSKERD	253	
QY	121	VIECLQPPDDDDYSMWDLFMKICVEIFAEVAFIPVLIIIVCYITLMLTRKXVRLLSGSKERD	180	
Db	254	RSKRITLTMVLYVVGAFVVCAPLHIEIVTWLVLDINRDPDLVVAALHLCALATYANSSL	313	
QY	181	XNLRITFLVLYVVAVFVVCWPIHIFLIVLALGSTSHSA-ALSSYFCIALGYTNSSL	239	
Db	314	NPVLAFDENFKRCEROLC	333	
QY	240	NPILYAFDENFKRCERDFC	259	
RESULT	12			
ID	OPRX	RAT	STANDARD;	PRT; 367 AA.
AC	P35370;			
DT	01-JUN-1994	(REL. 29, CREATED)		
DT	01-JUN-1994	(REL. 29, LAST SEQUENCE UPDATE)		
DT	01-NOV-1997	(REL. 35, LAST ANNOTATION UPDATE)		
DE	NOICIGPTIN RECEPTOR (ORPHANIN FQ RECEPTOR) (KAPPA-TYPE 3 OPIOID RECEPTOR) (KOR-3) (KOR-C) (XOR1).			
DE	RECEPTOR (KOR-3) (KOR-C) (XOR1).			
GN	OPRL1 OR COR.			
OS	RATUUS NORVEGETICUS (RAT).			
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
OC	EUTHERIA; RODENTIA.			
FN	[1]			
FP	SEQUENCE FROM N.A.			
SC	STRAIN=WISTAR; TISSUE=BRAIN;			


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RN [5]
RE SEQUENCE FROM N.A.
RA MEDLINE; 95327076.
RA PAN Y.X., CHENG J., XU J., ROSSI G., JACOBSON E., RYAN-MORO J.,
RA BROOKS A.L., DEAN G.E., STANDIFER K.M., PASTERNAK G.W.;
RA MOL. PHARMACOL. 47:1180-1188(1995).
RN [6]
RP SEQUENCE OF 1-357 FROM N.A.
RC STRAIN-BALB/C; TISSUE=SPLEEN;
RA HALFORD W.P., GERHARDT B.M., CARR D.J.J.;
RA SUBMITTED (AUG-1994) TO EMBL/GENBANK/DDJ DATA BANKS.
CC -1- FUNCTION: RECEPTOR FOR THE NEUROPEPTIDE NOCICEPTIN/ORPHANIN FQ.
CC HAS A POTENTIAL ROLE IN MODULATING A NUMBER OF BRAIN FUNCTIONS,
CC INCLUDING INSTINCTIVE BEHAVIOURS AND EMOTIONS. THE ACTIVITY OF
CC THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH INHIBITS ADENYLYL
CC CYCLASE.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; U04952; G440880; -.
DR EMBL; D31667; G808874; -.
DR EMBL; D31666; G808874; JOINED.
DR EMBL; X91813; G1008982; -.
DR EMBL; U32932; G1464791; -.
DR EMBL; U32928; G1464791; JOINED.
DR EMBL; U32930; G1464791; JOINED.
DR EMBL; U09421; G551485; -.
DR EMBL; U14165; G540093; -.
DR GCRDB; GCR_0891; -.
DR MGI; MGI:97440; OPL.
DR PROSITE; PS00237; G-PROTEIN_RECEPTOR; 1.
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
KW PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.
FT DOMAIN 1 47
FT TRANSMEM 48 74
FT DOMAIN 75 84
FT TRANSMEM 85 106
FT DOMAIN 107 121
FT TRANSMEM 122 143
FT DOMAIN 144 162
FT TRANSMEM 163 185
FT DOMAIN 186 208
FT TRANSMEM 209 233
FT DOMAIN 234 261
FT TRANSMEM 262 285
FT DOMAIN 286 297
FT TRANSMEM 298 319
FT DOMAIN 320 366
FT DISULFID 120 197
FT LIPID 331 331
FT CARBOHYD 21 21
FT CARBOHYD 26 26
FT CARBOHYD 36 36
FT CONFILCT 348 349
SQ SEQUENCE 367 AA; 40491 MW; 3F472156 CRC32;

Query Match 60.3%; Score 1343; DB 1; Length 367;
Best Local Similarity 62.1%; Pred. No. 2,166-244;
Matches 174; Conservative 46; Mismatches 55; Indels 5; Gaps 5;

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QY 161 XNLRITRLVIVVAVFVGCWTPVQVFLVQGLGVQPSSETAVALLRCTALGVYNSCLN 240
DB 313 PLIVAFIDENFKACRRCFCASALREMOVSDRVRSIARD 352
QY 241 PLIVAFIDENFKRCDRCFCPLKMMERKSTRVANTYQD 280

RESULT 14
ID OPRX_HUMAN STANDARD; PRT; 370 AA.
AC P41146;
DT 01-FEB-1995 (REL. 31, CREATED)
DI 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
DI 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE NOCICEPTIN RECEPTOR (ORPHANIN FQ RECEPTOR) (KAPPA-TYPE 3 OPIOID
DE RECEPTOR) (KOR- 3).
GN OPR1 OR ORL1 OR OOR.
OS HOMO SAPIENS (HUMAN).
OC EURARCTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN STEM;
RX MEDLINE; 94185768.
RA MOLLEREAU C., PARMENTIER M., MAILLET P., BUTOUR J.L., MOISAND C.,
RA CHAILON P., CAPUT D., VASSART G., MEDNIR C.;
RL FEBS LETT. 341:33-38(1994).
RN [2]
RP SEQUENCE FROM N.A.
RA LEE P.H., ZHU J., LIU-CHEN L., CHANG K.;
RL SUBMITTED (JAN-1996) TO EMBL/GENBANK/DDJ DATA BANKS.
CC -1- FUNCTION: RECEPTOR FOR THE NEUROPEPTIDE NOCICEPTIN/ORPHANIN FQ.
CC HAS A POTENTIAL ROLE IN MODULATING A NUMBER OF BRAIN FUNCTIONS,
CC INCLUDING INSTINCTIVE BEHAVIOURS AND EMOTIONS. THE ACTIVITY OF
CC THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH INHIBITS ADENYLYL
CC CYCLASE.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; X77130; G471317; -.
DR EMBL; U30185; G1144297; -.
DR PIR; S43087; S43087.
DR GCRDB; GCR_0987; -.
DR PROSITE; PS00237; G-PROTEIN_RECEPTOR; 1.
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
KW PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.
FT DOMAIN 1 50
FT TRANSMEM 51 77
FT DOMAIN 78 87
FT TRANSMEM 88 109
FT DOMAIN 110 124
FT TRANSMEM 125 146
FT DOMAIN 147 165
FT TRANSMEM 166 188
FT DOMAIN 189 211
FT TRANSMEM 212 236
FT DOMAIN 237 264
FT TRANSMEM 265 288
FT DOMAIN 289 300
FT TRANSMEM 301 322
FT DOMAIN 323 370
FT DISULFID 123 200
FT LIPID 334 334
FT CARBOHYD 21 21
FT CARBOHYD 28 28
FT CARBOHYD 39 39
SQ SEQUENCE 370 AA; 40693 MW; BE3C3E8F CRC32;

Query Match 59.7%; Score 1331; DB 1; Length 370;
Best Local Similarity 60.6%; Pred. No. 7,056-742;
Matches 171; Conservative 49; Mismatches 57; Indels 5; Gaps 5;

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 WISE (TM)

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Msrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu Apr 16 13:36:28 1998; MasPar time 15.63 Seconds

Tabular output not generated. 794,520 Million cell updates/sec

Title: >US-08-292-694A-12

Description: (1-295) from US08292694A.pep

Perfect Score: 2229

Sequence: 1 YTKMTATNIIYFNALAD.....NTVQDPAYLRIDGMNRPV 295

Scoring table: PAM 150

Searched: 140555 seqs, 42109429 residues

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database:

sptrmb15
 1:sp_fungi 2:sp_human 3:sp_invertebrate 4:sp_mammal
 5:sp_mnc 6:sp_organelle 7:sp_phase 8:sp_plant
 9:sp_bacteria 10:sp_rodent 11:sp_virus 12:sp_vertebrate
 13:sp_unclassified

Statistics: Mean 46.849; Variance 117.237; scale 0.400

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	1520	68.2	392	2	012930	1.74e-225
2	1489	66.8	401	4	P79350	1.90e-220
3	1461	65.5	383	12	042324	2.50e-215
4	1328	59.6	240	10	064120	3.34e-193
5	856	38.4	117	10	060733	1.17e-114
6	643	28.8	119	10	064206	6.90e-78
7	635	28.5	98	10	P97266	1.35e-78
8	522	23.4	372	10	008726	1.74e-60
9	483	21.7	354	10	035313	2.60e-54
10	474	21.3	352	4	P97405	6.81e-53
11	473	21.2	352	4	002746	9.79e-53
12	473	21.2	352	10	P97308	9.79e-53
13	472	21.2	359	12	P79785	1.41e-52
14	470	21.1	359	10	035210	2.90e-52
15	468	21.0	352	2	014705	5.98e-52
16	468	21.0	354	10	035891	5.98e-52
17	467	21.0	361	10	035811	8.59e-52
18	461	20.7	333	2	014694	7.53e-51
19	462	20.7	352	2	014697	5.24e-51
20	462	20.7	352	2	014692	5.24e-51

21	462	20.7	352	4	018770	CCRS RECEPTOR (FRAGMENT)	5.24e-51
22	461	20.7	352	2	014702	CCRS RECEPTOR (FRAGMENT)	7.53e-51
23	461	20.7	352	2	015388	CCRS RECEPTOR (FRAGMENT)	7.53e-51
24	461	20.7	352	2	014699	CCRS RECEPTOR (FRAGMENT)	7.53e-51
25	461	20.7	352	2	014701	CCRS RECEPTOR (FRAGMENT)	7.53e-51
26	461	20.7	352	2	014707	CCRS RECEPTOR (FRAGMENT)	7.53e-51
27	461	20.7	352	2	014700	CCRS RECEPTOR (FRAGMENT)	7.53e-51
28	461	20.7	352	2	014704	CCRS RECEPTOR (FRAGMENT)	7.53e-51
29	462	20.7	362	12	091383	ANGIOTENSIN II RECEPTOR	5.24e-51
30	459	20.6	352	4	002778	CC CHEMOKINE RECEPTOR	1.55e-50
31	459	20.6	352	2	014695	CCRS RECEPTOR (FRAGMENT)	1.55e-50
32	458	20.5	352	2	014706	CCRS RECEPTOR (FRAGMENT)	2.29e-50
33	457	20.5	352	4	018772	CCRS RECEPTOR (FRAGMENT)	3.12e-50
34	455	20.4	352	2	014696	CCRS RECEPTOR (FRAGMENT)	6.57e-50
35	454	20.4	352	2	014703	CCRS RECEPTOR (FRAGMENT)	9.43e-50
36	453	20.3	352	2	014693	CCRS RECEPTOR (FRAGMENT)	1.35e-49
37	450	20.2	383	11	089609	G PROTEIN-COUPLED RECE	3.99e-49
38	449	20.1	352	4	018771	CCRS RECEPTOR (FRAGMENT)	5.72e-49
39	448	20.1	352	2	014698	CCRS RECEPTOR (FRAGMENT)	8.20e-49
40	445	20.0	352	2	015133	PURINERGIC RECEPTOR P2	2.42e-48
41	444	19.9	352	2	014708	CCRS RECEPTOR (FRAGMENT)	3.45e-48
42	442	19.8	678	3	094736	TACHYKININ-LIKE RECEPT	7.11e-48
43	436	19.6	353	12	P79960	MESSENGER-ASSOCIATED	6.15e-47
44	415	18.6	238	12	092158	ANGIOTENSIN II RECEPTO	1.14e-43
45	415	18.6	360	4	018793	CHEMOKINE RECEPTOR	1.14e-43

ALIGNMENTS

RESULT	ID	PRELIMINARY	PRT	392 AA.
AC	012930			
DI	01-NOV-1996 (TREMBLREL. 01, CREATED)			
DI	01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)			
DI	01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)			
DE	MU OPIOID RECEPTOR VARIANT.			
GN	MOR.			
OS	HOMO SAPIENS (HUMAN).			
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
OC	EUTHERIA; PRIMATES.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE-BRAIN;			
RX	MEDLINE; 95046336.			
RA	BARE L.A., MANSSON E., YANG D.;			
RL	FEBS LETT. 354:213-216(1994).			
RN	[2]			
RP	SEQUENCE OF 1-388 FROM N.A.			
RC	TISSUE-BRAIN;			
RX	MEDLINE; 94139928.			
RA	WANG J.B., JOHNSON P.S., PERSICO A.M., HAWKINS A.L., GRIFFIN C.A.,			
RL	UHL G.R.;			
RL	FEBS LETT. 338:217-222(1994).			
DR	EMBL; D12569; G607912; ..			
DR	PROSITE; PS00237; G-PROTEIN RECEPTOR: 1.			
FT	VARIANT 40	D -> N (IN REF. 2).		
FT	VARIANT 51	D -> N (IN REF. 2).		
FT	VARIANT 207	I -> M (IN REF. 2).		
FT	VARIANT 234	L -> V (IN REF. 2).		
SQ	SEQUENCE 392 AA; 43939 MW; 3359DB4 CRC22;			

Query Match 68.2%; Score 1520; DB 2; Length 392;
 Best Local Similarity 67.1%; Pred. No. 1.74e-225;
 Matches 188; Conservative 43; Mismatches 46; Indels 3; Gaps 3;

Db	98	YTKMTATNIIYFNALADALSTIPPOSVYIMGTGFTLCTIVISIDYNNFTS	157
QY	1	YTKMTATNIIYFNALADALVTTIMPFSYIMNSPFGVGLCKIVISIDYNNFTSI	60
Db	158	FTFCTSVSVRYIAVCPVAKLDFRIPRNKINVCWIISSAIGLPVNFIAATKYRG-S	216
QY	61	FTITMGSVDRIYAVCPVAKLDFRIPRNKINVCWIISSAIGLPVNFIAATKYRG-S	120


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Db 217 -ICGLTSHPTW-YWELLATCYPIFAFIMPVLLITCYGIMTLRLKSYMLSGSEKRD 274
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 121 VIECLCLPDDDSYMWDLDMKICVEIFAEFVLPVLLITCYLMTLRLKXYMLLSGSEKRD 180
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 275 RNLRLTRFMVAVVAVAFVCMTPPIHVIYIKALVYIPETTFQVSWHFCMLGYTNSCLN 334
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 181 XNLRLTRFLVLYVAVAFVCMTPPIHIFLVLALDSTSHSTALSTSYFCIALGTNSSLN 240
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 335 PVLVAFLDENKRCFRCFCIPITSSNIEDQNSTRIKQNTD 374
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 241 PLVAFLDENKRCFRCFCIPKXMXMERXSTSRKVNVD 280
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 2
ID P79350 PRELIMINARY; PRT; 401 AA.
AC P79350;
DT 01-MAY-1997 (TREMBLREL_03, CREATED)
DT 01-MAY-1997 (TREMBLREL_03, LAST SEQUENCE UPDATE)
DT 01-JAN-1998 (TREMBLREL_05, LAST ANNOTATION UPDATE)
DE MU OPFOID RECEPTOR.
OS BOS TAURUS (BOVINE).
CC EUCARYOTA; METAQCA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; ARTIODACTYLA.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=STRIATUM;
RA SIMON E.J., VILLEM S., ANDRIA M., ONOPRISHVILI I., HILLER J.M.;
RL SUBMITTED (MAR-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -1 - SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
EMBL: U896777. GI881731.
DR PROSITE, PS00237; G-PROTEIN RECEPTOR; 1.
DR G-PROTEIN COUPLLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN.
SQ SEQUENCE 401 AA; 45045 MW; 56735988 CIRC32;

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	Query Match	66.8%	Score 1489	DB 4	Length 401
	Best Local Similarity	66.1%	Pred. No. 2,90e-220		
	Matches 185	Conservative 45	Mismatches 47	Indels 3	Gaps 3
Db	99 YTKKKTATNTIYIFENALADALATSTLPDEOSGNVYMGWPGIILCKIVISIDYNNMTST 158				
Qy	1 YTKKKTATNTIYIFENALADALATSTLPDEOSGNVYMGWPGIILCKIVISIDYNNMTST 60				
Db	159 FTLCTMGVDRIYACHPKVALDPTPRNNKLTINICNNILSSALDGLPYWPMATKYRQG-S 217				
Qy	61 FTLCTMGVDRIYACHPKVALDPTPRNNKLTINICNNILSSALDGLPYWPMATKYRQGDVD 120				
Db	218 -LSDTLFSEHPT-YTNNLKLICVYFAITMPDITITVYCGMLRLKSVPMGSGSEKD 275				
Qy	121 VIECCTLOFPDDQYSWMBLPMKICVYFAITMPDITITVYCGMLRLKSVPMGSGSEKD 180				
Db	276 RNLRTIRPMYLYVAAYVTCMTPPHIVIVILKLTIPETFOYVSMHFCALATVNSGLN 335				
Qy	181 XNLRIRIRLYVAVVAVVYVCTPPLHITILVDALGSTSHSAALSSYFCALDGTNSLN 240				
Db	336 PVLYAFLEDNFKRCFRFCIPTSSILIQONSTRLRONTRD 375				
Qy	241 PLYAFLEDNFKRCFRFCIPTSSILIQONSTRLRONTRD 280				
RESULT	3				
ID	042324	PRELIMINARY	PRT	383 AA.	
AC	042324				
DT	01-JAN-1998 (TREMBREL. 05, CREATED)				
DT	01-JAN-1998 (TREMBREL. 05, LAST SEQUENCE UPDATE)				
DT	01-JAN-1998 (TREMBREL. 05, LAST ANNOTATION UPDATE)				
DE	MO-OPLOID RECEPTOR.				
OS	CATOSYOMUS COMMERSONI (WHITE SUCKER).				
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; PISCES; GNATHOSTOMATA;				
OC	OSTEICHTHYES; ACTINOPTERYGII; CYPRINIFORMES.				
OC	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSE-CNS;				
RA	DARLISON M.G., HARVEY R.J., GRETEN F.R., KREIENKAMP H.J., ZWIERS H.				

RA STEMER, T., LEDERIS, K., RICHTER, D.,
 RL SUBMITTED (NOV-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 CC 1: SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 EMBL, Y10904; E1169530; -.
 DR PROSITE, PS00237; G-PROTEIN-RECEPTOR; 1.
 KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN.
 SQ SEQUENCE 383 AA; 44332 MW; 00B0CBAD CRC32;

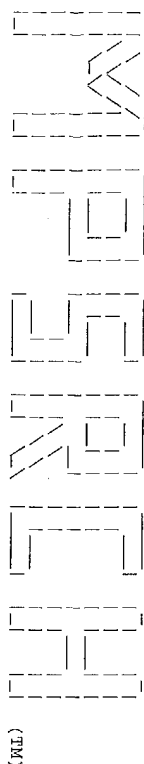
Query Match	65.5%;	Score 1461;	DB 12;	Length 383;
Best Local Similarity	65.1%;	Pred. No. 1.50e-215;		
Matches	183;	Conservative	42;	Indels 6;
				Gaps 4;

Db 85 YTKMTATNIIYFNALADALATATSEPOSNYLMGMPEDVACIKYMSIDYNNMTSI 144
 Qy 1 YTKKTAATNIIYFNALADALVYTTMTPEOSIVYLMNSPREDVACIKYVLSIDYNNMTSI 60
 Db 145 FTLTMSIDRYIAVCHPKALDEPTPRNAKIVNYCNMILSSAIGLPYMAVASTIENONS 204
 Qy 61 FTLTMSVDRYIAVCHPKALDEPTPIKAKTINICIMILSSVSGISAIVIGTKV -RED- 118
 Db 205 PLOYSNEDCULTEPHHPM-YWETLLKICVFELAIIMVYLITVYCYGMLIRKSVRLSG 263
 Qy 119 -VDV-TECCLOPEPDDISWMDLEMKICVFPAFVIVPILIIYVYTTMLIRLKKVRLSG 175
 Db 264 SKEDRNLRRTIRRVLVVVAFFICQTPHIFVYIKALVTIPNSLFOYTMHPCFALGYI 323
 Qy 176 SREKDXNLRRTIRRVLVVVAFFVQWPIRHFILVEALGSHSHSTALSSYFCIALGYT 235
 Db 324 NSCLNPVLYIAFLDENFKRRECECPSPSVLDIONSTRNKS 364
 Qy 236 NSSLNPILYIAFLDENFKRCEDFECPILKMKMERKSTRVRN 276

RESULT	4		
TD	Q64120	PRELIMINARY;	PRT; 240 AA.
AC	Q64120;		
DT	01-NOV-1996	(TREMBL,REL. 01, CREATED)	
DT	01-NOV-1996	(TREMBL,REL. 01, LAST SEQUENCE UPDATE)	
DT	01-JAN-1998	(TREMBL,REL. 05, LAST ANNOTATION UPDATE)	
DE	MU-COPIPOID RECEPTOR MOR. (FRAGMENT).		
OS	RATTUS NORVEGICUS (RAT).		
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;		
OC	EUTHERIA; RODENTIA.		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE; 93521654.		
RA	SEDOI M., ROY S., RAMAKRISHNAN S., ELDE R., LOH H.H.;		
RL	BIOCHEM. BIOPHYS. RES. COMMUN. 209:563-574(1995).		
CC	-1 SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).		
DR	EMBL; S77863; E199800.		
DR	PROSITE; PS00237; G_PROTEIN_RECEPTOR; 1.		
KR	G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN.		
FT	NON_TER	1	
EQ	SEQUENCE	240 AA; 27408 MW; D3C58BFF CRC32;	

Query Match	59.6%	Score 1328	DB 10	Length 240
Best Local Similarity	68.3%	Pred. No. 3.34e-193		
Matches 166	Conservative 36	Mismatches 38	Indels 3	Gaps 3
Db	1	TAINIYFNTALADALATSTLPQSVNVLNGTWEPFGTILCKIYISIDYNNMPTISFTLCT	60	
QY	6	TATNIIYFNTALADALATSTLPQSVNVLNGTWEPFGTILCKIYISIDYNNMPTISFTLCT	65	
Db	61	MSVRYIAYCHPVYALDFETRPNNKIVNVCNWLLSSAIGLVPVFMATITKRGQ-S-IDCT	118	
QY	66	MSVRYIAYCHPVYALDFETRPNNKIVNVCNWLLSSAIGLVPVFMATITKRGQ-S-IDCT	125	
Db	119	LTSEHPFW-IWENILKTCVFLPAFIMELIILVYCYGLMILRLKSVMLSGSKSKDKNLR	177	
QY	126	LQPDDEDSYMWDLPMKTCVFLPAFIMELIILVYCYGLMILRLKSVMLSGSKSKDKNLR	185	
Db	178	ITKAVLVVAVFVYCWPFIHIVYIKALITLIPETQVITSWMFCIALGYNSCLNPVLY	237	

Qy	186	ITRLVAVVAEYVCCWPIHIFLVEALGSHSTALSLSYPCIALGYNSSLNPILYA	243
Db	238	FLD 240	
Qy	246	FLD 248	



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MSearch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Thu Apr 16 13:34:37 1998; Maspar time 10.52 Seconds
Tabular output not generated. 501.584 Million cell updates/sec

Title: >US-08-292-694A-2
Description: (1-380) from US08282694A.pep
Perfect score: 2839
Sequence: 1 MESPDQIFRSDPGPTCSPSA.....RNTVQDPAKMDVGNKRPV 380

Scoring table: PAM 150
Gap 11

Searched: 111726 seqs, 13889129 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database:

a-geneseq30
1:part8 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23

Statistics: Mean 34.914; Variance 155.554; scale 0.224

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	2839	100.0	380	12	R67669		Mouse kappa opioid re	8.42e-257
2	2839	99.6	380	13	R76783		Rat kappa opiate rece	7.76e-256
3	2833	99.4	380	13	R72591		Mammalian kappa opioi	2.94e-255
4	2746	96.7	380	17	R88722		Human kappa opioid re	7.80e-248
5	2130	75.0	295	12	R67672		Human kappa opioid re	1.53e-188
6	1683	59.3	356	11	R65188		Murine mu-subtype opi	1.15e-145
7	1677	59.1	400	13	R71966		Human mu opioid recep	4.31e-145
8	1676	59.0	398	13	R76781		Rat mu opiate recepto	5.37e-145
9	1675	59.0	398	13	R71964		Rat mu opiate recepto	6.35e-145
10	1670	56.7	400	13	R76780		Human mu opiate rece	6.70e-145
11	1610	56.7	372	13	R76782		Rat delta opiate rece	1.11e-138
12	1597	56.3	372	9	R48629		Sequence of murine de	1.94e-137
13	1597	56.3	372	12	R66503		Mouse delta opioid re	1.94e-137
14	1499	52.8	371	10	R66503		Murine delta opioid r	4.50e-128
15	1473	51.9	367	13	R71968		Rat opiod receptor.	1.37e-125
16	1471	51.8	367	12	R67671		Mouse opiod receptor	2.12e-125
17	1464	51.6	367	13	R76638		Rat opiorph receptor	9.89e-125
18	1195	42.1	367	13	R74298		Mouse kappa-3 opiod	4.13e-99
19	980	34.5	391	7	R32650		Murine somatostatin r	9.71e-79
20	976	34.4	391	7	R32659		Human somatostatin r	2.32e-78

21	922	32.5	369	7	R32622	Murine somatostatin r	2.89e-73
22	912	32.1	369	7	R32621	Human somatostatin re	2.53e-72
23	912	32.1	369	18	R97269	Human somatostatin re	2.53e-72
24	901	31.7	369	5	R27504	Pituitary somatostati	2.75e-71
25	850	29.9	333	13	R72985	Epsilon opiod recept	1.73e-66
26	817	28.8	322	15	R48754	Rat RGH G-protein cou	2.18e-63
27	817	28.8	322	19	W02726	Rat RGH G-protein cou	2.18e-63
28	815	28.7	418	7	R39263	Human somatostatin re	3.36e-63
29	792	27.9	328	13	R72984	Epsilon opiod recept	4.83e-61
30	732	25.8	428	7	R39264	Murine somatostatin r	2.00e-55
31	679	23.9	242	22	W10017	G-protein coupled rec	1.76e-50
32	623	21.9	355	23	W25751	Human MRP-alpha/ANAT	2.82e-45
33	623	21.9	355	10	R52749	C-C chemokine recept	2.82e-45
34	614	21.6	349	14	R79443	Galanin receptor.	1.92e-44
35	614	21.6	349	17	R95070	Human galanin recepto	1.92e-44
36	604	21.3	321	22	W10016	G-protein coupled rec	1.62e-43
37	603	21.2	325	15	W02702	G-protein coupled bo	2.01e-43
38	603	21.2	325	15	R48730	G-protein coupled bo	2.01e-43
39	588	20.7	348	17	R91229	Mouse pancreas G-prot	4.91e-42
40	588	20.7	348	17	R95069	Mouse pancreas beta-c	4.91e-42
41	587	20.7	355	18	W03376	CC-chemokine receptor	6.07e-42
42	587	20.7	355	22	W10100	Human C-C chemokine r	6.07e-42
43	584	20.6	355	23	W27124	Human chemokine recep	1.15e-41
44	584	20.6	355	18	W03377	CC-chemokine receptor	1.15e-41
45	580	20.4	352	23	W27125	Maceque chemokine rec	2.69e-41

ALIGNMENTS

RESULT 1
ID R67669 standard; Protein: 380 AA.
AC R67669;
DE 17-AUG-1995 (first entry)
DI Mouse kappa opiod receptor MOR1.
DE Mouse; kappa; delta; mu; opiod receptor; brain; primer: PCR; amplify;
KW transmembrane domain; somatostatin; receptor; human; expression vector;
KW truncate; chimeric; assay; probe.
OS Mus musculus.
PN W09428132-A.
PD 08-DEC-1994.
PE 20-MAY-1994; U05747.
PR 20-MAY-1993; US-066296.
PR 30-JUL-1993; US-100694.
PR 05-NOV-1993; US-147592.
PA (ARCH-) ARCH DEV CORP.
PI Bell GI, Reisine T, Yasuda K;
DR WPT. 95-022804/03.
DR N-PED3; Q75926.
PT Polynucleotides and peptides derived from opiod receptor
PT screening assays for useful drug substances.
PS Claim 8: Page 207-211: 300pp; English.
CC The amino acid sequence of the novel mouse kappa opiod receptor MOR1.
CC a fragment (amplified from the cDNA library with primers Q75929-30) as a
CC probe. The primers are based on the conserved sequences present in the
CC second and third transmembrane domains of somatostatin (SRI) receptor
CC subtypes SSTR1, SSTR2 and SSTR3. The 1.2 kb SBT1 fragment from the mouse
CC kappa opiod receptor clone, lambda msl-1, was subcloned into the CMV
CC promoter-based expression vector PCMV-6b. The resultant construct
CC PCMV-msl-1 was transfected into COS-1 cells for protein production. The
CC gene encoding the opiod receptor can be used to produce complete,
CC truncated or chimeric opiod receptor proteins. The opiod receptors
CC thus produced are useful for the development of novel assays designed to
CC select or improve substances, capable of interacting with the opiod
CC receptor proteins, for use in diagnosis, drug design and therapeutic
CC applications.
SQ Sequence 380 AA;

Query Match 100.0%; Score 2839; DB 12; Length 380;
Best Local Similarity 100.0%; Pred. No. 8.42e-257;
Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


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Db      1  mespiqifrgdpgptcspacallpnsswfpmaesdngsvsgdqqlsahispaipy 60
QY      1  |||||
Db      61  iitavsvfvgvlgvngslvmfviirytkmktatniyifnlaladalvtltmpfgsaayl 120
QY      61  |||||
Db      121 mmswpgfdvclkvlsidgymftsifltlmsvdyiavchpvkaldftlplkakiini 180
QY      121 |||||
Db      181 ciwllassvgisaiylvgtkvredvdiacsldfpddeyswldlfnkicvfvfaftipyvl 240
QY      181 |||||
Db      241 iitvctylmlrlksvryllsgsrekdrnlrrtkllyvvavflicwtpihifilvealg 300
QY      241 |||||
Db      301 stshsraalsstiffcalgtntslmpvlyafdenfkrcfrcfcpikmmrgstnry 360
QY      301 |||||
Db      361 rntvqgpaasmrdygmknkpy 380
QY      361 |||||
QY      361 RNTVQDPASMRDYGANKRPV 380

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RESULT 2
ID      R76783 standard; Protein; 380 AA.
AC      R76783;
DE      11-DEC-1995 (first entry)
DE      Rat kappa opiate receptor.
KW      kappa opiate receptor; mu opiate receptor; hMOR; opiate agonist;
        opiate antagonist; drug abuse; analgesic.
OS      Rattus sp.
PN      WO9520667-A1.
PR      03-AUG-1995.
PR      30-JAN-1995; 001144.
PR      28-JAN-1994; US-188275.
PA      (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA      (USSH ) US SEC DEPT HEALTH.
PI      Johnson PS. Persico AM, Uhl G, Wang J;
DR      MPI: 95-275452/36.
PT      New DNA encoding human mu opiate receptor - used esp. for screening
PT      opds. for activity as opiate agonists or antagonists
PS      Disclosure; Page 29-30; 49pp; English.
CC      hMOR cDNA was obtd. from a human cerebral cortical cDNA library
CC      screened with fragments of a rat mu opiate receptor. The encoded
CC      protein showed homology to rat mu, delta and kappa opiate
CC      receptors (R76781-83).
SQ      Sequence 380 AA:

```

```

Query Match          99.6%; Score 2829; DB 13; Length 380;
Best local Similarity 98.9%; Pred. No. 7,76e-256;
Matches 376; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

```

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Db      1  mespiqifrgdpgptcspacallpnsswfpmaesdngsvsgdqqlsahispaipy 60
QY      1  |||||
Db      61  iitavsvfvgvlgvngslvmfviirytkmktatniyifnlaladalvtltmpfgsaayl 120
QY      61  |||||
Db      121 mmswpgfdvclkvlsidgymftsifltlmsvdyiavchpvkaldftlplkakiini 180
QY      121 |||||
Db      181 ciwllassvgisaiylvgtkvredvdiacsldfpddeyswldlfnkicvfvfaftipyvl 240
QY      181 |||||
QY      181 ciwllassvgisaiylvgtkvredvdiacsldfpddeyswldlfnkicvfvfaftipyvl 240

```

```

Db      241 iitvctylmlrlksvryllsgsrekdrnlrrtkllyvvavflicwtpihifilvealg 300
QY      241 |||||
Db      301 stshsraalsstiffcalgtntslmpvlyafdenfkrcfrcfcpikmmrgstnry 360
QY      301 |||||
Db      361 rntvqgpaasmrdygmknkpy 380
QY      361 |||||
QY      361 RNTVQDPASMRDYGANKRPV 380

```

```

RESULT 3
ID      R72591 standard; Protein; 380 AA.
AC      R72591;
DE      01-DEC-1995 (first entry)
DE      Mammalian kappa opiod receptor protein.
KW      Mammalian kappa opiod receptor; mouse delta opiod receptor; analgesic;
        amplification; primer; rat; probe; E.coli; Rt-PCR; hypnotic compound; ds.
OS      Rattus rattus.
FH      Key
FT      CDS          Location/Qualifiers
FT      /tag= a
FT      /product= kappa opiod receptor
PN      J07070191-A.
PD      14-MAR-1995.
PE      30-JUL-1993; 190261.
PR      09-JUL-1993; JP-170591.
PA      (TAKE ) TAKEDA CHEM. IND. LTD.
DR      MPI: 95-144857/19.
DR      N-FSDB; Q86725.
PT      Kappa opiod receptor protein and cells expressing it - useful
PT      for the screening of compounds for analgesic and hypnotic
PT      properties
PS      Claim 2; Page 9-10; 15pp; Japanese.
CC      The amino acid sequence of the novel mammalian kappa opiod receptor.
CC      The gene was isolated by amplifying a fragment from rat brain mRNA by
CC      reverse transcriptase-PCR (RT-PCR) using primers Q86726-7 derived from
CC      the mouse delta-opiod receptor gene. This fragment was cloned into the
CC      plasmid pCRII to produce pRII. The plasmid pRII was used to probe a rat
CC      brain DNA library in lambda ZAP1 to obtain a clone of the rat kappa
CC      opiod receptor gene, designated pXOR2. This clone was introduced into
CC      E.coli JM109 for production of the receptor protein. The receptor protein
CC      is useful for screening of analgesic and hypnotic compounds including
CC      peptides and proteins.
SQ      Sequence 380 AA:

```

```

Query Match          99.4%; Score 2823; DB 13; Length 380;
Best local Similarity 98.7%; Pred. No. 2.94e-235;
Matches 375; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

```

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Db      1  mespiqifrgdpgptcspacallpnsswfpmaesdngsvsgdqqlsahispaipy 60
QY      1  |||||
Db      61  iitavsvfvgvlgvngslvmfviirytkmktatniyifnlaladalvtltmpfgsaayl 120
QY      61  |||||
Db      121 mmswpgfdvclkvlsidgymftsifltlmsvdyiavchpvkaldftlplkakiini 180
QY      121 |||||
Db      181 ciwllassvgisaiylvgtkvredvdiacsldfpddeyswldlfnkicvfvfaftipyvl 240
QY      181 |||||
QY      181 ciwllassvgisaiylvgtkvredvdiacsldfpddeyswldlfnkicvfvfaftipyvl 240
QY      241 iitvctylmlrlksvryllsgsrekdrnlrrtkllyvvavflicwtpihifilvealg 300

```


Db	301	ststataistavysciaalgyrnslnpylaflidenkrcfrdcfcfakrmernglnrv	360
Oy	301	STSHSTALSSYYCICALGYTNSLNPVLAFLDENKRCFRDCFPKKRMERQSTNRY	360
Db	361	rnttqdpasmrdivvgmknkv	380
Oy	361	RNTVDPSAMRDKVGGMKNKV	380

RESULT 4
ID R88722 standard; Protein; 380 AA.
AC R88722;
DT 04-SEP-1996 (first entry)
DE Human kappa opioid receptor.
KW Human, kappa opioid receptor; psychiatric disorder; cardiovascular
KW neurology; diagnosis.
OS Homo sapiens.
PN W09601898-A1.
PD 25-JAN-1996.
PF 07-JUL-1995; F00912.
PR 11-JUL-1994; F9-008531.
PA (VYSI-) UNIV PASTEUR STRASBOURG LOTIS.
PI Kieffer B, Simonin F;
DR WPI: 96-097628/10.
DR N-PSDB: T12550.
DT New nucleic acid encoding the human Kappa opioid receptor - useful
PT in diagnosis and therapy, and for isolating receptor ligands and
PT modulators
PS Claim 7; Page 13-15; 30pp; French.
CC The sequence coding for the human kappa opioid receptor was
CC obtained from two overlapping cDNA fragments isolated from a
CC human placental cDNA library. The fragments were amplified from
CC the library using PCR primers based on the sequence of human
CC genomic clones which hybridised with a murine delta receptor cDNA
CC probe. Nucleotide probes derived from the kappa opioid receptor
CC coding sequence are useful for diagnosis of neurological, cardio-
CC vascular and psychiatric disorders associated with opioid
CC receptors. The receptor can be used for identifying e.g. agonists
CC of its activity for potential use as analgesics.
QC Sequence 380 AA;

Query Match:	96.7%	Score 2746;	DB 17;	Length 380;
Best Local Similarity:	93.7%;	Pred. No. 7,80e-248;		
Matches 356;	Conservative 18;	Mismatches 6;	Indels 0;	Gaps 0;
Db	1	msdpqiftrgpgfpcapacacippnssawfpgyweapdsngsagsedaglepahispapv	60	
Qy	1	MSDPQIRGPDGPICPSACLLNSSSWRFNMLSDSDNGSVGGEDQLEAHHSPIAPV	60	
Db	61	itavsvyfvvgvayvgsalvmfvaiirvkmktnaiyifnlaladalvtttmpqgstvyl	120	
Qy	61	ITAVSVYFVVGIVGNSLVMEFVIRYKMTANIIYFNLALDALVATTTMPQSAVYL	120	
Db	121	maswpgfvclcklvtasldyymfesiifltumsvdrylavchpkaldfttptlakini	180	
Qy	121	MNSWPGFVCLCKLYISLDYIMFESITFLTMASVDRIACHPKALDFTPTLAKIINI	180	
Db	181	civilssvsgisaivaylgvltkvegdvylecsiqfpdddysswdlfnkicvfiiafvipvl	240	
Qy	181	CIVLSSVSGISAVIYLGVTKREBDVYLECSIQFPDDEYSWMDLFMKICVFVFAFVPL	240	
Db	241	ititcytlmliirllksvlllsgsrkdnrlritltlvvvaavfvcktcphlfiilveaig	300	
Qy	241	IITCYTLMIRLLKSVRLSGSRKDRRLRIRITLVVVAVFICWPIHIFILVYALG	300	
Db	301	sthsstaalseyfciaaygnsslnpilaiflaiefnkrctfcdcfjllmmmergstary	360	
Qy	301	STHSSTAALSSYFCIALGYNSSLNPYLAFIDENKRCRCDFCFJLKMMERQSTNRY	360	
Db	361	entvgdpeaylidigmnkpv	380	
Qy	361	ENTVGDPEAYLIDIGMNNKPV	380	

ID	Result	5	Standard	Protein	295	AA
AC	R67672					
DT	18-AUG-1995					(first entry)
DE	Human kappa opioid receptor partial protein.					
KW	Mouse; kappa; delta; mu; opioid receptor; brain; primer; PCR; amplify;					
KW	transmembrane domain; somatostatin receptor; human; expression vector;					
KW	truncate; Chlmaeric; assay; probe.					
OS	Homo sapiens.					
FH	Key					Location/Qualifiers
FT	Misc.difference 169					/label= Any amino acid
FT	Misc.difference 181					/label= Any amino acid
FT	Misc.difference 265					/label= Any amino acid
FT	Misc.difference 269					/label= Any amino acid
PN	W09428132-A.					
PD	08-DEC-1994.					
PF	20-MAY-1994.					U05747.
PR	20-MAY-1993.					US-066296.
PR	30-JUL-1993.					US-100694.
PR	05-NOV-1993.					US-147592.
PA	(ARCH-) ARCH DEV CORP.					
PI	Bell GI, Reisine T, Yasuda K;					
DR	WPI; 95-022804/03.					
DR	N-PSDB: Q75931.					
PT	Polynucleotides and peptides derived from opioid receptor					
PT	polypeptides - for use in therapeutic compositions and in					
PT	screening assays for useful drug substances.					
PS	Claim 12; Page 236-239; 500pp; English.					
CC	The partial amino acid sequence of the novel human kappa opioid receptor					
CC	The corresponding gene was isolated from a human brain hippocampus cDNA					
CC	library using a probe from the mouse kappa opioid receptor gene (Q75926).					
CC	The gene is missing the N-terminal sequence. The C-terminal sequence is					
CC	very similar to the mouse kappa opioid receptor sequence. Of the					
CC	C-terminal 293 amino acids, 281 residues are identical and 6 residues					
CC	have conservative substitutions. The gene encoding the human opioid					
CC	receptor can be placed in a suitable expression vector for production of					
CC	the protein in a cell. The opioid receptors thus produced are useful for					
CC	the development of novel assays designed to select or improve substances,					
CC	capable of interacting with the opioid receptor proteins, for use in					
CC	diagnosis, drug design and therapeutic applications.					

Query	Match	Similarity	Score	DB	Length
Query Maccs	75.0%	92.5%	2130	12	255
Best Local	92.5%	156	186		
Matches	273	Conservative	13	Mismatches	8
				Indels	1
				Gaps	

RESULT 6


```

ID R65188 standard; Protein; 356 AA.
AC R65188;
DE 19-APR-1995 (first entry)
DE Murine mu-subtype opioid receptor.
KW Mu-subtype opioid receptor; MOR; drug addiction.
OS Rattus rattus.
FH Key Location/Qualifiers
FT Modified site 10..12
FT /note= "Putative N-linked glycosylation site"
FT Modified site 230
FT /note= "Threonine residue especially favourable
FT for protein kinase A phosphorylation"
FT Region 25..48
FT /note= "hydrophobic membrane spanning region"
FT Region 58..78
FT /note= "hydrophobic membrane spanning region"
FT Region 96..118
FT /note= "hydrophobic membrane spanning region"
FT Region 139..166
FT /note= "hydrophobic membrane spanning region"
FT Region 187..212
FT /note= "hydrophobic membrane spanning region"
FT Region 236..257
FT /note= "hydrophobic membrane spanning region"
FT Region 274..294
FT /note= "hydrophobic membrane spanning region"
FT Region 31..403-1994.
FT 31-AUG-1994.
FT 09-FEB-1994; 101968.
PR 26-FEB-1993; US-026140.
PA (AMCY ) AMERICAN CYANAMID CO.
PI Corbett MJ, Eppler CM, Shieh H, Zysk JR;
DR WPI: 94-265963/33.
DR N-PDB: Q79199.
PT Pure mu-type opioid receptor protein - and nucleic acid coding
PT for it
PS Claim 2; Fig 9; 39pp; English.
CC R65188 is the rat mu-subtype opioid receptor protein purified
CC from rat brain membranes, with biotinyl-D-endorphin (R5666)
CC as its ligand. It is encoded by the nucleotide sequence Q79199
CC which was synthesised using Q71022 and Q71023 as PCR primers.
CC R65188 is useful for identifying other receptor subtypes, for
CC screening new opioid ligands, and for studying mechanisms of
CC opioid action, e.g. drug addiction.
SQ Sequence 356 AA.

Query Match 59.3%; Score 1683; DB 11; Length 356;
Best Local Similarity 62.8%; Pred. No. 1.15e-145;
Matches 213; Conservative 60; Mismatches 62; Indels 4; Gaps 4;

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RESULT 7
ID R71966 standard; Protein; 400 AA.
AC R71966;
DE 20-OCT-1995 (first entry)
DE Human mu opioid receptor.
DE Mu opioid receptor; MOR; gene therapy; diagnostic.
OS Homo sapiens.
FH Homo sapiens.
FT W09507983-A.
FT 23-MAR-1995.
FT 13-SEP-1994; U10358.
FT 13-SEP-1993; US-120601.
PA (INDV ) UNIV INDIANA FOUND.
PI Yu L,
DR WPI: 95-131351/17.
DR N-PDB: Q89226.
PT New nucleic acid encoding new human mu opioid receptor - and
PT related vectors, transfected cells, antibodies etc., useful in
PT diagnosis, treatment and drug screening.
PS Claim 4; Page 211-214; 26pp; English.
CC A cDNA library constructed from human caudate nucleus mRNA was
CC screened with rat mu opioid receptor cDNA under conditions of
CC low stringency. One positive clone included the sequence given in
CC Q89226, encoding a mu opioid receptor MOR (R71964). The cDNA
CC is used for prodn. of recombinant MOR, in gene therapy, etc.
SQ Sequence 400 AA.

Query Match 59.1%; Score 1677; DB 13; Length 400;
Best Local Similarity 66.6%; Pred. No. 4.31e-145;
Matches 207; Conservative 52; Mismatches 45; Indels 3; Gaps 3;

```


CC opiate specific ligand. Recombinant hMOR1 can be used to screen
CC compounds for analgesic activity.
SQ Sequence 400 AA.

Query Match 59.0%; Score 1675; DB 13; Length 400;
Best Local Similarity 66.6%; Pred. No. 6,70e-145;
Matches 207; Conservative 52; Mismatches 49; Indels 3; Gaps 3;

Db 70 altlmalyicvavglfngflvmvviyrytknktatniylfnaladalatsclpfqsvn 129
:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 59 PVLITAVSVVVEVGLVGNLSLVEFVIRTKMTATNIYFNALADALVTTMPQSAV 118
130 ylmgtwpgftllckivisldymmfscftlcmsvdyriavchpkaiddftprnakii 189
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 119 YLMSWPFEDVLCIKYISIDYIMFTSITLLMMSVDRYIAVCHPKAIDFRIPLAKKII 178
190 nvcnwflssaajlpvmfmatkkyrg-s-ldctllfsbptw-ywenlvkicvifafamp 246
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 179 NCIWMLASSVGSIAIVLGITKVRVEDVIEGSLQFPDDEYSWDLFMKICVFAFAVFP 238
247 vllitvcyglmlrlkkyvmlsgskednrlrltmvlyvvaavfvcwplhiyvilka 306
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 239 VALLVCYGLMLRLKSVLSSGSKEDNRLRLTKVLYVVAVFTICWPHIFLVEA 298
307 lvtibetltqtwshfclalgytnsclnpylvaflidenkrcfrefcitsnlegqust 366
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 299 LSTSHSTALSSYFCIALGTNSSLNLYIAFLDENKRCFRCFRIKMKMEQSTN 358
Db 367 rlrqtridhps 377
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 359 RVNMYVODPAS 369

RESULT 11
ID R76782 standard; Protein; 372 AA.
AC R76782;
DE 11-DEC-1995 (first entry)
DE Rat delta opiate receptor.
KW Delta opiate receptor; mu opiate receptor; hMOR; opiate agonist;
KW opiate antagonist; drug abuse; analgesic.
OS Rattus sp.
PN W09523667-A1.
PD 03-AUG-1995.
PR 30-JAN-1995; U01144.
PR 28-JAN-1994; US-188275.
PA (USCH) US DEPT HEALTH & HUMAN SERVICES.
PA (USCH) US SEC DEPT HEALTH.
PI Johnson PS, Persico AM, Uhl G, Wang J;
PI WPI; 95-275452/36.
PT New DNA encoding human mu opiate receptor - used esp. for screening
PT cpds. for activity as opiate agonists or antagonists
PS Disclosure; Page 28-29; 49pp; English.
CC hMOR cDNA was obtd. from a human cerebral cortical cDNA library
CC screened with fragments of a rat mu opiate receptor. The encoded
CC protein showed homology to rat mu, delta and kappa opiate
CC receptors (R76781-83).
SQ Sequence 372 AA;

Query Match 56.7%; Score 1610; DB 13; Length 372;
Best Local Similarity 65.6%; Pred. No. 1.11e-138;
Matches 214; Conservative 55; Mismatches 48; Indels 9; Gaps 7;

Db 15 llansvdfpsafpsaanaasgpar--sas-slalalatalysavcavglignvym 71
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 22 LCPNSSWPPMAESDSNGVSGEDQQLSASHTSPALPIITIAVSVVVEVGLVGNLSLW 81
Db 72 fglvvytklktatniylfnaladalatsclpfqsvnylmwtpfgellckavlsidyn 131
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 82 FVILITAVSVVVEVGLVGNLSLVEFVIRTKMTATNIYFNALADALVTTMPQSAV 141
132 mftsifcltmvsvdyriavchpkaiddftprnakiihclvnlavsgvypimvavtqp 191
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 142 MFTSIFCLTMVSVDYRIAVCHPKAIDFRIPLAKKIIINCIWMLASSVGSIAIVLGITKV 201

Db 192 rdga-vv-cltqfssp-swydwlvkicvrlfafafovplllitvcygmrlkrlsvrlls 247
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 202 REDVAVIECSLQFPDDEYSW-MDLFMKICVFAFAVFTIPLIIVCTLMILRLKSRFLLS 260
Db 248 gskedrlsrirtlmvlyvvgafvcwaphihfvylwclvdhnrqplvvaalhlclalq 307
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 261 GSREKDRNRLRTKVLVYVVAVFTICWPHIFLVEALGSSHSYA-ALSSYFCIALG 319
Db 308 yanssnpylvaflidenkrcfrcqlc 333
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 320 YTNSSLNLYIAFLDENKRCFRCRDFC 345

RESULT 12
ID R48629 standard; Protein; 372 AA.
AC R48629;
DE 15-SEP-1994 (first entry)
DE Sequence of murine delta opiod receptor deduced from the
DE DOR-1 cDNA clone.
KW Opioid receptor; morphine; opiate.
OS Mus musculus.

FM Key Location/Qualifiers
FT Region 46..75
FT /label= putative membrane spanning region
FT Region 85..102
FT /label= see above
FT Region 125..144
FT /label= see above
FT Region 168..189
FT /label= see above
FT Region 215..238
FT /label= see above
FT Region 262..284
FT /label= see above
FT Region 295..308
FT /label= see above
PN W09404552-A.

PD 03-MAR-1994.
PF 13-AUG-1993; U07665.
PR 13-AUG-1992; US-929200.
PA (REGC) UNIV CALIFORNIA.
PI Edwards RH, Evans CJ, Kaufman D, Keith DE;
PI WPI; 94-083099/10.

DR N-PSDB; Q36700.
PT DNA encoding opiod receptors and antibodies against this
PT receptor - used to express and locate these receptors, and screen
PT cpds. for opiod (ant)agonist activity
PS Claim 10; Fig 5; 74pp; English.

CC A cDNA library was constructed using mRNA isolated from the NG109-15
CC cell line. A single clone, named the DOR-1 clone was isolated.
CC Comparisons with known sequences in Genbank showed highest homology
CC between DOR-1 and the G-protein-coupled somatostatin receptor. Other
CC features of the DOR-1 clone AA sequence deduced from the cDNA
CC sequence include 3 consensus glycosylation sites at residues 18 and
CC 33 (predicted to be in the extracellular N-terminal domain), and at
CC residue 310 (close to the C-terminus and predicted to be
CC intracellular). Phosphokinase C consensus sites are present within
CC predicted intracellular domains, at residues 242,255, 344 & 352.
CC Seven putative membrane-spanning regions were identified. The DOR-1
CC clone produces a delta receptor with a predicted mol. wt. of 40,556
CC kdaltons prior to post-translational modifications.

Query Match 56.3%; Score 1597; DB 9; Length 372;
Best Local Similarity 66.7%; Pred. No. 1.94e-137;
Matches 206; Conservative 51; Mismatches 46; Indels 6; Gaps 5;

Db 47 alalatalysavcavglignvymfgivrytklktatniylfnaladalatsclpfqs 106
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 57 ALPVLITAVSVVVEVGLVGNLSLVEFVIRTKMTATNIYFNALADALVTTMPQSAV 116
107 akymwtpfgellckavlsidynmfscftlcmsvdyriavchpkaiddftprnak 166


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QY 117 AYVLMNSMFGVCLKIVISIDYNNFTSLFTILMASVRYIAVCHPVALDPRILKAK 176
Db 167 llniclwlasvgvpydimwvtpqrdga-vv-cmlqfisp--swydwetvklcivlfaif 222
QY 177 INICIMWLASSVGSAIVLGSTKVAEDVDYIECSIQPFDDDEYSW-WDLFMKICVFEVAF 235
Db 223 vvpilittvcygmllrlsvllssgskedslriltmavlvvgaafvvcapilifv1 282
QY 236 VLPVLIITVCYTLMLIRLSVRLSSGSKEDRNIRIKLVIVVAVFIICWPIHIFIL 295
Db 283 wtlvdinrrdpijvaalhlcalagyanslnpvlafidenfkrcfrqlcrtpcrgqp 342
QY 296 VEAIGSTSHSTA-ALSSYFCIALGTNSLNPVLAFLDENFKRCFRDCEPIKRMER 354
Db 343 gslrrprga 351
QY 355 GSNRYRYNT 363

RESULT 13
ID R67670 standard; Protein: 372 AA.
AC R67670;
DE 17-AUG-1995 (first entry)
KW Mouse delta opioid receptor MOR1.
KW Transmembrane domain; delta; mu; opioid receptor; brain; primer; PCR; amplify;
KW Truncate; chimeraic; assay; probe.
OS Mus musculus.
PN 009428132-A.
PD 08-DEC-1994.
PF 20-MAY-1994; U05747.
PR 30-JUL-1993; US-066296.
PR 05-NOV-1993; US-147592.
PA (ARCH-) ARCH DEV CORP.
PI Bell GI, Reisine T, Yasuda K;
DR WPI: 95-022804/03.
DR N-PSDB: Q75927
PT polynucleotides and peptides derived from opioid receptor
PT polypeptides - for use in therapeutic compositions and in
PT screening assays for useful drug substances.
PS Claim 5; Page 215-221; 300pp; English.
CC The amino acid sequence of the novel mouse delta opioid receptor MOR1.
CC The corresponding gene was isolated from a mouse brain cDNA library using
CC a fragment (amplified from the cDNA library with primers Q75929-30) as a
CC probe. The primers are based on the conserved sequences present in the
CC second and third transmembrane domains of somatostatin (SMT) receptor
CC subtypes SSTR1, SSTR2 and SSTR3. The 1.3 kb SSTR1-SSTR3 fragment from the
CC mouse delta opioid receptor clone, lambda msl-2, was subcloned into the
CC CMV promoter-based expression vector pCMV-6c. The resultant construct
CC pCMV-msl-2 was transfected into COS-1 cells for protein production. The
CC gene encoding the opioid receptor can be used to produce complete,
CC truncated or chimeric opioid receptor proteins. The opioid receptors
CC thus produced are useful for the development of novel assays designed to
CC select or improve substances, capable of interacting with the opioid
CC receptor proteins, for use in diagnosis, drug design and therapeutic
CC applications.
SQ Sequence 372 AA;

Query Match 56.3%; Score 1597; DB 12; Length 372;
Best Local Similarity 66.7%; Pred. No. 1,94e-137;
Matches 206; Conservative 51; Mismatches 46; Indels 6; Gaps 5;
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QY 177 INICIMWLASSVGSAIVLGSTKVAEDVDYIECSIQPFDDDEYSW-WDLFMKICVFEVAF 235
Db 223 vvpilittvcygmllrlsvllssgskedslriltmavlvvgaafvvcapilifv1 282
QY 236 VLPVLIITVCYTLMLIRLSVRLSSGSKEDRNIRIKLVIVVAVFIICWPIHIFIL 295
Db 283 wtlvdinrrdpijvaalhlcalagyanslnpvlafidenfkrcfrqlcrtpcrgqp 342
QY 296 VEAIGSTSHSTA-ALSSYFCIALGTNSLNPVLAFLDENFKRCFRDCEPIKRMER 354
Db 343 gslrrprga 351
QY 355 GSNRYRYNT 363

RESULT 14
ID R66503 standard; Protein: 371 AA.
AC R66503;
DE 19-JAN-1995 (first entry)
KW Murine delta opioid receptor.
KW delta opioid; enkephalin; receptor; mouse; murine; analgesic; pain;
KW drug addiction; neurological disorder; psychiatric; disorder;
KW cardiovascular disorder.
OS Mus musculus.
PN FR2697850-A.
PD 13-MAY-1994.
PF 10-NOV-1992; 013526.
PR 10-NOV-1992; FR-013526.
PA (USTR-) UNIV PASTEUR STRASBOURG LOUIS.
PI Kieffer B;
DR WPI: 94-178255/22.
DR N-PSDB: 066656.
PT New nucleic acid encoding opioid receptor - and related
PT polypeptide, antisense nucleic acid, probes, recombinant cells
PT and ligands, useful in diagnosis and treatment of e.g.
PT neurological disorders
PS Claim 8; Page 19-20; 29pp; French.
CC A cDNA bank constructed from hybridoma NG108-15, was used to
CC transfect COS-1 cells. The cells were tested for ability to bind
CC tritium labelled Tyr-D-Thr-Gly-Phe-Den-Phe, in the presence or
CC absence of the opioid antagonist naloxone. Clone K56 was isolated
CC from a positive colony and found to contain a 221bp insert. This
CC cDNA encodes a delta opioid (enkephalin) receptor with apparent
CC dissociation constant 1.4nM and Bmax 3.9-6.4 pmole/mg protein.
SQ Sequence 371 AA;

Query Match 52.8%; Score 1499; DB 10; Length 371;
Best Local Similarity 64.9%; Pred. No. 4.50e-128;
Matches 200; Conservative 52; Mismatches 51; Indels 5; Gaps 5;
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(TM)

MSearch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Thu Apr 16 13:33:04 1998; MasPar time 19.37 Seconds
Tabular output not generated. 840.647 Million cell updates/sec

Title: >US-08-292-694A-2
Description: (1-380) from US08292694A.pep
Perfect Score: 2839
Sequence: 1 MESPIQIFRGDPGPCTCSFSA.....RNTVDPASMRDYGKKNRPV 380

Scoring table:
PAM 150
Gap 11

Searched: 195121 seqs, 42852602 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: p1r55
1:p1r1 2:p1r2 3:p1r3 4:p1r4

Statistics: Mean 40.199; Variance 186.150; scale 0.216

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	2839	99.6	380	2	S36143	A:Accession: S36143.	1.15e-243
2	2816	99.2	380	2	JC2434	A:Accession: JC2434.	1.85e-242
3	2747	96.8	380	2	JC2338	TOIG of: jc2338 check	4.55e-236
4	2746	96.7	380	2	157005	TOIG of: 157005 check	5.55e-236
5	2610	91.9	380	2	A53259	TOIG of: a53259 check	2.10e-223
6	2350	82.8	310	2	MESPIQIFRG	This is a DE line.	2.34e-199
7	1680	59.2	392	2	S65693	TOIG of: s65693 check	1.23e-197
8	1678	59.1	392	2	A57510	A:Status: nucleic acid	1.87e-137
9	1677	59.1	400	2	156553	A:Accession: 156553.	2.31e-137
10	1674	59.0	398	2	156517	TOIG of: 156517 check	4.35e-137
11	1659	58.4	398	2	156504	TOIG of: 156504 check	1.04e-135
12	1612	56.8	372	2	138657	A:Accession: 138657.	2.13e-131
13	1610	56.7	372	2	S34592	TOIG of: s34592 check	3.25e-131
14	1597	56.3	372	2	B48227	TOIG of: b48227 check	5.06e-130
15	1473	51.9	367	2	156520	A:Accession: 156520.	1.15e-118
16	1471	51.8	367	2	JC2421	A:Accession: JC2421.	1.77e-118
17	1470	51.8	367	2	149022	A:Title: Cloning and f	2.18e-118
18	1465	51.6	367	2	S43087	TOIG of: s43087 check	6.25e-118
19	980	34.5	391	2	C41795	A:Accession: C41795.	8.85e-74
20	978	34.4	391	2	A39297	TOIG of: a39297 check	1.34e-73
21	976	34.4	391	2	A41795	F:95-120/Domain: trans	2.04e-73
22	968	34.1	388	2	JN0605	F:84-109/Domain: trans	1.09e-72
23	963	33.9	384	2	A47249	TOIG of: a47249 check	3.04e-72

ALIGNMENTS

RESULT ID	1	STANDARD:	PRT:	380 AA.
XX	S36143			
XX	xxxxxx			
DT	01-PAN-1900			
XX		A:Accession: S36143.		
CC		A:Accession: S36143		
CC		A:Status: preliminary		
CC		A:Molecule type: mRNA		
CC		A:Residues: 1-380 <NIS>		
CC		R:Chen, Y.; Mestek, A.; Liu, J.; Yu, L.		
CC		Biochem. J. 295, 625-628, 1993		
CC		A:Title: Molecular cloning of a rat kappa opioid receptor reveals sequence simi		
CC		A:Reference number: S36825		
CC		A:Accession: S36825		
CC		A:Status: preliminary		
CC		A:Molecule type: mRNA		
CC		A:Residues: 1-380 <CHP>		
CC		A:Cross-references: GB:I22001; NID:9409236; PID:9409237		
CC		R:Minami, M.; Toyota, T.; Katano, Y.; Maekawa, K.; Nakamura, S.; Onogi, T.; Kaneko		
CC		FEBS Lett. 329, 291-295, 1993		
CC		A:Title: Cloning and expression of a cDNA for the rat kappa-opioid receptor.		
CC		A:Reference number: S36102		
CC		A:Accession: S36102		
CC		A:Molecule type: mRNA		
CC		A:Residues: 1-41, 1-43-380 <MIN>		
CC		R:Li, S.; Zhu, J.; Chen, C.; Chen, Y.W.; Dertel, J.K.; Ashby, B.; Liu-Chen, L.Y		
CC		Biochem. J. 295, 629-633, 1993		
CC		A:Title: Molecular cloning and expression of a rat kappa opioid receptor.		
CC		A:Reference number: S39015		
CC		A:Accession: S39015		
CC		A:Molecule type: mRNA		
CC		A:Residues: 1-344, 1-346-380 <LIS>		
CC		R:Meng, F.; Xie, G.		
CC		Proc. Natl. Acad. Sci. U.S.A. 90, 9954-9958, 1993		
CC		A:Title: Cloning and pharmacological characterization of a rat kappa opioid rec		
CC		A:Reference number: A46789; MUID:94052210		
CC		A:Accession: A46789		
CC		A:Status: preliminary; translated from GB/EMBL/DBJ		
CC		A:Molecule type: mRNA		
CC		A:Residues: 1-380 <RES>		
CC		A:Cross-references: EMBL:000442; NID:9403486; PID:9403487		
CC		A:Keywords: G protein-coupled receptor; transmembrane protein		
CC		SEQUENCE 380 AA: 42688 MW: 808499 CN;		


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Query Match          99.6%; Score 2829; DB 2; Length 380;
Best Local Similarity 98.9%; Pred. No. 1.16e-243;
Matches 376; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 1 MESPQIFEGGEGPCAPACILPNSSSWFPMWAEEDSGSGSEDOQLESAHISPAIV 60
QY 1 MESPQIFEGGEGPCAPACILPNSSSWFPMWAEEDSGSGSEDOQLESAHISPAIV 60
Db 61 IITAVSVVFFVGVGNLSVMFVIRYTKMTATNTIYNLALADLVTTMPFOSAVYL 120
QY 61 IITAVSVVFFVGVGNLSVMFVIRYTKMTATNTIYNLALADLVTTMPFOSAVYL 120
Db 61 IITAVSVVFFVGVGNLSVMFVIRYTKMTATNTIYNLALADLVTTMPFOSAVYL 120
QY 61 IITAVSVVFFVGVGNLSVMFVIRYTKMTATNTIYNLALADLVTTMPFOSAVYL 120
Db 121 MNSWPGDVLCKIVISIDYNNFTSIFLTLMMSVDRIYAVCHPVKALDPRTPKAKIINI 180
QY 121 MNSWPGDVLCKIVISIDYNNFTSIFLTLMMSVDRIYAVCHPVKALDPRTPKAKIINI 180
Db 121 MNSWPGDVLCKIVISIDYNNFTSIFLTLMMSVDRIYAVCHPVKALDPRTPKAKIINI 180
QY 121 MNSWPGDVLCKIVISIDYNNFTSIFLTLMMSVDRIYAVCHPVKALDPRTPKAKIINI 180
Db 181 C1WLLASVGISAIYVGKRVREDVDVIECSIQFPDDEYSWMDLEFKICVFYFAEYIPVL 240
QY 181 C1WLLASVGISAIYVGKRVREDVDVIECSIQFPDDEYSWMDLEFKICVFYFAEYIPVL 240
Db 241 IITVCYTLMLIKKSVRLISGSRKRDNRIRITKLVVAVFIICWPIIHIFIIIEALG 300
QY 241 IITVCYTLMLIKKSVRLISGSRKRDNRIRITKLVVAVFIICWPIIHIFIIIEALG 300
Db 301 S1SHSTALSSYFICATAGYTNSLNPLVYAFLEDFEKRCFDFCPPIKMREROSTNRV 360
QY 301 S1SHSTALSSYFICATAGYTNSLNPLVYAFLEDFEKRCFDFCPPIKMREROSTNRV 360
Db 361 RNTVODPASMARDVGGMKRPV 380
QY 361 RNTVODPASMARDVGGMKRPV 380

RESULT 2
ID JC2434 STANDARD; PRT; 380 AA.
AC xxxxxx
XX 01-JAN-1900
DE A:Accession: JC2434.
XX A:Accession: JC2434
XX A:Molecule type: mRNA
CC A:Residues: 1-380 <MIS>
CC A:Cross-references: DDBJ:D31663
CC C:Genetics:
CC A:Map position: 1A2-3
CC A:Introns: 86/2; 204/1
CC C:Keywords: receptor
CC SEQUENCE 380 AA; 42630 MW; 803251 CN;

Query Match          99.2%; Score 2816; DB 2; Length 380;
Best Local Similarity 99.5%; Pred. No. 1.85e-242;
Matches 378; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 1 MESPQIFEGGEGPCAPACILPNSSSWFPMWAEEDSGSGSEDOQLESAHISPAIV 60
QY 1 MESPQIFEGGEGPCAPACILPNSSSWFPMWAEEDSGSGSEDOQLESAHISPAIV 60
Db 61 IITAVSVVFFVGVGNLSVMFVIRYTKMTATNTIYNLALADLVTTMPFOSAVYL 120
QY 61 IITAVSVVFFVGVGNLSVMFVIRYTKMTATNTIYNLALADLVTTMPFOSAVYL 120
Db 61 IITAVSVVFFVGVGNLSVMFVIRYTKMTATNTIYNLALADLVTTMPFOSAVYL 120
QY 61 IITAVSVVFFVGVGNLSVMFVIRYTKMTATNTIYNLALADLVTTMPFOSAVYL 120
Db 121 MNSWPGDVLCKIVISIDYNNFTSIFLTLMMSVDRIYAVCHPVKALDPRTPKAKIINI 180
QY 121 MNSWPGDVLCKIVISIDYNNFTSIFLTLMMSVDRIYAVCHPVKALDPRTPKAKIINI 180
Db 121 MNSWPGDVLCKIVISIDYNNFTSIFLTLMMSVDRIYAVCHPVKALDPRTPKAKIINI 180
QY 121 MNSWPGDVLCKIVISIDYNNFTSIFLTLMMSVDRIYAVCHPVKALDPRTPKAKIINI 180
Db 181 C1WLLASVGISAIYVGKRVREDVDVIECSIQFPDDEYSWMDLEFKICVFYFAEYIPVL 240
QY 181 C1WLLASVGISAIYVGKRVREDVDVIECSIQFPDDEYSWMDLEFKICVFYFAEYIPVL 240

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Db 241 IITVCYTLMLIKKSVRLISGSRKRDNRIRITKLVVAVFIICWPIIHIFIIIEALG 300
QY 241 IITVCYTLMLIKKSVRLISGSRKRDNRIRITKLVVAVFIICWPIIHIFIIIEALG 300
Db 301 S1SHSTALSSYFICATAGYTNSLNPLVYAFLEDFEKRCFDFCPPIKMREROSTNRV 360
QY 301 S1SHSTALSSYFICATAGYTNSLNPLVYAFLEDFEKRCFDFCPPIKMREROSTNRV 360
Db 361 RNTVODPASMARDVGGMKRPV 380
QY 361 RNTVODPASMARDVGGMKRPV 380

RESULT 3
ID JC2338 STANDARD; PRT; 380 AA.
AC xxxxxx
XX 01-JAN-1900
DE T01G of: jc2338 check: 8304 from: 1 to: 380.
XX T01G of: jc2338 check: 8304 from: 1 to: 380
CC >P1:JC2338
CC kappa opioid receptor - human
CC C:Species: Homo sapiens (man)
CC C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 10-Sep-1997
CC C:Accession: JC2338; A55354
CC R:Manuscript: E. J. Bare, L. J. Yang, D.
CC Biochem. Biophys. Res. Commun. 202, 1431-1437, 1994
CC A:Title: Isolation of a human kappa opioid receptor cDNA from placenta.
CC A:Reference number: JC2338
CC A:Accession: JC2338
CC A:Molecule type: mRNA
CC A:Residues: 1-380 <MAN>
CC A:Experimental source: placenta
CC R:Wang, J.B.; Johnson, P.S.; Wu, J.M.; Wang, W.F.; Uhl, G.R.
CC J. Biol. Chem. 269, 25966-25969, 1994
CC A:Title: Human kappa opiate receptor second extracellular loop elevates dynorph
CC A:Reference number: A55354
CC A:Accession: A55354
CC A:Status: preliminary
CC A:Molecule type: mRNA
CC A:Residues: 136-279 <MAN>
CC A:Cross-references: GB:I36130; NID:9598184; PID:9598185
CC C:Comment: This receptor preferentially binds to dynorphins.
CC C:Keywords: G protein-coupled receptor; receptor; transmembrane protein
CC F:60-85/Domain: transmembrane #status predicted <TM2>
CC F:95-114/Domain: transmembrane #status predicted <TM2>
CC F:133-154/Domain: transmembrane #status predicted <TM3>
CC F:177-199/Domain: transmembrane #status predicted <TM4>
CC F:228-251/Domain: transmembrane #status predicted <TM5>
CC F:275-296/Domain: transmembrane #status predicted <TM6>
CC F:311-333/Domain: transmembrane #status predicted <TM7>
CC SEQUENCE 380 AA; 42655 MW; 802911 CN;

Query Match          96.8%; Score 2747; DB 2; Length 380;
Best Local Similarity 93.9%; Pred. No. 4.52e-236;
Matches 357; Conservative 17; Mismatches 6; Indels 0; Gaps 0;

Db 1 MESPQIFEGGEGPCAPACILPNSSSWFPMWAEEDSGSGSEDOQLESAHISPAIV 60
QY 1 MESPQIFEGGEGPCAPACILPNSSSWFPMWAEEDSGSGSEDOQLESAHISPAIV 60
Db 61 IITAVSVVFFVGVGNLSVMFVIRYTKMTATNTIYNLALADLVTTMPFOSAVYL 120
QY 61 IITAVSVVFFVGVGNLSVMFVIRYTKMTATNTIYNLALADLVTTMPFOSAVYL 120
Db 61 IITAVSVVFFVGVGNLSVMFVIRYTKMTATNTIYNLALADLVTTMPFOSAVYL 120
QY 61 IITAVSVVFFVGVGNLSVMFVIRYTKMTATNTIYNLALADLVTTMPFOSAVYL 120
Db 121 MNSWPGDVLCKIVISIDYNNFTSIFLTLMMSVDRIYAVCHPVKALDPRTPKAKIINI 180
QY 121 MNSWPGDVLCKIVISIDYNNFTSIFLTLMMSVDRIYAVCHPVKALDPRTPKAKIINI 180

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Db 18: C1WLSSSVGISAIVLGTKVREDVYIECSLOFPDDDXSWMDLPMKICVETFAFVPTL 240
QY 181 C1WLSSSVGISAIVLGTKVREDVYIECSLOFPDDDXSWMDLPMKICVETFAFVPTL 240
Db 241 IIVCYTILMLRLKSVRLSGSRKDRNLRIIRLVLVVAFAVVCWMPPIHIFILVEALG 300
QY 241 IIVCYTILMLRLKSVRLSGSRKDRNLRIIRLVLVVAFAVVCWMPPIHIFILVEALG 300
Db 301 STSHSTAALSSYYFCIALGYTNSLNPVLYAFLEDFKSCFDFCPPIKMREROSTNRV 360
QY 301 STSHSTAALSSYYFCIALGYTNSLNPVLYAFLEDFKSCFDFCPPIKMREROSTNRV 360
Db 361 RNTVODPAPALRIDGDKMKPV 380
QY 361 RNTVODPAPALRIDGDKMKPV 380

RESULT 4
ID 157005 STANDARD; PRT; 380 AA.
AC xxxxxx
XX
XX 01-JAN-1900
DI
XX
DE TOIG of: 157005 check: 8302 from: 1 to: 380.
XX
XX TOIG of: 157005 check: 8302 from: 1 to: 380
CC
CC >PI:157005
CC opiod receptor kappa-1 - human
CC C/Species: Homo sapiens (man)
CC C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 29-Aug-1997
CC C/Accession: 157005
CC R/Zhu, J.; Chen, C.; Xue, J.
CC Life Sci. 56, 201-207, 1995
CC A/Title: Cloning of a human .kappa. opiod receptor from the brain.
CC A/Reference number: 157005
CC A/Accession: 157005
CC A/Status: preliminary; translated from GB/EMBL/DBJ
CC A/Molecule type: mRNA
CC A/Residues: 1-380 <RES>
CC A/Cross-references: GB:L37362; NID:g722617; PID:g722618
CC C/Genetics:
CC A/Genes: GDB:OPRK1; KOR
CC A/Cross-references: GDB:132651; OMIM:165196
CC C/Map position: 8q11.2-8q11.2
CC A/SEQUENCE 380 AA: 42645 MW: 802905 CN:
SQ

Query Match 96.7%; Score 2746; DB 2; Length 380;
Best Local Similarity 93.7%; Pred. No. 5,59e-236;
Matches 356; Conservative 18; Mismatches 6; Indels 0; Gaps 0;

Db 1 MDSPIOIEFGEGPCAPACLPSPNSAMPGAPPDNSNGSSEAOLEPAHISAIIV 60
QY 1 MDSPIOIEFGEGPCAPACLPSPNSAMPGAPPDNSNGSSEAOLEPAHISAIIV 60
Db 61 IITAVSVYVVGGLVNSLMEVYIIRYTKMTAFENIIFNLALADLVTTIMFQSEVYL 120
QY 61 IITAVSVYVVGGLVNSLMEVYIIRYTKMTAFENIIFNLALADLVTTIMFQSEVYL 120
Db 61 IITAVSVYVVGGLVNSLMEVYIIRYTKMTAFENIIFNLALADLVTTIMFQSEVYL 120
QY 61 IITAVSVYVVGGLVNSLMEVYIIRYTKMTAFENIIFNLALADLVTTIMFQSEVYL 120
Db 121 MNSWPGDVLCIKVIVSDIYNNFTSIFILPMASVDRIYAVCHPVKALDPRTPKAKIINT 180
QY 121 MNSWPGDVLCIKVIVSDIYNNFTSIFILPMASVDRIYAVCHPVKALDPRTPKAKIINT 180
Db 121 MNSWPGDVLCIKVIVSDIYNNFTSIFILPMASVDRIYAVCHPVKALDPRTPKAKIINT 180
QY 121 MNSWPGDVLCIKVIVSDIYNNFTSIFILPMASVDRIYAVCHPVKALDPRTPKAKIINT 180
Db 181 C1WLSSSVGISAIVLGTKVREDVYIECSLOFPDDDXSWMDLPMKICVETFAFVPTL 240
QY 181 C1WLSSSVGISAIVLGTKVREDVYIECSLOFPDDDXSWMDLPMKICVETFAFVPTL 240
Db 181 C1WLSSSVGISAIVLGTKVREDVYIECSLOFPDDDXSWMDLPMKICVETFAFVPTL 240
QY 181 C1WLSSSVGISAIVLGTKVREDVYIECSLOFPDDDXSWMDLPMKICVETFAFVPTL 240
Db 241 IIVCYTILMLRLKSVRLSGSRKDRNLRIIRLVLVVAFAVVCWMPPIHIFILVEALG 300
QY 241 IIVCYTILMLRLKSVRLSGSRKDRNLRIIRLVLVVAFAVVCWMPPIHIFILVEALG 300
Db 301 STSHSTAALSSYYFCIALGYTNSLNPVLYAFLEDFKSCFDFCPPIKMREROSTNRV 360
QY 301 STSHSTAALSSYYFCIALGYTNSLNPVLYAFLEDFKSCFDFCPPIKMREROSTNRV 360
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QY 301 STSHSTAALSSYYFCIALGYTNSLNPVLYAFLEDFKSCFDFCPPIKMREROSTNRV 360
Db 361 RNTVODPAPALRIDGDKMKPV 380
QY 361 RNTVODPAPALRIDGDKMKPV 380

RESULT 5
ID A55259 STANDARD; PRT; 380 AA.
AC xxxxxx
XX
XX 01-JAN-1900
DI
XX
DE TOIG of: a55259 check: 7081 from: 1 to: 380.
XX
XX TOIG of: a55259 check: 7081 from: 1 to: 380
CC
CC >PI:A55259
CC kappa opiod receptor - guinea pig
CC N/Alternate names: dynorphin receptor
CC C/Species: Cavia porcellus (guinea pig)
CC C/Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 10-Sep-1997
CC C/Accession: A55259
CC R/Xie, G.; Meng, F.; Mansour, A.; Thompson, R.C.; Hoyersten, M.T.; Goldstein, A
CC Proc. Natl. Acad. Sci. U.S.A. 91, 3779-3783, 1994
CC A/Title: Primary structure and functional expression of a guinea pig kappa opio
CC A/Reference number: A55259
CC A/Accession: A55259
CC A/Status: preliminary
CC A/Molecule type: mRNA
CC A/Residues: 1-380 <XIE>
CC A/Cross-references: GB:U04092; NID:g476106; PID:g476107
CC C/Keywords: transmembrane protein
CC A/SEQUENCE 380 AA: 42736 MW: 800736 CN:
SQ

Query Match 91.9%; Score 2610; DB 2; Length 380;
Best Local Similarity 92.9%; Pred. No. 2,16e-223;
Matches 338; Conservative 21; Mismatches 5; Indels 0; Gaps 0;

Db 17 ARNACILPNSGAMLPQWAPPDGNSAGPDEQOLEPAHISPAIVITAVSVYVVGGLV 76
QY 17 ARNACILPNSGAMLPQWAPPDGNSAGPDEQOLEPAHISPAIVITAVSVYVVGGLV 76
Db 17 ARNACILPNSGAMLPQWAPPDGNSAGPDEQOLEPAHISPAIVITAVSVYVVGGLV 76
QY 17 ARNACILPNSGAMLPQWAPPDGNSAGPDEQOLEPAHISPAIVITAVSVYVVGGLV 76
Db 77 NSIVMFVITIRYTKMTAFENIIFNLALADLVTTIMFQSAVYLANSPFGDVLCIKVIVS 136
QY 77 NSIVMFVITIRYTKMTAFENIIFNLALADLVTTIMFQSAVYLANSPFGDVLCIKVIVS 136
Db 77 NSIVMFVITIRYTKMTAFENIIFNLALADLVTTIMFQSAVYLANSPFGDVLCIKVIVS 136
QY 77 NSIVMFVITIRYTKMTAFENIIFNLALADLVTTIMFQSAVYLANSPFGDVLCIKVIVS 136
Db 137 IDYNNFTSIFILPMASVDRIYAVCHPVKALDPRTPKAKIINTIC1WLSSSVGISAIVL 196
QY 137 IDYNNFTSIFILPMASVDRIYAVCHPVKALDPRTPKAKIINTIC1WLSSSVGISAIVL 196
Db 137 IDYNNFTSIFILPMASVDRIYAVCHPVKALDPRTPKAKIINTIC1WLSSSVGISAIVL 196
QY 137 IDYNNFTSIFILPMASVDRIYAVCHPVKALDPRTPKAKIINTIC1WLSSSVGISAIVL 196
Db 197 GGIKVRADVYIECSLOFPDDDXSWMDLPMKICVETFAFVPTLIIIVCYTILMLRLKSV 256
QY 197 GGIKVRADVYIECSLOFPDDDXSWMDLPMKICVETFAFVPTLIIIVCYTILMLRLKSV 256
Db 197 GGIKVRADVYIECSLOFPDDDXSWMDLPMKICVETFAFVPTLIIIVCYTILMLRLKSV 256
QY 197 GGIKVRADVYIECSLOFPDDDXSWMDLPMKICVETFAFVPTLIIIVCYTILMLRLKSV 256
Db 257 RLISGSRKDRNLRIIRLVLVVAFAVVCWMPPIHIFILVEALGSSSTAALSSYYFCI 316
QY 257 RLISGSRKDRNLRIIRLVLVVAFAVVCWMPPIHIFILVEALGSSSTAALSSYYFCI 316
Db 257 RLISGSRKDRNLRIIRLVLVVAFAVVCWMPPIHIFILVEALGSSSTAALSSYYFCI 316
QY 257 RLISGSRKDRNLRIIRLVLVVAFAVVCWMPPIHIFILVEALGSSSTAALSSYYFCI 316
Db 317 ALGYTNSLNPVLYAFLEDFKSCFDFCPPIKMREROSTNRVNTVODPAPALRIDGDKMKPV 376
QY 317 ALGYTNSLNPVLYAFLEDFKSCFDFCPPIKMREROSTNRVNTVODPAPALRIDGDKMKPV 376
Db 377 NKPV 380
QY 377 NKPV 380

RESULT 6
ID MESPQIQRDPGPTCSPACLLPNSSSWFPNMAESDSNGSVGSEDOQLESIAHISPAIVITAVSVYV 360
XX
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RESULT	9	STANDARD;	PRT;	400 AA.
ID	156553			
XX	XXXXXX			
XX	01-JAN-1900			
DT				
DE	A:Accession: I56553.			
XX				
CC	A:Accession: I56553			
CC	A:Status: nucleic acid sequence not shown; translated from GB/EMBL/DBJ			
CC	A:Molecule type: mRNA			
CC	A:Residues: 1-400 <RES>			
CC	A:Cross-references: GB:I29301; NID:g459831; PID:g459832			
CC	R:Wang, J.B.; Johnson, P.S.; Persico, A.M.; Hawkins, A.L.; Griffin, C.A.; Uhl, G.F.			
CC	submitted to GenBank, August 1994			
CC	A:Reference number: A58991			
CC	A:Accession: A58991			
CC	A:Status: translated from GB/EMBL/DBJ			
CC	A:Molecule type: mRNA			
CC	A:Residues: 1-50, 'N', 52-233, 'V', 235-400 <MAN>			
CC	A:Cross-references: GB:I25119; PID:g452073			
CC	R:Wang, J.B.; Johnson, P.S.; Persico, A.M.; Hawkins, A.L.; Griffin, C.A.; Uhl, G.F.			
CC	FEBS Lett. 338, 217-222, 1994			
CC	A:Title: Human mu opiate receptor, cDNA and genomic clones, pharmacologic character			
CC	A:Reference number: S41075			
CC	A:Accession: S41075			
CC	A:Status: nucleic acid sequence not shown			
CC	A:Molecule type: mRNA			
CC	A:Residues: 1-50, 'N', 52-400 <MA2>			
CC	R:Bare, U.A.; Kansson, E.; Yang, D.			
CC	FEBS Lett. 354, 213-216, 1994			
CC	A:Title: Expression of two variants of the human mu opiate receptor mRNA in SK-N-S			
CC	A:Reference number: S51215			
CC	A:Accession: S51215			
CC	A:Status: preliminary			
CC	A:Molecule type: mRNA			
CC	A:Residues: 387-400 <BAR>			
CC	C:Genetics:			
CC	A:Gene: GDB:G:OPRML			
CC	A:Cross-references: GDB:I37216; OMIM:600018			
CC	A:Map position: 6q24-6q25			
CC	C:Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein			
CC	F:73-96/Domain: transmembrane #status predicted <TM1>			
CC	F:107-133/Domain: transmembrane #status predicted <TM2>			
CC	F:144-165/Domain: transmembrane #status predicted <TM3>			
CC	F:188-208/Domain: transmembrane #status predicted <TM4>			
CC	F:236-257/Domain: transmembrane #status predicted <TM5>			
CC	F:283-304/Domain: transmembrane #status predicted <TM6>			
CC	F:323-344/Domain: transmembrane #status predicted <TM7>			
CC	F:9,12,33,40,48/Binding site: carbonylate (asn) (covalent) #status predicted			
CC	SEQUENCE 400 AA: 44779 MW: 873826 CN;			
SC				
Query Match	59.1%;	Score 1677;	DB 2;	Length 400;
Best local similarity	65.6%;	Pred. No. 2, 31e-137;		
Matches	207;	Conservative	52;	Mismatches 49; Indels 3; Gaps 3;
Db	70	ATTNATSYICVCGVLGFENFLMYIVTRYTKKRNATINITYFNALADALASTLPQSYN	129	
Qy	59	PVLIATVSVFVGVGLVGSILVMEVILIRTKRTATNIIYFNLALADALVTTTFQSAV	118	
Db	130	YIMGTWPGTGLICIVISIDYNNMFTSTFLLCTMVDVRIANCHEVKALDFETPNAKTI	189	
Qy	119	YLMNSWPGVDVCKIVISIDYNNMFTSTFLLTMVDVRIANCHEVKALDFETPNAKTI	178	
Db	190	NVCNMLSSAIGLPYPMFAITKRYQG-S-IDCIITFFSHPTW-YWENLIKICVFIPAFIMP	246	
Qy	179	NICIMLLASVQISAIYIGGVTKREDVDIECSLQFPDDEYSWMDLPMKICVFVAFVFP	238	
Db	247	VALITVCGIMLTRKSVAMLSGSKEDRNLRRTIRMYLVYVAVITVCTPHIYITKA	306	

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QY 239 VLIIVCTATLILRLKFSYRLSSSRKDRNLRLTICLVLVWVAFLICWPIHIFLVEA 298
Db 307 LVITPEITFQVSVNHFCIALGYTNSCLNPVLYALIDENFRCFREPIPIPTSSNEQNST 366
QY 299 LGSTSHSFAALSYFCIALGYTNSLNPVLYALIDENFRCFREPIPIKMEROSIN 358
Db 367 RIRONIRDHPS 377
QY 359 RVRNTVDDPAS 369

RESULT 10
XX AC ID I56517 STANDARD: PRT; 398 AA.
XX AC xxxxxx
XX 01-JAN-1900
DE TOIG of: I56517 check: 8374 from: 1 to: 398.
XX TOIG of: I56517 check: 8374 from: 1 to: 398
CC >P1,I56517
CC mu-opioid receptor - rat
CC C:Species: Rattus norvegicus (Norway rat)
CC C>Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 13-Mar-1997
CC C:Accession: I56517; I57951; A49680; I52314; S34593; A48799; I58154
CC C:R.Burrows, J.R.; Zhang, G.; Bouvier, C.; Saez, C.; Rommelspach, O.K.; Kelly, M.C.
CC C: J. Neurochem. 64, 14-24, 1995
CC A>Title: Characterization and distribution of a cloned rat mu-opioid receptor.
CC A:Reference number: I56517; MUID:95096825
CC A:Accession: I56517
CC A:Status: preliminary; translated from GB/EMBL/DBJ
CC A:Residues: 1-398 <RES>
CC A:Molecule type: mRNA
CC A:Cross-references: EMBL:U02083; NID:G403573; PID:G403574
CC R.Chen, Y.; Mestek, A.; Liu, J.; Hurrey, J.A.; Yu, L.
CC Moll. Pharmacol. 44, 8-12, 1993
CC A>Title: Molecular cloning and functional expression of a mu-opioid receptor fr
CC A:Reference number: I57951; MUID:93341493
CC A:Accession: I57951
CC A:Status: preliminary; translated from GB/EMBL/DBJ
CC A:Molecule type: mRNA
CC A:Residues: 1-398 <RES>
CC A:Cross-references: GB:U3069; NID:G348250; PID:G348251
CC R.Eppler, C.M.; Hulmes, J.D.; Wang, J.B.; Johnson, B.; Corbett, M.; Luthin, D.R.
CC J. Biol. Chem. 268, 26447-26451, 1993
CC A>Title: Purification and partial amino acid sequence of a mu opioid receptor f
CC A:Reference number: A49680; MUID:9407533
CC A:Accession: A49680
CC A:Status: preliminary
CC A:Molecule type: protein
CC A:Residues: 272-291 <RPP>
CC A:Experimental source: brain membranes
CC A>Note: sequence extracted from NCBI Dackbone (NCBI:140841)
CC R.Sedgell, M.; Roy, S.; Ramakrishnan, S.; Elde, R.; Ioh, H.H.
CC Biochem. Biophys. Res. Commun. 209, 563-574, 1995
CC A>Title: Complementary DNA cloning of a mu-opioid receptor from rat peritoneal
CC A:Reference number: I52314; MUID:95251654
CC A:Accession: I52314
CC A:Status: preliminary
CC A:Molecule type: mRNA
CC A:Residues: 101-340 <SED>
CC A:Cross-references: GB:S77863; NID:G998526
CC A:Experimental source: Sprague Dawley, peritoneal macrophages
CC R.Fukuda, K.; Kato, S.; Mori, K.; Nishi, M.; Takeshima, H.
CC FEBS Lett. 327, 311-314, 1993
CC A>Title: Primary structures and expression from cDNAs of rat oploid receptor de
CC A:Reference number: S34593
CC A:Accession: S34593
CC A:Molecule type: mRNA
CC A:Residues: 1-244, V', 246-398 <FUX>
CC R.Wang, J.

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Db 308 YANSLNPLYALFDENKRCRFOJCRKPCGSPDPSRAREA 351
QY 320 YTNSSLNPLYALFDENKRCRFOJCRKPCGSPDPSRAREA 363

RESULT 13
ID S34592 STANDARD; PRT; 372 AA.
XX xxxxxx
XX 01-JAN-1900
DE TOIG of: s34592 check: 2221 from: 1 to: 372.
XX
XX TOIG of: s34592 check: 2221 from: 1 to: 372
CC
CC >P1:S34592
CC delta opioid receptor - rat
CC C:Species: Rattus norvegicus (Norway rat)
CC C>Date: 10-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 23-Feb-1997
CC C:Accession: S34592; 156571
CC R:Rukuda, K.; Kato, S.; Mori, K.; Nishi, M.; Takeshima, H.
CC FEES Lett. 327, 311-314, 1993
CC A>Title: Primary structures and expression from cDNAs of rat opioid receptor delta
CC A:Reference number: S34592
CC A:Accession: S34592
CC A:Molecule type: mRNA
CC A:Residues: 1-372 <FUK>
CC R:Aboud, M.E.
CC J. Neurosci. Res. 27, 714-719, 1994
CC A>Title: Molecular cloning and expression of a rat delta opioid receptor from rat
CC A:Reference number: 156571
CC A:Accession: 156571
CC A>Status: preliminary; translated from GB/EMBL/DBJ
CC A:Molecule type: mRNA
CC A:Residues: 1-372 <RES>
CC A:Cross-references: EMBL:U00475; NID:g403488; PID:g514211
CC C:Genetics:
CC A:Gene: dori
CC C:Keywords: G protein-coupled receptor; transmembrane protein
SQ SEQUENCE 372 AA; 40449 KM; 719618 CN;

Query Match 56.7%; Score 1610; DB 2; Length 372;
Best Local Similarity 65.6%; Pred. No. 3,25e-131;
Matches 214; Conservative 55; Mismatches 46; Indels 9; Gaps 7;

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ID B48227 STANDARD; PRT; 372 AA.
XX
XX xxxxxx
XX 01-JAN-1900
DE TOIG of: b48227 check: 3372 from: 1 to: 372.
XX
XX TOIG of: b48227 check: 3372 from: 1 to: 372
CC
CC >P1:B48227
CC delta opioid receptor 1 - Mouse
CC C:Species: Mus musculus (house mouse)
CC C>Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 10-Sep-1997
CC C:Accession: B48227; #sequence_revision 26-May-1994 #text_change 10-Sep-1997
CC R:Yasuda, K.; Raynor, K.; Kong, H.; Breder, C.D.; Takeda, J.; Reisine, T.; Bell
CC Proc. Natl. Acad. Sci. U.S.A. 90, 6736-6740, 1993
CC A>Title: Cloning and functional comparison of kappa and delta opioid receptors
CC A:Reference number: B48227
CC A:Accession: B48227
CC A:Molecule type: mRNA
CC A>Status: preliminary
CC A:Residues: 1-372 <YAS>
CC A:Cross-references: GB:U1064; NID:g348246; PID:g348247
CC R:Kieffer, B.L.; Beffert, K.; Gaveriaux-Ruff, C.; Hirth, C.G.
CC submitted to the EMBL Data Library, February 1993
CC A:Reference number: S37807
CC A:Accession: S37807
CC A>Status: preliminary
CC A:Molecule type: mRNA
CC A:Residues: 1-372 <KID>
CC A:Cross-references: EMBL:L06322; NID:g192942; PID:g192943
CC R:Bezdega, T.; Chin, H.; Kim, E.; Jung, H.H.; Kozak, C.A.; Klee, W.A.
CC Proc. Natl. Acad. Sci. U.S.A. 90, 9305-9309, 1993
CC A>Title: Regional expression and chromosomal localization of the delta opiate r
CC A:Reference number: A48685; MCID:94022364
CC A:Accession: A48685
CC A>Status: preliminary
CC A:Molecule type: mRNA
CC A:Residues: 8-372 <B2D>
CC A:Experimental source: NG108-15 hybrid cells
CC A>Note: sequence extracted from NCBI backbone (NCBIN:138618, NCBI:138619)
CC R:Kieffer, B.L.; Beffert, K.; Gaveriaux-Ruff, C.; Hirth, C.G.
CC Proc. Natl. Acad. Sci. U.S.A. 89, 12048-12052, 1992
CC A>Title: The delta-opioid receptor: isolation of a cDNA by expression cloning a
CC A:Reference number: S36745
CC A:Accession: S36745
CC A:Molecule type: mRNA
CC A:Residues: 1-189, 'N', '191', 'GMVQ', '207-208', 'ACSSSPYQVL', '210-372 <KID>
CC A:Cross-references: EMBL:L06322
CC C:Keywords: brain; G protein-coupled receptor; glycoprotein; phosphoprotein; tr
SQ SEQUENCE 372 AA; 40561 KM; 727422 CN;

Query Match 56.3%; Score 1597; DB 2; Length 372;
Best Local Similarity 66.7%; Pred. No. 5,06e-130;
Matches 206; Conservative 51; Mismatches 46; Indels 6; Gaps 5;

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 W O R L D
 (TM)

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Msrch_pp protein - protein database search, using Smith-Waterman algorithm
 Run on: Thu Apr 16 13:30:34 1998; Maspar time 10.94 Seconds
 Tabular output not generated. 871.365 Million cell updates/sec

Title: >US-08-292-694A-2
 Description: (1-380) From US08292694A.pep
 Perfect Score: 2839
 Sequence: 1 MESPIQIFRSDPGFTCSPSA.....RNTVQDPASMDVGMKRPV 380

Scoring table: PAM 150
 Gap 11

Searched: 69112 seqs, 25083644 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: swiss-prot35
 1:swiss1

Statistics: Mean 50.098; Variance 102.197; scale 0.490

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	2839	100.0	380	1	OPRK_MOUSE	KAPPA-TYPE OPIOID RECE	0.00e+00
2	2829	99.6	380	1	OPRK_RAT	KAPPA-TYPE OPIOID RECE	0.00e+00
3	2747	96.8	380	1	OPRK_HUMAN	KAPPA-TYPE OPIOID RECE	0.00e+00
4	2610	91.9	380	1	OPRK_CAYO	KAPPA-TYPE OPIOID RECE	0.00e+00
5	1678	59.1	388	1	OPRM_MOUSE	MU-TYPE OPIOID RECEPTO	0.00e+00
6	1676	59.0	398	1	OPRM_RAT	MU-TYPE OPIOID RECEPTO	0.00e+00
7	1675	59.0	400	1	OPRM_HUMAN	MU-TYPE OPIOID RECEPTO	0.00e+00
8	1672	58.9	401	1	OPRM_PIG	MU-TYPE OPIOID RECEPTO	0.00e+00
9	1610	56.7	372	1	OPRD_RAT	DELTA-TYPE OPIOID RECE	1.46e-293
10	1608	56.6	372	1	OPRD_HUMAN	DELTA-TYPE OPIOID RECE	3.79e-293
11	1597	56.3	372	1	OPRD_MOUSE	DELTA-TYPE OPIOID RECE	7.09e-291
12	1473	51.8	367	1	OPRX_RAT	NOCICEPTIN RECEPTOR (O	2.65e-265
13	1471	51.8	370	1	OPRX_MOUSE	NOCICEPTIN RECEPTOR (O	6.84e-265
14	1465	51.6	370	1	OPRX_HUMAN	NOCICEPTIN RECEPTOR (O	1.18e-263
15	1459	51.4	370	1	OPRX_PIG	NOCICEPTIN RECEPTOR (O	2.02e-263
16	1447	51.0	370	1	OPRX_CAYO	NOCICEPTIN RECEPTOR (O	5.98e-260
17	1273	44.8	228	1	OPRD_PIG	DELTA-TYPE OPIOID RECE	3.25e-224
18	980	34.5	391	1	SSR1_MOUSE	SOMATOSTATIN RECEPTOR	1.65e-164
19	978	34.4	391	1	SSR1_RAT	SOMATOSTATIN RECEPTOR	4.20e-164
20	976	34.4	391	1	SSR1_HUMAN	SOMATOSTATIN RECEPTOR	1.07e-163
21	968	34.1	388	1	SSR4_HUMAN	SOMATOSTATIN RECEPTOR	4.44e-162
22	963	33.9	384	1	SSR4_RAT	SOMATOSTATIN RECEPTOR	4.56e-161
23	954	33.6	384	1	SSR4_MOUSE	SOMATOSTATIN RECEPTOR	3.01e-155

24	938	33.0	368	1	SSR2_BOVIN	SOMATOSTATIN RECEPTOR	5.16e-156
25	936	33.0	369	1	SSR2_PIG	SOMATOSTATIN RECEPTOR	1.37e-155
26	927	32.7	369	1	SSR2_RAT	SOMATOSTATIN RECEPTOR	8.59e-154
27	922	32.5	369	1	SSR2_MOUSE	SOMATOSTATIN RECEPTOR	8.78e-153
28	912	32.1	369	1	SSR2_HUMAN	SOMATOSTATIN RECEPTOR	9.14e-151
29	850	29.9	333	1	GPB8_HUMAN	PROBABLE G PROTEIN-COU	2.77e-138
30	819	28.8	363	1	SSR5_HUMAN	SOMATOSTATIN RECEPTOR	4.60e-132
31	815	28.7	418	1	SSR3_HUMAN	SOMATOSTATIN RECEPTOR	2.91e-131
32	812	28.6	363	1	SSR5_MOUSE	SOMATOSTATIN RECEPTOR	1.16e-130
33	792	27.9	328	1	GPB7_HUMAN	PROBABLE G PROTEIN-COU	1.17e-126
34	788	27.8	363	1	SSR5_RAT	SOMATOSTATIN RECEPTOR	7.39e-126
35	724	25.9	428	1	SSR3_RAT	SOMATOSTATIN RECEPTOR	4.37e-115
36	732	25.8	428	1	SSR3_MOUSE	SOMATOSTATIN RECEPTOR	1.09e-114
37	639	22.5	359	1	AG2R_CANFA	TYPE-1A ANGIOTENSIN II	2.83e-96
38	629	22.2	359	1	AG2R_HUMAN	TYPE-1A ANGIOTENSIN II	2.63e-94
39	626	22.1	359	1	AG2R_PIG	TYPE-1 ANGIOTENSIN II	1.02e-93
40	623	21.9	355	1	CKR1_HUMAN	C-C CHEMOKINE RECEPTOR	3.98e-93
41	617	21.7	359	1	AG2R_RABIT	TYPE-1 ANGIOTENSIN II	6.00e-92
42	616	21.7	359	1	AG2R_BOVIN	TYPE-1B ANGIOTENSIN II	9.42e-92
43	615	21.7	359	1	AG2S_RAT	TYPE-1B ANGIOTENSIN II	1.48e-91
44	614	21.6	349	1	GALR_HUMAN	GALANIN RECEPTOR (GALI	2.33e-91
45	610	21.5	359	1	AG2S_MOUSE	TYPE-1B ANGIOTENSIN II	1.42e-90

ALIGNMENTS

RESULT ID	1	OPRK_MOUSE	STANDARD:	PRT:	380 AA.
AC	P33534:				
DT	01-FEB-1994 (REL. 28, CREATED)				
DT	01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)				
DT	01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)				
DE	KAPPA-TYPE OPIOID RECEPTOR (KOR-1) (MSL-1).				
GN	OPRK1.				
OS	MUS MUSCULUS (MOUSE).				
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;				
OC	EUTHERIA; RODENTIA.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE-BRAIN;				
RX	MEDLINE: 93342064.				
RA	YASUDA K., RATNOR K., KONG H., BREDDER C.D., TAKEDA J., RELSINE T.,				
RA	BELL G.I.;				
RL	PROC. NATL. ACAD. SCI. U.S.A. 90:6736-6740(1993).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE: 95100967.				
RA	NISET M., TAKASHIMA H., MORI M., NAKAGAWA K.I., TAKUCHI I.;				
RA	BIOCHEM. BIOPHYS. RES. COMMUN. 205:1353-1357(1994).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE: 95251663.				
RA	LIU H.C., LU S., AUGUSTIN L.B., FELSHEIM R.F., CHEN H.C.;				
RA	LOH H.H., WEI L.N.;				
RL	BIOCHEM. BIOPHYS. RES. COMMUN. 209:639-647(1995).				
RN	[4]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE: 96084989.				
RA	BEKOWSKI S.M., ZHU J., LIU-CHEN L.Y., EISENSTEIN T.K.;				
RA	ADLER M.W., ROGERS T.J.;				
RL	J. NEUROIMMUNOL. 62:113-117(1995).				
CC	-1- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM				
CC	ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. RECEPTOR				
CC	FOR DYNORPHINS. MAY PLAY A ROLE IN ACOSUAL AND REGULATION OF				
CC	AUTONOMIC AND NEUROENDOCRINE FUNCTIONS.				
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.				
CC	-1- TISSUE SPECIFICITY: BRAIN (NEOCORTEX, HIPPOCAMPUS, AMYGALA,				
CC	MEDIAL HABENULA, HYPOTHALAMUS, LOCOS CERULEUS, AND PARABRACHIAL				
CC	NUCLEUS).				
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.				
DR	EMBL: L11065; G348249; -.				
DR	EMBL: D31665; G808876; -.				
DR	EMBL: D31663; G808876; JOINED.				

DR EMBL; D31664; G808876; JOINED.
 DR EMBL; S77872; G998532; -.
 DR EMBL; S77868; G998532; JOINED.
 DR EMBL; S77869; G998532; JOINED.
 DR EMBL; S8111; E257489; -.
 DR PIR; A48227; A48227.
 DR GCRDB; GCR_0635; -.
 DR GMD; MGI:97439; OPR1.
 DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; 1.
 DR G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
 KW PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.
 KW DOMAIN 1 58
 FT DOMAIN 1 58
 FT TRANSMEM 59 85
 FT DOMAIN 86 95
 FT TRANSMEM 96 117
 FT DOMAIN 118 132
 FT TRANSMEM 133 154
 FT DOMAIN 155 173
 FT TRANSMEM 174 196
 FT DOMAIN 197 222
 FT TRANSMEM 223 247
 FT DOMAIN 248 275
 FT TRANSMEM 276 299
 FT DOMAIN 300 311
 FT TRANSMEM 312 333
 FT DOMAIN 334 380
 FT DISULFID 131 210
 FT LIPID 345 345
 FT CARBOHYD 25 345
 FT CARBOHYD 39 39
 FT CONFLICT 211 211
 FT CONFLICT 231 231
 SQ SEQUENCE 380 AA; 42652 MW; C6F33212 CRC32;

Query Match 100.0%; Score 2839; DB 1; Length 380;
 Best Local Similarity 100.0%; Pred. No. 0.00e+00;

Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MESPIDIFRGDPPPTGSPGACILPNSSSWEPNNAESDSNGSVSEDOLESATISPAIV 60
 QY 1 MESPIDIFRGDPPPTGSPGACILPNSSSWEPNNAESDSNGSVSEDOLESATISPAIV 60
 Db 61 IITAVYVAVVGVGVNSIVMFIIRYTKMKATNTIIFNLALADLVTTMFGSAVL 120
 QY 61 IITAVYVAVVGVGVNSIVMFIIRYTKMKATNTIIFNLALADLVTTMFGSAVL 120
 Db 121 MNSWPGDVLCIKIVISIDYNNMTSIFTLTMSVDRYIAVCHFKALDPRTPKAKINI 180
 QY 121 MNSWPGDVLCIKIVISIDYNNMTSIFTLTMSVDRYIAVCHFKALDPRTPKAKINI 180
 Db 181 CWTLLASVGSIAIVGTRVEDVVICSLQPPDEYSWMDLPMKIGVFAFVPIVL 240
 QY 181 CWTLLASVGSIAIVGTRVEDVVICSLQPPDEYSWMDLPMKIGVFAFVPIVL 240
 Db 241 IITVCTMLILRIKSVRLISGRKENDRNIRITKLVLVVAVFIICWPIHIFIIIEALG 300
 QY 241 IITVCTMLILRIKSVRLISGRKENDRNIRITKLVLVVAVFIICWPIHIFIIIEALG 300
 Db 301 STSHSTAAISSTYFCIALGYTNSLNPVLYALDENFKRCFDECPITAKRMRGSTNRY 360
 QY 301 STSHSTAAISSTYFCIALGYTNSLNPVLYALDENFKRCFDECPITAKRMRGSTNRY 360
 Db 361 RNTVODPASMADVGGMKRPV 380
 QY 361 RNTVODPASMADVGGMKRPV 380

RESULT 2
 ID OPRK_RAT STANDARD; PRT; 380 AA.
 AC P34975;
 DT 01-FEB-1994 (REL. 28, CREATED)
 DT 01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)

DE KAPPA-TYPE OPTOID RECEPTOR (KOR-1).
 GN OPRK1 OR KOR-D.
 OS RATTUS NORVEGICUS (RAT).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN;
 RX MEDLINE; 94059008.
 RA CHEN Y., MESTER A., LIU J., YU L.,
 RL BIOCHEM. J. 295:625-628(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC MEDLINE; 93374033.
 RA KINAMI M., TOYA T., KATAO Y., MAEKAWA K., NAKAMURA S., ONOGI T.,
 RA KANEKO S., SATOH M.,
 RN FEBS LETT. 329:291-295(1993).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SPRAGUE-DAWLEY; TISSUE-BRAIN;
 RX MEDLINE; 94059009.
 RA LI S., ZHU J., CHEN C., CHEN Y.-W., DERIBL J.K., ASHBY B.,
 RA LIU-CHEN L.-Y.,
 RN BIOCHEM. J. 295:629-633(1993).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SPRAGUE-DAWLEY; TISSUE-BRAIN;
 RX MEDLINE; 94052210.
 RA MENG F., XIE G.-X., THOMPSON R.C., MANSOUR A., GOLDSTEIN A.,
 RA WATSON S.J., AKIL H.,
 RL PROC. NATL. ACAD. SCI. U.S.A. 90:9954-9958(1993).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN-WISTAR; TISSUE-BRAIN;
 RX MEDLINE; 93380575.
 RA NISHI M., TAKESHITA H., FUKUDA K., KATO S., MORI K.,
 RL FEBS LETT. 330:77-80(1993).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SPRAGUE-DAWLEY;
 RX MEDLINE; 95204422.
 RA YAKOVLEV A.G., KRUEGER K.E., FADEN A.I.,
 RL J. BIOL. CHEM. 270:6421-6424(1995).
 CC -1- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM
 ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. RECEPTOR
 FOR DOPAMINE AND NEUROENDOCRINE FUNCTIONS.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DR EMBL; I22001; G409237; -.
 DR EMBL; D16829; G404116; -.
 DR EMBL; I22536; G425189; -.
 DR EMBL; U00442; G403487; -.
 DR EMBL; D16534; G415310; -.
 DR EMBL; U17995; G727260; -.
 DR EMBL; U17993; G727260; JOINED.
 DR EMBL; U17994; G727260; JOINED.
 DR PIR; S36143; S36143.
 DR GCRDB; GCR_0635; -.
 DR GCRDB; GCR_0724; -.
 DR GCRDB; GCR_0790; -.
 DR GCRDB; GCR_0804; -.
 DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; 1.
 KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
 KW PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.
 KW DOMAIN 1 58
 FT DOMAIN 1 58
 FT TRANSMEM 59 85
 FT DOMAIN 86 95
 FT TRANSMEM 96 117
 FT DOMAIN 118 132
 FT TRANSMEM 133 154
 FT DOMAIN 155 173


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RESULT 4
ID OPERK_CANVO STANDARD: PRT: 380 AA.
AC P41144;
DT 01-FEB-1995 (REL. 31, CREATED)
DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE KAPPA-TYPE OPIOID RECEPTOR (KOR-1).
GN OPERK1
OS CAVIA PORCELLUS (GUINEA PIG).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-HARTLEY; TISSUE-BRAIN;
RX MEDLINE: 94224825.
RA XIE G.X., MENG F., MANSOUR A., THOMPSON R.C., HOVERSTEN M.T.,
RA GOLDSTEIN A., WATSON S.J., AKIL H.;
RA PROC. NATL. ACAD. SCI. U.S.A. 91:3779-3783(1994).
CC -1- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM
CC ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. RECEPTOR
CC FOR DYNORPHINS. MAY PLAY A ROLE IN AROUSAL AND REGULATION OF
CC AUTONOMIC AND NEUROENDOCRINE FUNCTIONS.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL: U04092; G476107; -.
DR GCRDB: GCR.0991; -.
DR PROSITE: PS00237; G-PROTEIN RECEPTOR; 1.
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
KW PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.
FT DOMAIN 1 58
FT TRANSMEM 59 85
FT DOMAIN 86 95
FT TRANSMEM 96 117
FT DOMAIN 118 132
FT TRANSMEM 133 154
FT DOMAIN 155 173
FT TRANSMEM 174 196
FT DOMAIN 197 222
FT TRANSMEM 223 247
FT DOMAIN 248 275
FT TRANSMEM 276 299
FT DOMAIN 300 311
FT TRANSMEM 312 333
FT DOMAIN 334 380
FT DISULFID 131 210
FT LIPID 345 345
FT CARBOHYD 25 25
FT CARBOHYD 39 42
SQ SEQUENCE 380 AA; 42736 MW; F9F34C4C CRC32;

Query Match 91.98; Score 2610; DB 1; Length 380;
Best Local Similarity 92.98; Pred. No. 0.00e+00;
Matches 338; Conservative 21; Mismatches 5; Indels 0; Gaps 0;

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QY 257 RLISGRKDRNRLRITRLVLVAVAFIICWPIHIFILVEALGSTSHSTAALSYFECI 316
317 ALGYNSSLNPIIYAFIDENKRCFDFCPFKRMEROSTSFVNTVDDPAYMRNVDSV
DB 317 ALGYNSSLNPIYAFIDENKRCFDFCPFKRMEROSTSFVNTVDDPAYMRNVDSV 376
QY 317 ALGYNSSLNPIYAFIDENKRCFDFCPFKRMEROSTSFVNTVDDPAYMRNVDSV 376
DB 377 NKPV 380
QY 377 NKPV 380
|||||
QY 377 NKPV 380

RESULT 5
ID OPERK_MOUSE STANDARD: PRT: 398 AA.
AC P42866; Q60768;
DT 01-NOV-1995 (REL. 32, CREATED)
DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE MU-TYPE OPIOID RECEPTOR (MOR-1).
GN OPERM1 OR OPERM OR MOR.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-C57BL/6; TISSUE-LIVER;
RX MEDLINE: 94377496.
RA MIN B.H., AUGUSTIN L.B., FELSHEIM R.F., FUCHS J.A., LOH H.H.;
RA PROC. NATL. ACAD. SCI. U.S.A. 91:9081-9085(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RX MEDLINE: 95377399.
RA ROSSI G.C., PAN Y.X., BROWN G.P., PASTERNAK G.W.;
RA FEBS LETT. 369:192-196(1995).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C; TISSUE-BRAIN;
RX MEDLINE: 95316184.
RA KAUBMAN D.L., KEITH D.E., ANTON B., TIAN J., MAGENDZO K.,
RA NEWMAN D., TRAN T., LEE D.S., WEN C., XIA Y., LOSIS A.C.,
RA EVANS C.J.;
RA J. BIOL. CHEM. 270:15877-15883(1995).
CC -1- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM
CC ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. RECEPTOR
CC FOR BETA-ENDORPHIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL: U10561; G565069; -.
DR EMBL: U10558; G565069; JOINED.
DR EMBL: U10559; G565069; JOINED.
DR EMBL: U10560; G565069; JOINED.
DR EMBL: U26915; G1055231; -.
DR EMBL: U19380; G8858865; -.
DR MGD: MGI:97441; OPERM.
DR PROSITE: PS00237; G-PROTEIN RECEPTOR; 1.
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
KW PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.
RN DOMAIN 1 64
FT TRANSMEM 65 94
FT DOMAIN 95 103
FT TRANSMEM 104 121
FT DOMAIN 122 143
FT TRANSMEM 144 163
FT DOMAIN 164 193
FT TRANSMEM 194 209
FT DOMAIN 210 234
FT TRANSMEM 235 257
FT DOMAIN 258 280
FT TRANSMEM 281 303
FT DOMAIN 304 311
FT TRANSMEM 312 328
FT DOMAIN 329 398
CYTOPLASMIC (POTENTIAL).

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FT DISTLTD 140 217 BY SIMILARITY.
 FT LIPID 351 351 PALMITATE (POTENTIAL).
 FT CARBOHYD 9 9 POTENTIAL.
 FT CARBOHYD 31 31 POTENTIAL.
 FT CARBOHYD 38 38 POTENTIAL.
 FT CARBOHYD 46 46 POTENTIAL.
 FT CONFLICT 22 22 C -> W (IN REF. 3).
 SQ SEQUENCE 398 AA; 44421 MW; C021489 CRC32;
 Query Match 59.1%; Score 1678; DB 1; Length 398;
 Best Local Similarity 65.8%; Pred. No. 0.00e+00;
 Matches 209; Conservative 55; Mismatches 49; Indels 4; Gaps 4;
 DB 68 AITMALISIVCVGLFSGFLVYIVRYTKKTAATNIYIENLALADALATSLPPOSVN 127
 QY 59 PYLITAVSVFVGVGVNSLVMEVILRYTKKTAATNIYIENLALADALATSLPPOSVN 118
 DB 128 YLMGMPENLICKIVISIDYNNMFTSTLTCTMSYDRIACHPYKALDEFTPRAKIV 187
 QY 119 YLMSNPEDVDICKIVISIDYNNMFTSTLTCTMSYDRIACHPYKALDEFTPRAKIV 178
 DB 188 NYCNWILSSAIGLPMFMATTKYKQ8-S-IDCTLFESHTW-YMENLTKICVFIAFTMP 244
 QY 179 NCIMWILSSAIGLPMFMATTKYKQ8-S-IDCTLFESHTW-YMENLTKICVFIAFTMP 238
 DB 245 VLIITVCGILMLRLKSVNMLSGSKEDNRLRITRMVAVVAVIVCWTPIHIVVILKA 304
 QY 239 VLIITVCGILMLRLKSVNMLSGSKEDNRLRITRMVAVVAVIVCWTPIHIVVILKA 298
 DB 305 LTIETETQYVSMHECTALGTNSCLNVLAFIDENKRCFPRECIPTSTIEQNSA 364
 QY 299 LSTISHSTALSSYFCALGTNSCLNVLAFIDENKRCFPRECIPTSTIEQNSA 358
 DB 365 RIRONTREHSTANTY 380
 QY 359 RVR-NTVODPASMRY 373
 RESULT 6
 ID OPRL_RAT STANDARD; PRT; 398 AA.
 AC P33335; 064064; 062846;
 DT 01-FEB-1994 (REL. 28, CREATED)
 DT 01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
 DI 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
 DE MU-TYPE OPIOID RECEPTOR (MOR-1) (OPIOID RECEPTOR B) (MOR1).
 GN OPRL OR MOR-B.
 OS RATTUS NORVEGICUS (RAT).
 CC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 RN 11
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN;
 RX MEDLINE; 93351652.
 RA FUKUDA K., KATO S., MORI K., NISHI M., TAKESHIMA H.;
 RL FEBS LETT. 327:311-314(1993).
 RN 12
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN;
 RX MEDLINE; 94052137.
 RA WANG J.-B., IMAI Y., EPLER M.C., GREGOR P., SPIVAK C., UHL G.R.;
 RL PROC. NATL. ACAD. SCI. U.S.A. 90:10230-10234(1993).
 RN 13
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN;
 RX MEDLINE; 93341493.
 RA CHEN Y., WESTER A., LIU J., HURLEY J.A., YU L.;
 RL MOL. PHARMACOL. 44:8-12(1993).
 RN 14
 RP SEQUENCE FROM N.A.
 RC STRAIN-SPRAGUE-DAWLEY; TISSUE-BRAIN;
 RA BUNZOW J.R., GRANDY D.K., KELLY M.;
 RL SUBMITTED (SEP-1993) TO EMBL/GENBANK/DBD; DATA BANKS.
 RN 15

RP SEQUENCE FROM N.A.
 RC STRAIN-SPRAGUE-DAWLEY; TISSUE-OLFACTORY BULB;
 RX MEDLINE; 94059560.
 RA THOMPSON R.C., MANSOUR A., AKIL H., WATSON S.J.;
 RL NEURON 11:903-913(1993).
 RN 16
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN;
 RX MEDLINE; 94246380.
 RA ZASTAWY R.L., GEORGE S.R., NGUYEN T., CHENG R., ISANOS J.,
 RL J. NEUROCHEM. 62:2099-2105(1994).
 RN 17
 RP SEQUENCE OF 356-391 FROM N.A.
 RX MEDLINE; 95172221.
 RA ZIMMERICH A., SIMON T., HOLIF V.;
 RL FEBS LETT. 359:142-146(1995).
 CC -1- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM
 CC ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. RECEPTOR
 CC FOR BETA-ENDORPHIN.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: BRAIN. IS EXPRESSED IN THE CEREBRAL CORTEX,
 CC CAUDATE PUTAMEN, NUCLEUS ACCUMBENS, SEPTAL NUCLEI, THALAMUS,
 CC HIPPOCAMPUS, AND HABENULA. NOT DETECTED IN CEREBELLUM.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DR EMBL; D16349; G391867; -;
 DR EMBL; L20684; G409150; -;
 DR EMBL; L13069; G348251; -;
 DR EMBL; U02083; G403574; -;
 DR EMBL; L22455; G457572; -;
 DR EMBL; U35424; G1017732; -;
 DR EMBL; S75669; G861432; -;
 DR PIR; S34593; S34593.
 DR GCRDB; GCR_0633; -;
 DR GCRDB; GCR_0637; -;
 DR GCRDB; GCR_0639; -;
 DR GCRDB; GCR_0640; -;
 DR GCRDB; GCR_0644; -;
 DR PROSITE; PS00237; G-PROTEIN COUPLED RECEPTOR; 1.
 KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
 KM PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.
 FT DOMAIN 1 64
 FT TRANSMEM 94
 FT DOMAIN 95 103
 FT TRANSMEM 104 121
 FT DOMAIN 122 143
 FT TRANSMEM 144 163
 FT DOMAIN 164 193
 FT TRANSMEM 194 209
 FT DOMAIN 210 234
 FT TRANSMEM 235 257
 FT DOMAIN 258 280
 FT TRANSMEM 281 303
 FT DOMAIN 304 311
 FT TRANSMEM 312 328
 FT DOMAIN 329 398
 FT DISTLTD 140 217
 FT LIPID 351 351
 FT CARBOHYD 9 9
 FT CARBOHYD 31 31
 FT CARBOHYD 38 38
 FT CARBOHYD 46 46
 FT CONFLICT 237 237
 FT CONFLICT 245 245
 FT CONFLICT 367 367
 SQ SEQUENCE 398 AA; 44494 MW; 2C21013D CRC32;
 Query Match 59.0%; Score 1676; DB 1; Length 398;
 Best Local Similarity 66.1%; Pred. No. 0.00e+00;
 Matches 209; Conservative 53; Mismatches 50; Indels 4; Gaps 4;
 DB 68 AITMALISIVCVGLFSGFLVYIVRYTKKTAATNIYIENLALADALATSLPPOSVN 127

[illegible]


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FT TRANSMEM 147 166 3 (POTENTIAL).
FT DOMAIN 167 196 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 197 212 4 (POTENTIAL).
FT DOMAIN 213 237 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 238 260 5 (POTENTIAL).
FT DOMAIN 261 283 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 284 306 6 (POTENTIAL).
FT DOMAIN 307 314 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 315 331 7 (POTENTIAL).
FT DOMAIN 332 401 CYTOPLASMIC (POTENTIAL).
FT DISULFID 143 220 BY SIMILARITY.
FT LIPID 354 354 PALMITATE (POTENTIAL).
FT CARBOHYD 9 9 POTENTIAL.
FT CARBOHYD 12 12 POTENTIAL.
FT CARBOHYD 34 34 POTENTIAL.
FT CARBOHYD 41 41 POTENTIAL.
FT CARBOHYD 49 49 POTENTIAL.
SQ SEQUENCE 401 AA: 45098 MW; 6786FD94 CRC32;

Query Match 58.9%; Score 1672; DB 1; Length 401;
Best Local Similarity 66.6%; Pred. No. 0.00e+00;
Matches 207; Conservative 52; Mismatches 49; Indels 3; Gaps 3;

Db 71 ATTMAATGTCVGVGFEGFELVAVYVRYTKKTKATNTIEMALADALATSTIPROSN 130
QY 59 PVIITRAVSVVAVGVGLVGLVSLVAVIIRTKKTKATNTIEMALADALATVTTMPQSAV 118
Db 131 YMGWTFEGTILCKIVISIDYNNMFTSIFTLCTMSVDRIYAVCHPYKALDFPRNAKII 190
QY 119 YLMSWPFEGDVLCIKIVISIDYNNMFTSIFTLCTMSVDRIYAVCHPYKALDFPRNAKII 178
Db 191 NVCNMLLSAIGLVPYKFAATIKYRNG-S-IDCALTFSEHTG-YWENMLKICVPIEAFIMP 247
QY 179 NCICMLLASVGSISALVIGGIKRYEDVDYIECSLOPDPDEYSWMDLFMKICVFEAFVIP 238
Db 248 VLIITMVCVGLMTRKSVYMLSGSKKEDNRIETRMVTVVAVAFVTCVTPHIVYITKA 307
QY 239 VLIITVCTVLMTRKSVYMLSGSKKEDNRIETRMVTVVAVAFVTCVTPHIVYITKA 298
Db 308 LITTEPTTQIVYSWHPCIALGYTNSCLNPEVLAFLDENFKRCFREFCIPSTSTIEQNSA 367
QY 299 LSTSTSHALSTSYECIALGYTNSCLNPEVLAFLDENFKRCFREFCIPSTSTIEQNSA 358
Db 368 RIRQNTRHAPS 378
QY 359 RVANTYQDPAS 369

RESULT 9
ID OPED_RAT STANDARD; PRT: 372 AA.
AC P33533;
DT 01-FEB-1994 (REL. 28, CREATED)
DI 01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
DE 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE DELTA-TYPE OPIOID RECEPTOR (DOR-1) (OPIOID RECEPTOR A).
GN OPRI1 OR KOR-A.
OS RATTUS NORVEGICUS (RAT).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
CC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RX MEDLINE; 93351652.
RA FUKUDA K., KATO S., MORI K., NISHI M., TAKESHIMA H.;
RL FEBS LETT. 327:311-314(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-SPRAGUE-DAWLEY; TISSUE-BRAIN;
RX MEDLINE; 94322412.
RA ABOOD M.E., NOEL M.A., FARNSWORTH J.S., TAO Q.;
RL J. NEUROSCI. RES. 37:714-719(1994).
CC -1- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM
ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. HIGHLY

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CC STEREOSELECTIVE. RECEPTOR FOR ENKEPHALINS.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; D16348; G391865; -.
DR EMBL; U00475; G514211; -.
DR PIR; S34592; S34592.
DR GCRDB; GCR_0638; -.
DR GCRDB; GCR_0805; -.
DR PROSITE; PS00237; G-PROTEIN RECEPTOR. 1.
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
KW PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.
FT DOMAIN 1 45 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 46 75 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 76 84 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 85 102 2 (POTENTIAL).
FT DOMAIN 103 124 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 125 144 3 (POTENTIAL).
FT DOMAIN 145 174 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 175 190 4 (POTENTIAL).
FT DOMAIN 191 215 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 216 238 5 (POTENTIAL).
FT DOMAIN 239 261 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 262 284 6 (POTENTIAL).
FT DOMAIN 285 293 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 294 310 7 (POTENTIAL).
FT DOMAIN 311 372 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 18 18 POTENTIAL.
FT CARBOHYD 33 33 POTENTIAL.
FT DISULFID 121 198 BY SIMILARITY.
FT LIPID 333 333 PALMITATE (POTENTIAL).
SQ SEQUENCE 372 AA: 40449 MW; 39F5ED50 CRC32;

Query Match 56.7%; Score 1610; DB 1; Length 372;
Best Local Similarity 65.6%; Pred. No. 1.46e-293;
Matches 214; Conservative 55; Mismatches 48; Indels 9; Gaps 7;

Db 15 LIANVDFPSPAPSPASANASSPQAR--SAS-SALAIATATLYSACVAGLLGNVLM 71
QY 22 LIPNSSWPFPMNAESDSNGSVSGEDQLESIAISALPIITRAVSVVAVGVGLVGLVSLVM 81
Db 72 EGIIVYTKKTKATNTIEMALADALATSTIPROSAKIYEMWPGELCKAVLSIDYNN 131
QY 82 EGIIVYTKKTKATNTIEMALADALATVTTMPQSAVYIMNSWPGDVLCIKIVISIDYNN 141
Db 132 MFTSIFTLTMSVDRIYAVCHPYKALDFPRNAKALINICIVILASGVGPIMVAVTOP 191
QY 142 MFTSIFTLTMSVDRIYAVCHPYKALDFPRNAKALINICIVILASGVGISAVIGTFYV 201
Db 192 RDGA-VV-CTIOFPSPB--SWWDIVTKICVGLFAVAVPLIITVCGMLRLRSYRLS 247
QY 202 RDVDVYIECSLOPDPDEYSW-MDLPMKICVFEAFVAVIPVLIIVCYTLMILRLKSVRLS 260
Db 248 GSKREDRSLRRTKRVIVYVGAFAVWCWAPIHIFVYIWLVDINRBDPLVYALHICIAAG 307
QY 261 GSKREDRSLRRTKRVIVYVGAFAVWCWAPIHIFVYIWLVDINRBDPLVYALHICIAAG 319
Db 308 YANSLINPVLAFLDENFKRCFROLG 333
QY 320 YINSSLINPVLAFLDENFKRCFROLC 345

RESULT 10
ID OPED_HUMAN STANDARD; PRT: 372 AA.
AC P41143;
DT 01-FEB-1995 (REL. 31, CREATED)
DI 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
DI 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE DELTA-TYPE OPIOID RECEPTOR (DOR-1).
GN OPRI1 OR OPRI.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
CC EUTHERIA; PRIMATES.
RN [1]

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FT TRANSMEM 125 144 3 (POTENTIAL).
FT DOMAIN 145 174 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 175 190 4 (POTENTIAL).
FT DOMAIN 191 215 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 216 238 5 (POTENTIAL).
FT DOMAIN 239 261 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 262 284 6 (POTENTIAL).
FT DOMAIN 285 293 7 (POTENTIAL).
FT TRANSMEM 294 310 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 311 372 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 18 18 POTENTIAL.
FT CARBOHYD 33 33 POTENTIAL.
FT DISULFID 121 198 BY SIMILARITY.
FT LIPID 333 333 PALMITATE (POTENTIAL).
SQ SEQUENCE 372 AA; 40561 MW; 51402255 CRC32;

Query Match
Best Local Similarity 56.3%; Score 1597; DB 1; Length 372;
Matches 206; Conservative 51; Mismatches 46; Indels 6; Gaps 5;

DB 47 AATAITAIYSACVAGLIGNVMEGIVRYKLTAKNTITFNALADALATSTLPPOS 106
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 57 ALPVIITAVSYVGVGLVGNLSIMFVIRYTKMKATNITFNLADALVTTMPQS 116
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 107 AXYIMETWEGELCKAVSIDYNNMTSIFILTMASVRYTAVCHPYALDFRTPAKK 166
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 117 AYILNMSWPFGLVCLIVSIDYNNMTSIFILTMASVRYTAVCHPYALDFRTPAKK 176
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 167 LINCITWVLSAGVGPIMWAVTOPRDA-VV-CMLQFSP--SWIMDVTKICVLEFAF 222
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 177 LINCITWVLSAGVGSALVLTGKTRKEDVDYDSCIQFEDDEXSW-WDLFMKICVLEFAF 235
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 223 VPIILLIIVCYGIMLLRLSRVLLSSGSKKEDRSRLRTITMVAIVVGAIVVCAPIHIEFI 282
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 236 VLPVILIVCYTIMIRLKSVRLLSGSRKEDNLRITILVIVVAVFLICWTPHIIITL 295
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 283 VMTIVDINRDVLVVAALHCLALGYSANSLMPVYAFIDENPKRCFROLOCTPGGROEP 342
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 296 VEALSTGSHSTA-ALSTYFCIALGTNSLNPVYAFIDENPKRCFROCPPIKRMER 354
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 343 GSILRRPRA 351
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 355 QSTNRVNT 363
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

RESULT 12
ID OPER RAT STANDARD; PR: 367 AA.
AC P35370;
DT 01-JUN-1994 (REL. 29, CREATED)
DT 01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE NOCICEPTIN RECEPTOR (ORPHANIN F0 RECEPTOR) (KAPPA-TYPE 3 OPIOID
RECEPTOR) (KOR-3) (ROR-C) (XOR1).
GN OPER1 OR OOR.
OS RATTUS NORVEGICUS (RAT).
OC EURARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-WISTAR; TISSUE-BRAIN;
RX MEDLINE: 94215703.
RA FUKUDA K., KATO S., MORI K., NISHI M., TAKESHIMA H., IWABE N.,
RA KITATA T., HOUTANI T., SUGIMOTO T.;
RL FEBS LETT. 343:42-46(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-HIPPOCAMPUS;
RA MENG F., XIE G., ALFRED M., THOMPSON R., HOVERSTEN M., WATSON S.,
RA AKIL H.;
RL SUBMITTED (JAN-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-SPRAGUE-DAWLEY; TISSUE-BRAIN;

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RX MEDLINE: 94307401.
RA HUNZOW J.R., SAEZ C., MORENO M., BOUVIER C., WILLIAMS J.T., LOW M.,
RA GRANDY D.K.;
RL FEBS LETT. 347:284-288(1994).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE: 94307400.
RA CHEN Y., FAN Y., LIU J., WESTER A., TIAN M., KOZAK C.A., YU L.;
RL FEBS LETT. 347:279-283(1994).
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RX MEDLINE: 95096849.
RA IACHOWICZ J.E., SHEN Y., MONSMA F.J. JR., SIBLEY D.R.;
RL J. NEUROCHEM. 64:34-40(1995).
RN [6]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RX MEDLINE: 94298959.
RA WANG J.B., JOHNSON P.S., IMAI Y., PERSICO A.M., OZENBERGER B.A.,
RA EPPLEER C.M., UHL G.R.;
RL FEBS LETT. 348:75-79(1994).
RN [7]
RP SEQUENCE FROM N.A.
RC STRAIN-SPRAGUE-DAWLEY; TISSUE-BRAIN;
RX MEDLINE: 95182817.
RA WICK M.J., MINNERATH S.R., LIN X., ELDE R.P., LAW P.Y., LOH H.H.;
RL BRAIN RES. MOL. BRAIN RES. 27:37-44(1994).
RN [8]
RP FUNCTION: RECEPTOR FOR THE NEUROPEPTIDE NOCICEPTIN/ORPHANIN F0.
HAS A POTENTIAL ROLE IN MODULATING A NUMBER OF BRAIN FUNCTIONS,
INCLUDING INSTINCTIVE BEHAVIOURS AND EMOTIONS. THE ACTIVITY OF
THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH INHIBITS ADENYLYL
CYCLASE.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN SEVERAL BRAIN AREAS.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL: D16438; G533355; -
DR EMBL: U05239; G451844; -
DR EMBL: U01913; G487965; -
DR EMBL: L28144; G496230; -
DR EMBL: U07871; G606803; -
DR EMBL: L33916; G557200; -
DR EMBL: L29419; G510719; -
DR PIR: S46238; S46238.
DR PIR: S43655; S43655.
DR GCRDB: GCR_0834; -
DR GCRDB: GCR_0898; -
DR GCRDB: GCR_0912; -
DR PROSITE: PS00237; G-PROTEIN RECEPTOR; 1.
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
KW PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.
FT DOMAIN 1 47
FT TRANSMEM 48 74
FT DOMAIN 75 84
FT TRANSMEM 85 106
FT DOMAIN 107 121
FT TRANSMEM 122 143
FT DOMAIN 144 162
FT TRANSMEM 163 185
FT DOMAIN 186 208
FT TRANSMEM 209 233
FT DOMAIN 234 261
FT TRANSMEM 262 285
FT DOMAIN 286 297
FT TRANSMEM 298 319
FT DOMAIN 320 366
FT DISULFID 120 197
FT LIPID 331 331
FT CARBOHYD 21 21
FT CARBOHYD 26 26
FT CARBOHYD 35 36
FT CONFLICT 105 105
FT CONFLICT 226 226
L -> V (IN REF. 2).

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FT	CONFLICT	246	246	S -> P (IN REF. 2).
FT	CONFLICT	348	348	S -> T (IN REF. 3).
SEQ	SEQUENCE	367 AA	40523 MW	7ED40CCC CRC32:
	Query Match		51.9%;	Score 1473; DB 1; Length 367;
	Best Local Similarity	59.3%;	Pred. No. 2,658-265;	
	Matches 188; Conservative	63;	Mismatches 61;	Indels 5; Gaps 5
DB	40	SAPLESLKVTIVGIVYAVNCIGGLGNGLYVILRHTRKMTATNITYFNIALADLTVL	99	
QY	51	SAHISPAIPVITITAYVSVYVGVGNGSLVMFVILRTKMTATNITYFNIALADALT	110	
DB	100	TLPGDITLLGFMFPGALCKTATYIDYNNMFSTPLTMSVDRYALCHPRLADVR	159	
QY	111	TMPPDSAYVLLMNSMFPFGDLCKIYISIDYNNMFSTPLTMSVDRYALCHPRLADVR	170	
DB	160	TSSKQAVNAVIMVALSVGVPAVIMGSAQV-DEBE-TECVETIPADQV-WGQVFA-IC	215	
QY	171	TPLRKATINICIMVLASSVGSISAYVIGETKVRDYDYECSLQPD-DEISWMDLEFKIC	229	
DB	216	ILFSLFIPVLLISVYCSIMTRRLRGVRLLSGSRKDKNLRIRITLYLVVAVFVGQWP	275	
QY	230	VEVFAFVPLIIIVCYVLMILRLKSVLLSGSRKDKNLRIRITLYLVVAVFVLIOWTP	289	
DB	276	VQVYVVLGVQVQPSFETAVVAILRFTCLGVYNSCLNLIYAFEDENKACFRKFCASS	335	
QY	290	IHIFLVALGSTSHSLSTSYFCIALGTNSLSNVLVLAFFDENKRCQFRDCEPIK	349	
DB	336	LHRMGVSDFRSTAKD	352	
QY	350	MMEROSTNRVKNVYQD	366	
	RESULT 13			
ID	OPRX MOUSE	STANDARD;	PRG;	367 AA.
AC	P35377; 060645;			
DT	01-JUN-1994 (REL. 29, CREATED)			
DT	01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)			
DT	01-JUN-1997 (REL. 35, LAST ANNOTATION UPDATE)			
DE	NOOCEPTIN RECEPTOR (ORPHANIN FQ RECEPTOR) (KAPPA-TYPE 3 OPIOID			
DE	RECEPTOR) (KOR-2) (ORGC) (K3 OPIATE RECEPTOR).			
GN	OPRL1 OR OPRL OR OOR.			
OS	MUS MUSCULUS (MOUSE).			
OC	EDUARICOTA, METAEOA;			
OC	ETHERIA; RODENTIA.			
RN	11			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6N; TISSUE=BRAIN;			
RA	YASUDA K., JONES E., REISINE T., BELL G.I.;			
RL	SUBMITTED (JAN-1994) TO EMBL/GENBANK/DBJ DATA BANKS.			
RN	12			
RP	SEQUENCE FROM N.A.			
RC	MEDLINE; 95100967.			
RA	NISHI M., TAKEISHIMA H., MORI M., NAKAGAMARA K.I., TAKEUCHI T.;			
RL	BIOCHEM. BIOPHYS. RES. COMMUN. 205:1353-1357(1994).			
RN	13			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=BRAIN;			
RA	MATTHEWS H.W.D.;			
RL	SUBMITTED (SEP-1995) TO EMBL/GENBANK/DBJ DATA BANKS.			
RN	14			
RP	SEQUENCE FROM N.A.			
RA	PAN Y.X., XU J., PASTERNAK G.W.;			
RL	SUBMITTED (JUL-1996) TO EMBL/GENBANK/DBJ DATA BANKS.			
RN	15			
RP	SEQUENCE FROM N.A.			
RC	MEDLINE; 95327076.			
RA	PAN Y.X., CHENG J., XU J., ROSSI G., JACOBSON E., RYAN-MORO J.,			
RL	BROOKS A.T., DEAN G.E., STANDIFER K.M., PASTERNAK G.W.;			
RN	16			
RP	SEQUENCE OF 1-357 FROM N.A.			
RC	STRAIN=BALE/C; TISSUE=SPLEEN;			

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RA HALFORD W.P., GEBHARDT B.M., CARR D.J.J.;
RL SUBMITTED (AUG-1994) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -1- FUNCTION: RECEPTOR FOR THE NEUROPEPTIDE NOCICEPTIN/OREXANIN EQ.
CC HAS A POTENTIAL ROLE IN MODULATING A NUMBER OF BRAIN FUNCTIONS,
CC INCLUDING INSTINCTIVE BEHAVIOURS AND EMOTIONS. THE ACTIVITY OF
CC THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH INHIBITS ADENYLYL
CC CYCLASE.
CC
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
DR EMBL; U04952; G440880; -.
DR EMBL; D31667; G808874; -.
DR EMBL; D31666; G808874; JOINED.
DR EMBL; X91813; G1009882; -.
DR EMBL; U32932; G1464791; -.
DR EMBL; U32928; G1464791; JOINED.
DR EMBL; U32930; G1464791; JOINED.
DR EMBL; U09421; G551485; -.
DR EMBL; U14165; G540093; -.
DR GCRDB; GCR_0891; -.
DR MGD; MGI:97440; OPRL.
DR KW PROSITE; PS00237; G-PROTEIN RECEPTOR; 1.
DR KX G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE;
KW PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.
FT DOMAIN 1 47
FT TRANSSEG 48 74
FT DOMAIN 75 84
FT TRANSSEG 85 106
FT DOMAIN 107 121
FT TRANSSEG 122 143
FT DOMAIN 144 162
FT TRANSSEG 163 185
FT DOMAIN 186 208
FT TRANSSEG 209 231
FT DOMAIN 234 261
FT TRANSSEG 262 285
FT DOMAIN 286 297
FT TRANSSEG 298 319
FT DOMAIN 320 366
FT DISULFID 120 197
FT LIPID 331 331
FT CARBOHYD 26 26
FT CARBOHYD 36 36
FT CARBOHYD 348 349
FT CONFLICT SI -> TV (IN REF. 2).
SQ SEQUENCE 367 AA; 40491 MW; 3F472156 CRC32;

Query Match 51.8%; Score 1471; DB 1; Length 367;
Best Local Similarity 59.3%; Pred. No. 6,84e-265;
Matches 188; Conservative 63; Mismatches 61; Indels 5; Gaps 5

DB 40 SAFEPLGLKVTIGVGYLWVCIGGLGNCINWYVILFRHKMTATNIXLEFNALADITVL 99
|||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 51 SAHISPAIPVITITANYVYVYVGLVGNLVAIVILIRYTKMTATNIXYENFNLADALVTT 110
|||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 100 TLPEQGDITLGFWEFGNALCKYVAIDYVMKFTSTFTLMAVDYVAICHPRLADYR 159
|||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 111 TMPFQSAVYIWNMSPEFGDVLCKIYISIDYVMFTSIFTLIMASDXYIAVCHPYKALDFR 170
|||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 160 TSSKQANVAVTMAASVYGVPAVIMSGAQ-EEDE-TECVIIPAQDY-WGVAFA-IC 215
|||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 171 TPLKKNITICIMWLASSVGSISALVIGSTIKREDVDVEGSLQPPD-DESWMDLEFKIT 229
|||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 216 IFLFSITIPVILITVSYSLMIRLRNGVYLITGSGREKDNLRIRLVLVYVAVVGQWTP 275
|||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 230 VYVFAFVFPVLLITVYCYLIMILRLKSVLITGSGRKQDNLRIRITKIVLVYVAVFIIDWP 289
|||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 276 VQVFLVQGLQVQGSFTAVAILRFCTVALGYVNSCLNFIIYAFIDENKACFRKFCQASA 335
|||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 290 IHIIFLVALGISTHSPTALSSYYFCIALGYTNSLINFLVLAFLDENKRCFCFRDFCPPIK 349
|||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 336 LHREMOVSDRYVSIKAD 352
|||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 350 NMHERQSTNRVNRVIVQD 366
|||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

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ID	RESULT	14	STANDARD	PRI:	370	AA.
AC	OPRX	HUMAN				
AC	P41146					
DT	01-FEB-1995	(REL. 31, CREATED)				
DT	01-FEB-1995	(REL. 31, LAST SEQUENCE UPDATE)				
DT	01-NOV-1997	(REL. 35, LAST ANNOTATION UPDATE)				
DE	NOCICEPTIN RECEPTOR (ORPHANIN FQ RECEPTOR) (KAPPA-TYPE 3 OP10ID RECEPTOR) (KOR-3)					
GN	ORPRL OR ORL1 OR ORR					
OS	HOMO SAPIENS (HUMAN)					
OC	EUTHARCTA, METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; EUTHERIA; PRIMATES.					
RA	SEQUENCE FROM N.A.					
RC	TISSUE-BRAIN STEM;					
RX	MEDLINE; 94185768.					
RA	MOLLEREAU C., PARMENTIER M., MAILLEUX P., BOUTOUR J.L., MOISAND C., CHALON P., CAPUT D., VASSART G., MEUNIER C.;					
RL	FEBS LETT. 341:33-38(1994).					
RM	[2]					
RP	SEQUENCE FROM N.A.					
RA	LEE P.H., ZHU J., LIU-CHEN L., CHANG K.;					
RL	SUBMITTED (JAN-1996) TO EMBL/GENBANK/DBJ DATA BANKS.					
CC	-1- FUNCTION: RECEPTOR FOR THE NEUROPEPTIDE NOCICEPTIN/ORPHANIN FQ. HAS A POTENTIAL ROLE IN MODULATING A NUMBER OF BRAIN FUNCTIONS, INCLUDING INSTINCTIVE BEHAVIOURS AND EMOTIONS. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH INHIBITS ADENYLYL CYCLASE.					
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.					
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.					
DR	EMBL; X7130; G471317; -					
DR	EMBL; U30185; G1144297; -					
DR	PIR; S43087; S43087; -					
DR	GCDB; GC8_0987; -					
DR	PROSITE; PS00237; G-PROTEIN RECEPTOR. 1.					
KW	G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.					
KW	DOMAIN 1					
FT	DOMAIN	51	77			
FT	DOMAIN	78	87			
FT	TRANSMEM	88	109			
FT	DOMAIN	110	124			
FT	TRANSMEM	125	146			
FT	DOMAIN	147	165			
FT	TRANSMEM	166	188			
FT	DOMAIN	189	211			
FT	TRANSMEM	212	236			
FT	DOMAIN	237	264			
FT	TRANSMEM	265	288			
FT	DOMAIN	289	300			
FT	TRANSMEM	301	322			
FT	DOMAIN	323	370			
FT	DISULFID	123	200			
FT	LIPID	334	334			
FT	CARBOHYD	21	21			
FT	CARBOHYD	28	28			
FT	CARBOHYD	39	39			
SO	SEQUENCE	370	AA;	40693	MM;	B3C3E8F CRC32;
Query Match		51.6%;	Score 1465;	DB 1;	Length 370;	
Best Local Similarity		58.3%;	Pred. No. 1.18e-263;			
Matches 186;	Conservative	65;	Mismatches 63;	Indels 5;	Gaps 5;	
Db	43	GATPLGLKXIVTIGVGLYAVCYGSLGNLVVYVYLRLHRTKMTANINITYFNALADLYVL	102			
OY	51	SAHISPAFLVITIAVYSVVFVGLVSNLVAFVIRTKMTATNINITYFNALADALVLT	110			
103	TLPLPGTDLILGLFPEFGALCKIVAIADYVYMTSTFLIMASDVRAVCHPRLADVR	162				
OY	111	IMFGASAVYLVNSWPEFGVGLCKIVAIISIDYVYMTSTFLIMASDVRIACHPRLADFR	170			

[illegible]


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QY 51 SAHISPAIPVITITAYSVYFVGVGLVGNLSLMEVITIRYMKMTATNITYIFNLALADALVTT 110
Db 103 TTPFGDVLIGFWPEGNALCKAVTAIDYNNMTSAFTLTANSVDRYAICHPIRALDVR 162
QY 111 TWPFGSAVYLNMSWPEGDVLCRVISIDYNNMTSIFTLTMSVDRYIAVCHPVKALDFR 170
Db 163 TSSKAQAVNVAIWALASTYGVPAVIMGSAQV-EDEE-TECLVEIPAPQDY-WGPYFA-VC 218
QY 171 TPLKAKIINICIMWLASSVGSIAIVGGRKREDVDVIECSLOFPD-DEYSWMDLFMKIC 229
Db 219 IFLSEFVIFVLLIISVYCSLWVRRLRGVRLSSGREKRNLRITRLVLYVAVFGCTP 278
QY 230 VEVFAFVIFVLLIIVCYTLMILRLKSVRLSSGREKRNLRITKLVLYVAVFLICWTP 289
Db 279 VQVENVLVQGLSVQPSSENAVAVLRFCTALGYVNSCINPILYAFIDENFRACERKFCAPT 338
QY 290 IHIFLIVEALGSTSHSTALSSYFCIALGYTNSSLNPLYAFIDENFRKCFRDFCEPIK 349
Db 339 RRREOVSDRVRSLAKDVA 357
QY 350 MREROSTNRNRNVQDPA 368
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Search completed: Thu Apr 16 13:31:11 1998
Job time : 37 secs.

[illegible]

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DE 01-Jan-1998 (TREMBLREL_05, LAST ANNOTATION UPDATE)
DB MU OPIOID RECEPTOR.
OS BOS TAURUS (BOVINE).
OC EUKAROTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
CC EUHERERIA; ARTIODACTYLA.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=STRATUM.
RA SIMON E.J., VILLEM S., ANDRIA M., ONOIRISHVILI I., HILLER J.M.;
RT SUBMITTED (MAR-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
DR EMBL; U69677; GI861731; -.
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN.
SQ SEQUENCE 401 AA: 45045 MW: 5673B988 CRC32;

Query Match          58.1%; Score 1650; DB 4; Length 401;
Best Local Similarity 65.9%; Pred. No. 2,37e-248; Indels 3; Gaps 3;
Matches 205; Conservative 54; Mismatches 49;

Db      71 AIIIMAYSIYCVGELRGNFVMIVRYTKMTAINIIFNLADALASTLPQSYN 130
Qy      ::::|::::|::::|::::|::::|::::|::::|::::|::::|::::| 118
        59 PVLITAVYAVEVGVGLVNSLVMEVIIRYTKMKTATNIYIFNLADALVTTMPQSAY 118
Db      131 YLMGTVEPGTILCTIVSIDYNNFISIFPLCTMSVDYRATACHPKALDIRPRNAKTI 190
Qy      ||::|::::|::::|::::|::::|::::|::::|::::|::::|::::| 178
        119 YLMSWEPGDVLCIKIVISIDYNNFISIFPLTMASVDYRATACHPKALDERFLPAKTI 178
Db      191 NICMWLLSATGLVPMFMATTKYQG-S-IDSTVFSGPTM-YWMNLKICVIFAFAIMP 247
Qy      ::||::|::::|::::|::::|::::|::::|::::|::::|::::|::::| 238
        179 NICMLILASSVGIALVIGGRKYAEVDVLECSIQPFEDDEYSMDLFMKICYVEAFVIP 238
Db      248 ILITVCGLMIERLKSVRMISGSKEKDRIIRTRAVLYVAVAVFYCWTPIHIYYIKA 307
Qy      ::||::|::::|::::|::::|::::|::::|::::|::::|::::|::::| 298
        239 VLIIIVYTLMIILKSKVRLSGSRREDNRIRTKYLVAVVAVFIICWPPIHIFLVA 298
Db      308 LITIPETPEQVSHEPICALGYMSCINPLYAFLDENEKRCREPCIPSSITEOONS 367
Qy      |:::|::::|::::|::::|::::|::::|::::|::::|::::|::::| 358
        289 LGSHSHSTAALSIFYFCIALGYTNSSLNPVLIAPLDENFKRCRFDFCPILKMENQSTIN 358
Db      368 RIRONTIRDPDS 378
Qy      |:|::|::::|::::|::::|::::|::::|::::|::::|::::|::::| 369
        359 RVKNTVDDPAS 369

RESULT 4
ID Q64120 PRELIMINARY; PRI; 240 AA.
AC Q64120;
DE 01-NOV-1996 (TREMBLREL_01, CREATED)
DT 01-NOV-1996 (TREMBLREL_01, LAST SEQUENCE UPDATE)
DT 01-Jan-1998 (TREMBLREL_05, LAST ANNOTATION UPDATE)
DE MU-OPIOID RECEPTOR MOR (FRAGMENT).
OS RATUUS NORVEGETICUS (RAT).
OC EUKAROTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
CC EUHERERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE; 95251654.
RX SEOTI M., ROY S., RAMAKRISHNAN S., ELDE R., LOH H.H.;
RA BIOCHEM. BIOPHYS. RES. COMMUN. 209:563-574(1995).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
DR EMBL; S77863; E199500; -.
KW PROSITE; PS00237; G-PROTEIN RECEPTOR; 1.
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN.
FT NON_TER 1
SQ SEQUENCE 240 AA: 27408 MW: D3C6B8BF CRC32;

Query Match          47.2%; Score 1339; DB 10; Length 240;
Best Local Similarity 68.3%; Pred. No. 1.26e-195;
Matches 166; Conservative 39; Mismatches 35; Indels 3; Gaps 3;
1 TATNITFNALADALAISTLPQSVNTLMGTVEPGTILCTIVSIDYNNFISIFPLCT

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QY 92 TANNIYIFNLALADALVTTTMTPEQSAVILNMSWPGDVLCKIVISIDYNNMFTSTILTM 151
 DB 61 MSVDRIYAVCHVYKALDEFTPRNAKTVNCNILLSALPLVWENATIKYRG-S-IDCT 118
 QY 112 MSVDRIYAVCHVYKALDEFTPRNAKTVNCNILLSALPLVWENATIKYRG-S-IDCT 118
 DB 119 IFRSEPTM-YWENLTKICVFPAFVPIVLIITVCYTLMLRLKSVLLSGSREKDRNLR 177
 QY 212 IOPPDESWMLFMKICVFPAFVPIVLIITVCYTLMLRLKSVLLSGSREKDRNLR 271
 DB 178 IFRMVLVVAEIVVQVTFPIHIVITIKALITPETFQVSWFECIALGYTNSCLNPVLA 237
 QY 272 IFRMVLVVAEIVVQVTFPIHIVITIKALITPETFQVSWFECIALGYTNSCLNPVLA 237
 DB 238 FLD 240
 QY 332 FLD 334

RESULT 5
 ID Q60733 PRELIMINARY; PRT; 117 AA.
 AC Q60733;
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
 DE KAPPA OPIOID RECEPTOR (FRAGMENT).
 GN OPRK1.
 OS MUS MUSCULUS (MUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 CC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA GRANDY D. K.;
 RL SUBMITTED (DEC-1994) TO EMBL/GENBANK/DBJ DATA BANKS.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 DR EMBL; U16998; G595937;
 DR PROSITE; PS00237; G-PROTEIN RECEPTOR; 1.
 KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN.
 FT NON_TER 1
 FT NON_TER 117
 FT SEQUENCE 117 AA; 13071 MW; FCC68E1 CRC32;
 SQ
 Query Match 30.3%; Score 860; DB 10; Length 117;
 Best Local Similarity 98.3%; Pred. No. 2.17e-115;
 Matches 115; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 DB 1 YTKMTATNITFNLALADALVTTTMTPEQSAVILNMSWPGDVLCKIVISIDYNNMFTSI 60
 QY 87 YTKMTATNITFNLALADALVTTTMTPEQSAVILNMSWPGDVLCKIVISIDYNNMFTSI 146
 DB 61 FTLMMSVDRIYAVCHVYKALDEFTPRNAKTVNCNILLSALPLVWENATIKYRG-S-IDCT 118
 QY 147 FTLMMSVDRIYAVCHVYKALDEFTPRNAKTVNCNILLSALPLVWENATIKYRG-S-IDCT 203

RESULT 6
 ID Q64206 PRELIMINARY; PRT; 119 AA.
 AC Q64206;
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
 DE DELTA OPIOID RECEPTOR/DOR (FRAGMENT).
 OS MUS MUSCULUS (MUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 CC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA ROY S.; SEDOJ M.; RAMAKRISHNAN S.; BARKE R. A.; LOH H. H.;
 RL CELL. IMMUNOL. 169:271-277(1995).
 DR EMBL; S81965; E257299;
 FT NON_TER 1
 FT SEQUENCE 119 AA; 13380 MW; DEC85C30 CRC32;
 SQ

Query Match 23.3%; Score 662; DB 10; Length 119;
 Best Local Similarity 69.9%; Pred. No. 7.46e-83;
 Matches 86; Conservative 17; Mismatches 15; Indels 5; Gaps 4;
 DB 1 FTLMMSVDRIYAVCHVYKALDEFTPRNAKTVNCNILLSALPLVWENATIKYRG-S-IDCT 118
 QY 146 FTLMMSVDRIYAVCHVYKALDEFTPRNAKTVNCNILLSALPLVWENATIKYRG-S-IDCT 205
 DB 61 LV-CMLQFSP--SWYMDYTKICVFPAFVPIVLIITVCYTLMLRLKSVLLSGSRE 116
 QY 206 DYIESLQFPDEISW-WLFRKICVFPAFVPIVLIITVCYTLMLRLKSVLLSGSRE 264
 DB 117 KDR 119
 QY 265 KDR 267

RESULT 7
 ID P97266 PRELIMINARY; PRT; 98 AA.
 AC P97266;
 DT 01-MAY-1997 (TREMBLREL. 03, CREATED)
 DT 01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
 DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
 DE MU-OPPIOID RECEPTOR (FRAGMENT).
 OS CAVIA PORCELLUS (GUINEA PIG).
 CC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 CC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA RONNEKLEIV O. K.; BOSCH M. A.; CUNNINGHAM M. J.; WAGNER E. J.;
 RA GRANDY D. K.; KELLY M. J.;
 RL SUBMITTED (JAN-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 DR EMBL; U67928; G1763013;
 DR PROSITE; PS00237; G-PROTEIN RECEPTOR; 1.
 KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN.
 FT NON_TER 1
 FT NON_TER 98
 FT SEQUENCE 98 AA; 11161 MW; 28F749E6 CRC32;
 SQ

Query Match 22.4%; Score 635; DB 10; Length 98;
 Best Local Similarity 81.6%; Pred. No. 1.83e-78;
 Matches 80; Conservative 8; Mismatches 10; Indels 0; Gaps 0;
 DB 1 YTKMTATNITFNLALADALVTTTMTPEQSAVILNMSWPGDVLCKIVISIDYNNMFTSI 60
 QY 87 YTKMTATNITFNLALADALVTTTMTPEQSAVILNMSWPGDVLCKIVISIDYNNMFTSI 146
 DB 61 FTLMMSVDRIYAVCHVYKALDEFTPRNAKTVNCNILLSALPLVWENATIKYRG-S-IDCT 118
 QY 147 FTLMMSVDRIYAVCHVYKALDEFTPRNAKTVNCNILLSALPLVWENATIKYRG-S-IDCT 203

RESULT 8
 ID O08726 PRELIMINARY; PRT; 372 AA.
 AC O08726;
 DT 01-JUL-1997 (TREMBLREL. 04, CREATED)
 DT 01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
 DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
 DE GALANIN RECEPTOR TYPE 2.
 GN GALR2.
 OS RATTUS NORVEGICUS (RAT).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 CC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-HYPOTHALAMUS;
 RA HOWARD A. D.; TAN C.; SHIAO L. L.; PALYHA O. C.; MCKEE K. K.;
 RA WEINBERG D. H.; FEIGNER S. D.; CASCIERI M. A.; SMITH R. G.; PLOEG L. H. T.;
 RA SULLIVAN K. A.;
 RL SUBMITTED (MAY-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [2]
 RP SEQUENCE FROM N.A.

[illegible]

RESULT	13	PRELIMINARY:	PRT:	354 AA.
ID	P97405			
AC	P97405:			
DT	01-MAY-1997 (TREMBLREL. 03, CREATED)			
DT	01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)			
DT	01-MAY-1997 (TREMBLREL. 03, LAST ANNOTATION UPDATE)			
DE	BETA CHEMOKINE RECEPTOR.			
GN	CKRS.			
OS	MOS MUSCULUS (MOUSE).			
CC	EDUKAROTA, METAZOTA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
CC	EUTHERIA; ROSENTIA.			
RC	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-129/OLA;			
RA	KUZIEL W.A., BECK M.A., DAWSON T.C., MAEDA N.;			
RL	SUBMITTED (DEC-1996) TO EMBL/GENBANK/DBJ DATA BANKS.			
DR	EMBL, 068965; G1698716;..			
MO	SEQUENCE 354 AA; 40889 MW; B52D4BD7 CRC32;			
Query Match	20.6%;	Score 585;	DB 10;	Length 354;
Best Local Similarity	30.2%;	Pred. No. 2,24e-70;		
Matches	91;	Conservative 99;	Mismatches 101;	Indels 16; Gaps 13;
Db	23 OKINAKOIAADLPLPLYSIVIFGVGNMVFLLISCKKLSVVDIYLNTAISDLFL 82			
QY	50 ESASHSPALPIITAVIVSVFVGVGSLVAFVILIRYKMTATVYTFFNALADALV 109			
Db	83 LFLPLF-WAHYAAANEMIFGNIMCKVFTGYHNLGDEGIFLILITDRLAIYHAPALKY 141			
QY	110 TTPPQSAVYLIMNSPFDGLCKLIVTSIDYIMFTSIFLIMASVDRYAIVCHPVYALD 169			
Db	142 RIVNFGVTTVVYVWVAFAVASHPELITFRSQ-KSGFHYV-CSPHPHTGYEFWKSFOULR 199			
QY	170 RFLPKAKIINICITMLASVGSALVGLGTRKREVDVIECSLQCFDDYSWMDLFMKIC 229			
Db	200 MYLSLILPLVMICIS-GILH--T--LFRCKNKKR-RNV-RLIEAMIVYELFWTP 252			
QY	230 VEVFAEVFPIVILICITIMILIRKSVRLSREEDRMLRIITIKVIVVAVFIIICMP 289			
Db	253 YNIVLLTTFPOEFGILNCCSSNRDLQAMQATETLGMTCCRLNPYIYAVGKFRSGYSV 312			
QY	290 IHT-FILV--EAL-G-SISHSTALIS-STYFCIALGTYINSLNPFVILAFIDENKRCFND 343			
Db	313 F 313			

QY 344 F 344

RESULT 14
ID P97308 PRELIMINARY; PRT: 354 AA.
AC P97308;
DT 01-MAY-1997 (TREMBLREL. 03, CREATED)
DT 01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE C-CHEMOKINE RECEPTOR 5.
GN CCRS.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RA GUD B., KONO K., HARADA A., MATSUSHIMA K.;
RL SUBMITTED (JAN-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN=C57 BLACK/6; TISSUE=LIVER, KIDNEY AND SPLEEN;
RC KUMAMANN S.E., PLATT E.O., KOZAK S.L., KABAT D.;
RL J. VIROL. 71:8642-8656(1997).
RN [3]
RP SEQUENCE FROM N.A.
RA STRAIN=C57 BLACK/6; TISSUE=LIVER, KIDNEY AND SPLEEN;
RC KUMAMANN S.E., PLATT E.O., KABAT D.;
RL SUBMITTED (SEP-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL; D83648; G1777330; -.
DR EMBL; AF022990; G2444487; -.
SQ SEQUENCE 354 AA; 40785 MW; 78210143 CRC32;

Query Match 20.6%; Score 585; DB 10; Length 354;
Best Local Similarity 30.0%; Pred. No. 2,24e-70;
Matches 92; Conservative 93; Mismatches 105; Indels 17; Gaps 14;

Db 23 QKINVKQIAAQLPPLYSVIFGFGVGNMNVFLITSCKKLKVSDVILNLATISDLFL 82
QY 50 BSAHSPALPVITAVSYVFEVGLVNSLVMEVYIIRTKMTANITITFNALDALVT 109
Db 83 LILPF-WAHYANNEVPSNIMCKVFTGLYHIGFSGIFPIIITLIDRYLAIVAFALKV 141
QY 110 TTMPSQSAVYLNMSWPEGVLCIKIVISIDYNNMFTSIFLTMMSVDRYLAIVCHPYKALDF 169
Db 142 KTVNGVITSVYTWAVAFASLPILITFRSQ-KEGFHT-CSPHFPHQYHFWKSPQLK 199
QY 170 KPTLAKITINICWILASSVGSATVLGGTKVREDVDVIECSLOFPDDEYSWMDLFMKIC 229
Db 200 WYILSLILPLVAVICYS-GILH--T--LFCRNKKRH-RAV-RLIFAIMIVYFLFWTP 252
QY 230 YVVEFAVFPVILIIYCYITMLIRKSVRLSSGKREKRLRTKLVYVAVFIICTWTP 289
Db 253 YNIVLLTTFQEFPGINCCSSNRDLQAMQATLIGMTHCQINPVLYAVGKERSYLSV 312
QY 290 IHI-ETLV--EAL-G-STSHSPAALS-SYFICIALGYTNSLNPVLYAFLENDENKRCFRD 343
Db 313 F-FKKHM 318
QY 344 FCFPIKM 350

RESULT 15
ID Q91383 PRELIMINARY; PRT: 362 AA.
AC Q91383;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE ANGIOTENSIN II RECEPTOR (CLONE XAT).
XENOPUS LAEVIS (AFRICAN CLAWED FROG).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AMPHIBIA; ANURA.
RN [1]
RP SEQUENCE FROM N.A.
RA NISHIMATSU S., KOYASU N., SUGAYA T., OHNISHI J., YAMAGISHI T.,

RA MURAKAMI K., MIYAZAKI H.;
RL BIOCHIM. BIOPHYS. ACTA 1218:401-407(1994).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
DR EMBL; S73388; E136505; -.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; 1.
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN.
SQ SEQUENCE 362 AA; 41267 MW; 9704F695 CRC32;

Query Match 20.6%; Score 586; DB 12; Length 362;
Best Local Similarity 33.1%; Pred. No. 1.55e-70;
Matches 100; Conservative 80; Mismatches 105; Indels 17; Gaps 14;

Db 33 IAPITSTIVVGVGSMVAVIIVYSYKKKTKVASIPLMNLALSDLCFVITLDP-WAAV 91
QY 60 VITAVYVFEVGLVNSLVMEVYIIRTKMTANITITFNALDALVTMMPSQSAV 119
Db 92 TAMHYHMPGFLCKVASTATLNLVTTVFLITCISIDRYSAIVHMKSRIMRLAMARL 151
QY 120 L-MN-SWPEGVLCIKIVISIDYNNMFTSIFLTMMSVDRYLAIVCHPYKALDFRPLKAKI 177
Db 152 TCGVNLVAFPLASPSITRYQIYLFHDINQVCAIVY-DSGHIFMGMSLAKNIVGELI 210
QY 178 INICWILASSVGSATVLGGTKVREDVDVIECSLOFPDDEYSWMDLFMKICVFVFAFVI 237
Db 211 PFLITLSTYTLIGTKIKREV--YRAORARNDI--F-KMIVAVLLEFPCWIPYOVETPLD 265
QY 238 FVLIIYVYITMLIRKSVRLSSGKREKRLRTKLVYVAVFIICTWTPIHIFLIVE 297
Db 266 VLIQMDVIONCKMYDIDFGMPITICIAVENSCLNPELYGFGKMKRKHPLQLIYIPPK 325
QY 298 AL-G-STSHS-TA-ALSSYFICIAL--GYTNSLNPVLYAFLENDENKRCFRDFC-F-DIK 349
Db 326 MR 327
QY 350 MR 351

Search completed: Thu Apr 16 13:32:44 1998
Job time : 74 secs.

M O S E R
(TM)

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MPsrch_un n.a. - n.a. database search, using Smith-Waterman algorithm
Run on: Tue Apr 21 00:03:11 1998; Maspar time 1242.52 seconds
1341.823 Million cell updates/sec
Tabular output not generated.

Title: >US-08-292-694A-1
Description: (1-1410) From US08292694A.seq
Perfect Score: 1410
N.A. Sequence: 1 GCGCACCTTGCTGATCCCA.....AACCCAGATCAACTGCAG 1410
Comp: CGCGTGACAGACGATAGGGTT.....TTGGGTCAATGTTGAGGCTC

Scoring table: TABLE Jmetric
Gap 60

Nmatch STD : Dbase 0; Query 0
354530 seqs, 591221332 bases x 2

Searched: Minimum Match 0%
Post-processing: Listing first 1000 summaries

Database:

emb153
1:em_in 2:em_or 3:em_cm 4:em_ov 5:em_pl 6:em_bt5
7:em_hum1 8:em_hum2 9:em_ha 10:em_ro 11:em_un 12:em_vt
13:em_pat
genbank105
14:gb_ro 15:gb_cm 16:gb_ov 17:gb_in 18:gb_pl 19:gb_pa
20:gb_st 21:gb_vt 22:gb_ph 23:gb_sy 24:gb_un 25:gb_pat
26:gb_bt5

Statistics: Mean 9.323; Variance 3.013; scale 3.094

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the total score being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query	Match	Length	DB	ID	Description	Pred. No.
1	1410	100.0	1410	14	MUSKAPOPRE	Mouse kappa opioid rec	0.00e+00	
2	1208	85.7	1288	14	S81111	Kappa-opioid receptor	0.00e+00	
3	617	43.8	1186	14	MUSMOR6S3	Kappa-opioid receptor	0.00e+00	
4	526	37.3	638	14	MUSMOR6DP3	Mouse MOR6 gene for k	0.00e+00	
5	354	25.1	488	14	MUSMOR6DP2	Mouse MOR6 gene for k	0.00e+00	
6	354	25.1	1109	14	S7786882	Kappa opioid receptor	0.00e+00	
7	275	19.5	432	14	MUT16998	Mus musculus kappa opi	0.00e+00	
8	273	19.4	423	14	MUSMOR6DP1	Mouse MOR6 gene for k	0.00e+00	
9	273	19.4	2074	14	S7786881	Kappa opioid receptor	0.00e+00	
10	229	16.2	1273	14	RATRORP	Rat kappa for opioid re	1.90e-252	
11	229	16.2	1358	14	RATKOR1A	Rat kappa opioid recep	1.90e-252	
12	229	16.2	2094	14	RATKOR1B	Rattus norvegicus kapp	1.90e-252	
13	229	16.2	2481	25	E08674	CDNA coding rat kappa	1.90e-252	
14	229	16.2	2481	14	RATKOR	Rattus norvegicus mRNA	1.90e-252	

15	198	14.0	4742	14	RND00442	Rattus norvegicus kapp	1.50e-212	
16	160	11.3	658	14	RNKOR2	Rattus norvegicus kapp	4.51e-164	
17	68	4.8	4048	14	RNKOR3	Rattus norvegicus kapp	9.30e-51	
18	65	4.6	1733	14	CPU04092	Cavia porcellus Harle	2.86e-47	
19	38	2.7	1757	14	RNKOR1	Rattus norvegicus kapp	1.97e-17	
20	32	2.3	1142	25	R48343	Sequence 1 from Patent	2.02e-11	
21	29	2.1	1461	14	RATSR	Rat somatostatin recep	1.45e-08	
22	29	2.1	1699	14	RATSON	Rattus norvegicus mRNA	1.45e-08	
23	29	2.0	3615	14	RNGPCRRA	R. norvegicus mRNA for	1.45e-08	
24	28	2.0	2858	14	CFU04369	Cavia porcellus Harle	1.23e-07	
25	25	1.8	356	14	MMKOR3S06	Mus musculus opioid re	5.93e-05	
26	25	1.8	1079	14	MMU14165	Mus musculus orphan op	5.93e-05	
27	25	1.8	1083	14	MUSMOR6CP2	Mouse MOR6 gene for o	5.93e-05	
28	25	1.8	1253	14	RATOPRE	Rattus norvegicus opio	5.93e-05	
29	25	1.8	1304	14	RND05239	Rattus norvegicus opio	5.93e-05	
30	25	1.8	1338	14	MMU04052	Mus musculus C57BL/6N	5.93e-05	
31	25	1.8	1452	14	RND01913	Rattus norvegicus Spr	5.93e-05	
32	25	1.8	1452	25	162296	Sequence 3 from patent	5.93e-05	
33	25	1.8	1458	16	DNAJ1596	Danio rerio mRNA for o	5.93e-05	
34	25	1.8	1567	14	RATOPRECEP	Rat opioid receptor fa	5.93e-05	
35	25	1.8	1817	14	RATRORC	Rat mRNA for opioid re	5.93e-05	
36	25	1.8	2024	14	MMOPRECEP	M. musculus mRNA for op	5.93e-05	
37	25	1.8	2354	14	RND07871	Rattus norvegicus Spr	5.93e-05	
38	25	1.8	2600	14	MMU09421	Mus musculus K3 opiate	5.93e-05	
39	25	1.8	2706	14	RATKOR1A	Rattus norvegicus alte	2.97e-03	
40	23	1.6	1231	16	CCMUOP1	C. communis mRNA for	2.97e-03	
41	23	1.6	1366	14	RND00475	Rattus norvegicus Spr	2.97e-03	
42	23	1.6	1418	14	RATRORA	Rat mRNA for rat opioi	2.97e-03	
43	23	1.6	1834	14	S65335	delta opioid receptor	2.97e-03	
44	23	1.6	1835	14	MUSDOPRC	Mouse delta-opioid rec	2.97e-03	
45	23	1.6	2203	14	S66181	delta opiate receptor	2.97e-03	
46	23	1.6	2219	25	A38528	Sequence 1 from patent	2.97e-03	
47	23	1.6	2219	14	MUSDERO	Mus musculus delta-opi	2.97e-03	
48	23	1.6	2272	14	MUSDERO	Mouse delta opioid rec	2.97e-03	
49	20	1.4	36	25	A48344	Sequence 2 from Patent	7.14e-01	
50	20	1.4	39	25	A48347	Sequence 5 from Patent	7.14e-01	
51	20	1.4	356	14	S81965	delta opioid receptor/	7.14e-01	
52	20	1.4	555	14	MMKOR3S08	Mus musculus opioid re	7.14e-01	
53	20	1.4	720	14	S77863	mu-opioid receptor MOR	7.14e-01	
54	20	1.4	1367	14	RNT35424	Rattus norvegicus mu o	7.14e-01	
55	20	1.4	1401	14	RATROPTD	Rat mu opioid receptor	7.14e-01	
56	20	1.4	1415	15	BIT089677	Bos taurus mu opioid r	7.14e-01	
57	20	1.4	1448	14	RNT02083	Rattus norvegicus mu o	7.14e-01	
58	20	1.4	1586	14	RATMORA	Rattus norvegicus mu o	7.14e-01	
59	20	1.4	1881	15	PICMOPRA	Sus scrofa mu opioid r	7.14e-01	
60	20	1.4	2135	14	RATMOR1A	Rattus norvegicus Mu o	7.14e-01	
61	20	1.4	2205	15	S572758	Sus scrofa orphanin FQ	7.14e-01	
62	20	1.4	2397	14	RATRORE	Rat mRNA for rat opioi	7.14e-01	
63	20	1.4	2402	16	CHRM3MACR	Gallus gallus M3 musca	3.93e+00	
64	19	1.3	246	18	SCEMT4	S. cerevisiae EMT4 gene	2.02e+01	
65	18	1.3	962	15	RABCOR1A8	Rabbit alpha-1 collage	2.02e+01	
66	18	1.3	1041	18	GMAC114	Glycine max L. Merr MR	2.02e+01	
67	18	1.3	1207	21	MV087841	Monkeypox virus strain	2.02e+01	
68	18	1.3	1207	21	MV088543	Monkeypox virus tumor	2.02e+01	
69	18	1.3	1316	21	MV088142	Monkeypox virus strain	2.02e+01	
70	18	1.3	1317	21	MV087847	Monkeypox virus strain	2.02e+01	
71	18	1.3	1320	21	MV087845	Monkeypox virus strain	2.02e+01	
72	18	1.3	1763	19	CT083196	Chlamydia trachomatis	3.99e+00	
73	19	1.3	1832	15	HR5ADHS	Horse alcohol dehydrog	2.02e+01	
74	18	1.3	1902	21	P1WCOP05	Tobacco vein banding m	2.02e+01	
75	18	1.3	2540	14	SPHERGEN	Synchococcus sp. phae	3.99e+00	
76	18	1.3	3096	18	AF014813	Emicellula nidulans DN	2.02e+01	
77	19	1.3	3140	18	D76430	Yeast DNA for DIS pro	2.02e+01	
78	18	1.3	3268	15	BOYTMNT	Bos taurus nicotianid	2.02e+01	
79	18	1.3	3711	15	BOYNAD	Bovine mitochondriai n	2.02e+01	
80	18	1.3	3985	14	RNGPROCR	R. norvegicus mRNA for	2.02e+01	
81	18	1.3	4148	18	SCU66834	Saccharomyces cerevisi	2.02e+01	
82	18	1.3	4673	18	SCYLO21C	S. cerevisiae chromoso	2.02e+01	
83	18	1.3	5135	18	ATNATRTJMS	Arabidopsis thaliana A	2.02e+01	
84	18	1.3	6244	14	RNMATAP	R. norvegicus mRNA for	2.02e+01	
85	18	1.3	7071	14	SVPEPCA	S. vulgare PEPC gene.	2.02e+01	
86	18	1.3	8017	18	ATU76670	Arabidopsis thaliana r	2.02e+01	
87	18	1.3	8017	18	ATU76670	Arabidopsis thaliana r	2.02e+01	

C	88	1.3	9470	19	PD034346	Paracoccus denitrificans	2.02e+01	C	161	1.2	19112	21	MYTIRP	Marburg virus (Pop.) N	9.55e+01
C	89	1.3	10120	14	RATMEAP	Rattus norvegicus micr	2.02e+01	C	162	1.2	19116	17	DMDHGHOD	D. melanogaster hedgeho	9.55e+01
C	90	1.3	12787	19	MPAE000049	Helicobacter pylori se	2.02e+01	C	163	1.2	20712	17	CEP59F4	Caenorhabditis elegans	9.55e+01
C	91	1.3	13650	19	HPAE000582	Caenorhabditis elegans	2.02e+01	C	164	1.2	26600	17	CEP37B1	Caenorhabditis elegans	9.55e+01
C	92	1.3	31889	17	CELC070c11	Caenorhabditis elegans	2.02e+01	C	165	1.2	27336	17	CEP32F6A	Caenorhabditis elegans	9.55e+01
C	93	1.3	36626	17	CELC16D9	Caenorhabditis elegans	2.02e+01	C	166	1.2	27371	17	CEP31F4	Caenorhabditis elegans	9.55e+01
C	94	1.3	36753	17	CELC19F10	Caenorhabditis elegans	2.02e+01	C	167	1.2	31434	17	CEY68A4A	Caenorhabditis elegans	9.55e+01
C	95	1.3	37106	17	CEC04A11	Caenorhabditis elegans	2.02e+01	C	168	1.2	33371	26	CEK07H11	Caenorhabditis elegans	9.55e+01
C	96	1.3	39682	17	CEP22H6	Caenorhabditis elegans	2.02e+01	C	169	1.2	33477	17	CEK07G4	Caenorhabditis elegans	9.55e+01
C	97	1.3	41200	18	SC6520X	S. cerevisiae chromosom	2.02e+01	C	170	1.2	34033	17	CELR09G11	Caenorhabditis elegans	9.55e+01
C	98	1.3	43254	17	CELC1F57	Arabidopsis thaliana c	2.02e+01	C	171	1.2	35357	18	SPAC13F4	S. pombe chromosome I c	9.55e+01
C	99	1.3	95824	18	ATTU90439	Arabidopsis thaliana c	3.93e+00	C	172	1.2	37906	17	CELT08H4	Caenorhabditis elegans	9.55e+01
C	100	1.3	118155	26	HS884M20	Human DNA sequence ***	2.02e+01	C	173	1.2	38000	17	CEP58A4	Caenorhabditis elegans	9.55e+01
C	101	1.3	154557	26	AC002472	*** SEQUENCING IN PROG	2.02e+01	C	174	1.2	41397	17	CEB02B5	Caenorhabditis elegans	9.55e+01
C	102	1.3	169646	26	AC004019	Mollusca contigulsum	3.93e+00	C	175	1.2	79933	17	L49403	Drosophila melanogaste	9.55e+01
C	103	1.3	190289	21	MC060315	*** SEQUENCING IN PROG	2.02e+01	C	176	1.2	80531	26	HSV4460E1	Human DNA sequence ***	9.55e+01
C	104	1.3	231681	25	AC002470	*** SEQUENCING IN PROG	2.02e+01	C	177	1.2	122682	26	HS799F10	Human DNA sequence ***	9.55e+01
C	105	1.2	371	14	MM0R2	Sequence 4 from Patent	9.55e+01	C	178	1.2	126778	26	CEY68A4	Caenorhabditis elegans	9.55e+01
C	106	1.2	539	14	MM0R3	Mus musculus mu oploid	9.55e+01	C	179	1.2	129913	26	HS989H11	Human DNA sequence ***	9.55e+01
C	107	1.2	539	14	MM0R3	Mus musculus mu oploid	9.55e+01	C	180	1.2	136354	19	EC00W82	E. coli, the region fr	9.55e+01
C	108	1.2	654	16	CHKPOLITF	Gallus gallus POL-like	9.55e+01	C	181	1.2	137357	26	EC00R003	*** SEQUENCING IN PROG	9.55e+01
C	109	1.2	686	15	SS071149	Sus scrofa delta op101	9.55e+01	C	182	1.2	143339	26	AC004126	*** SEQUENCING IN PROG	9.55e+01
C	110	1.2	883	15	BOVIFCMB	Cow (clone bovmpl1) 1e	9.55e+01	C	183	1.2	160000	26	AC004057	*** SEQUENCING IN PROG	9.55e+01
C	111	1.2	920	17	PM084117	Psammecichnus mliaris	9.55e+01	C	184	1.2	172106	26	CEY67D11	Caenorhabditis elegans	9.55e+01
C	112	1.2	1127	19	STARPEP2	Plasmodium PC223 (from St	9.55e+01	C	185	1.2	180000	26	AC004063	*** SEQUENCING IN PROG	9.55e+01
C	113	1.2	1392	14	RAMPPLACS	Rat PPI alpha gene fo	9.55e+01	C	186	1.2	187816	26	CEY32E6	Caenorhabditis elegans	9.55e+01
C	114	1.2	1404	14	S76215	protein phosphatase 1	9.55e+01	C	187	1.2	226018	26	HS90L6	Human DNA sequence ***	9.55e+01
C	115	1.2	1407	14	RATPP1A	Rat PPI-alpha gene for cat	9.55e+01	C	188	1.2	261012	26	HS343C1	Human DNA sequence ***	9.55e+01
C	116	1.2	1610	14	MM026915	Mus musculus mu oploid	9.55e+01	C	189	1.2	291821	26	CEY48E1	Caenorhabditis elegans	9.55e+01
C	117	1.2	1796	25	I13407	Sequence 11 from Patent	9.55e+01	C	190	1.1	31	25	162294	Sequence 1 from Patent	4.15e+02
C	118	1.2	1797	14	MUSSTR3A	Mus somaticstatin rec	9.55e+01	C	191	1.1	35	25	A48820	Sequence 12 from Patent	1.63e+03
C	119	1.2	1880	19	SAPC223	Staphylococcus aureus	9.55e+01	C	192	1.1	54	25	A07526	Nucleotide sequence 6	4.15e+02
C	120	1.2	1998	18	ATCHSP60	A. thaliana mRNA for mi	9.55e+01	C	193	1.1	54	25	A12990	Nucleotide sequence 6	4.15e+02
C	121	1.2	2018	14	MUSCYR61A	Mouse CytR61 mRNA, comp	9.55e+01	C	194	1.1	54	25	AI2990	G. gallus type III coll	1.63e+03
C	122	1.2	2046	21	AF005755	Marburg virus strain M	9.55e+01	C	195	1.1	54	25	I55061	Sequence 16 from Patent	4.15e+02
C	123	1.2	2061	25	E08061	DNA encoding variant c	9.55e+01	C	196	1.1	70	25	SYN1NSP1	Rat insulin-I gene s:ig	4.15e+02
C	124	1.2	2061	25	I43345	Sequence 5 from Patent	9.55e+01	C	197	1.1	95	25	E00026	avian erythroblastosis	4.15e+02
C	125	1.2	2061	25	I23834	Sequence 5 from Patent	9.55e+01	C	198	1.1	112	21	ACBEBB2	19S (RNA [3' region])	4.15e+02
C	126	1.2	2061	25	I44694	Sequence 5 from Patent	9.55e+01	C	199	1.1	127	25	S81277	Nucleotide sequence 16	4.15e+02
C	127	1.2	2106	18	ATU18129	Arabidopsis thaliana 5	9.55e+01	C	200	1.1	128	25	A07535	Cyprinus carpio brain-	4.15e+02
C	128	1.2	2229	14	MM019360	Mus musculus mu oploid	9.55e+01	C	201	1.1	130	16	AF008558	Synthetic human insuli	4.15e+02
C	129	1.2	2232	16	CHKPOLID	Gallus gallus reverse	9.55e+01	C	202	1.1	171	23	SYN0UM1A	Sequence 12 from Patent	4.15e+02
C	130	1.2	2346	14	RNT36476	Rattus norvegicus 92-k	9.55e+01	C	203	1.1	186	25	I31100	M. musculus c-fes gene	4.15e+02
C	131	1.2	2462	19	EC11VEN	E. coli ilvBN operon f	9.55e+01	C	204	1.1	186	21	MMCFES186	Human herpesvirus 7 DN	4.15e+02
C	132	1.2	2470	19	EC011VPR	E. coli acetohydroxy ac	9.55e+01	C	205	1.1	186	21	HH7J1	Smythium clusatum nuc	4.15e+02
C	133	1.2	2477	19	AC0SLP	A. kitavi S-layer protei	9.55e+01	C	206	1.1	222	18	SORDNAITS2	Mouse Ig rearranged he	4.15e+02
C	134	1.2	2502	19	BACDGD	B. macerans cyclodextri	9.55e+01	C	207	1.1	223	14	M0S1GLHBD	Mouse K2 class I MHC g	1.63e+03
C	135	1.2	2631	19	BMCGTM	B. macerans cglm gene f	9.55e+01	C	208	1.1	229	14	MMK2MHC	Mouse T14 class I MHC	1.63e+03
C	136	1.2	2720	14	ABG06137	Rattus norvegicus F1A	9.55e+01	C	209	1.1	252	14	MMK14MHC	Mouse O6 class I MHC g	1.63e+03
C	137	1.2	2948	21	MAVSPA	Marburg Virus genomic	9.55e+01	C	210	1.1	267	14	MM06MHC	Mouse O8/9 class I MHC	1.63e+03
C	138	1.2	3261	19	LBAYVALS	Lactobacillus casei va	9.55e+01	C	211	1.1	272	14	MM089MHC	DNA sequence 2 from Patent	4.15e+02
C	139	1.2	3621	17	DRO20DC6Z	Drosophila melanogaste	9.55e+01	C	212	1.1	273	25	E00074	Sequence 2 from Patent	4.15e+02
C	140	1.2	3621	17	DMR81457	Drosophila melanogaste	9.55e+01	C	213	1.1	273	25	FH010316	Fasciola hepatica clon	1.63e+03
C	141	1.2	3753	17	DRO20DC7Z	Drosophila melanogaste	9.55e+01	C	214	1.1	273	17	MM0B8X55	B. mori bombyxin B-4 (1.63e+03
C	142	1.2	3668	15	S47919	p87-transposon-like p	9.55e+01	C	215	1.1	273	17	MM0B8X55	B. mori bombyxin B-5 (1.63e+03
C	143	1.2	4117	14	RNAJ696	Rattus norvegicus mRNA	9.55e+01	C	216	1.1	273	17	MM0B8X4X	B. mori bombyxin B-4 (1.63e+03
C	144	1.2	4558	16	GGU88211	Gallus gallus retinotro	9.55e+01	C	217	1.1	277	23	ARHSINS	Artificial gene for hu	4.15e+02
C	145	1.2	4790	18	SPALP1	S. pombe alp1 gene	9.55e+01	C	218	1.1	279	15	S75109	neurokinin receptor su	1.63e+03
C	146	1.2	4951	17	ABG07932	Bombyx mori mRNA for B	9.55e+01	C	219	1.1	282	17	MM0B8XJ5	B. mori bombyxin B-11	1.63e+03
C	147	1.2	5018	15	SSNAGATIT	Sus scrofa gene encodi	9.55e+01	C	220	1.1	286	20	SYN1NSGSA	Synthetic human proins	4.15e+02
C	148	1.2	5196	14	MMCYR61G	Mouse growth factor in	9.55e+01	C	221	1.1	290	23	PO1R1SLA	Parathelohania anophel	1.63e+03
C	149	1.2	5373	18	PCHCSB	P. hydrilia chsb gene fo	9.55e+01	C	222	1.1	301	17	DROCCOPAJ1	D. melanogaster copia	1.63e+03
C	150	1.2	5636	14	MUSALC801	Mus Musculus alpha-cr	9.55e+01	C	223	1.1	304	14	MMK17MHC	Mouse T17 class I MHC	1.63e+03
C	151	1.2	6751	17	DMGS378	Drosophila 68c glue ge	9.55e+01	C	224	1.1	305	14	MMENASCI	M. musculus tenascin mR	1.63e+03
C	152	1.2	7713	21	HPY25	Human papillomavirus t	9.55e+01	C	225	1.1	319	14	RATCARB02	Rat carboxypeptidase B	4.15e+02
C	153	1.2	8781	16	SAU18868	Squalus acanthias mult	9.55e+01	C	226	1.1	323	16	VALI2	Varanus albigularis 12	4.15e+02
C	154	1.2	10063	15	OA030306	Ovis aries y chromosom	9.55e+01	C	227	1.1	324	14	SYN0390S3	MHC RT1.H alpha -major	1.63e+03
C	155	1.2	10564	25	I47707	Sequence 5 from Patent	9.55e+01	C	228	1.1	331	25	I22421	Sequence 1 from Patent	4.15e+02
C	156	1.2	11378	19	AE000919	Methanobacterium therm	9.55e+01	C	229	1.1	336	25	E08679	CDNA encoding subunit	4.15e+02
C	157	1.2	11725	25	I07993	Sequence 1 from Patent	9.55e+01	C	230	1.1	342	15	AF007082	Monodelphis domestica	4.15e+02
C	158	1.2	11725	25	I05479	Sequence 13 from Patent	9.55e+01	C	231	1.1	343	14	RNCYTOBA08	Rattus norvegicus test	1.63e+03
C	159	1.2	12697	19	ECAE000444	Escherichia coli K-12	9.55e+01	C	232	1.1	345	15	S76746	Ig VH (rabbits, B-lymp	4.15e+02
C	160	1.2	15124	19	AE000934	Methanobacterium therm	9.55e+01	C	233	1.1	351	23	SYN1NSGS	Human (synthetic) insu	4.15e+02

380	16	1.1	1722 15	FDINRA	Feline gene for feline	4.15e+02
381	16	1.1	1731 14	AF006617	Rattus norvegicus micr	4.15e+02
382	15	1.1	1731 25	I55059	Sequence 13 from paten	4.15e+02
383	15	1.1	1736 14	RAISRI3	Rat SR13 myelin protei	1.63e+03
384	15	1.1	1736 14	SS5427	myelin protein SR13-gr	1.63e+03
385	16	1.1	1740 18	LLGPROA	L.luteus mRNA for alph	4.15e+02
386	15	1.1	1751 15	DB2053	Cynops pyrrhogaster mr	1.63e+03
387	16	1.1	1751 15	HR5ADHE	Horse pyridoxal dehydro	4.15e+02
388	15	1.1	1762 21	FLAEM76HA	Influenza A/equine/New	1.63e+03
389	15	1.1	1765 18	YSCSTP2	Saccharomyces cerevisi	1.63e+03
390	16	1.1	1770 16	ORZAIAR	Oryzias latipes alphas	4.15e+02
391	16	1.1	1775 18	CPCCMC1	Cryptococcus flavus mr	4.15e+02
392	16	1.1	1775 18	S45137	CMC1-carboxymethylcell	4.15e+02
393	16	1.1	1775 18	PS797043	Psidium sativum G protei	4.15e+02
394	15	1.1	1788 21	ACBYERBA	Avian erythroblastosis	4.15e+02
395	15	1.1	1788 21	OCTOMESCXY	Octopus dofleini omega	1.63e+03
396	15	1.1	1800 14	MUSGAS3A	Rattus norvegicus gluc	1.63e+03
397	16	1.1	1806 14	RATGLPR	R.norvegicus mRNA for	4.15e+02
398	15	1.1	1806 14	BNHRLP1	Bovine oestrogen sulfo	1.63e+03
399	15	1.1	1812 15	BOVOSTP	B. taurus mRNA for oest	1.63e+03
400	15	1.1	1812 15	BTOSTR	R.norvegicus mRNA for	1.63e+03
401	15	1.1	1816 14	RNCD25MR	Clostridium cellulopa	4.15e+02
402	16	1.1	1818 19	OC059414	Patinopecten yessoensi	4.15e+02
403	15	1.1	1825 17	AB006455	N.tubacum mRNA for inc	1.63e+03
404	15	1.1	1838 18	NT1PTVP17	A.thaliana mRNA for pu	4.15e+02
405	15	1.1	1864 18	ATGGS	Rat glucagon receptor	4.15e+02
406	16	1.1	1875 14	RATGLUCREC	Sarcocystis fusiformis	1.63e+03
407	15	1.1	1878 17	SPT03071	D.melanogaster G prote	4.15e+02
408	15	1.1	1889 17	DROSPND	Methanobacterium therm	4.15e+02
409	15	1.1	1901 19	MT037405	Sequence 3 from patent	4.15e+02
410	16	1.1	1904 14	MC010	Prunus persica (clone	1.63e+03
411	16	1.1	1909 25	166446	S.elegans gene encodin	4.15e+02
412	15	1.1	1912 18	PRDLHP	Bos taurus phosphatidy	1.63e+03
413	15	1.1	1914 17	SE1SRPN	A. nidulans mitochondr	1.63e+03
414	15	1.1	1917 15	BT021660	A.thaliana Chloroplast	1.63e+03
415	15	1.1	1917 18	MIANRN	S.cerevisiae chromosom	1.63e+03
416	15	1.1	1929 18	CHATGSHL	R. norvegicus (Sprague	4.15e+02
417	15	1.1	1936 14	SCY0123C	Salmonella enterica in	1.63e+03
418	15	1.1	1936 14	RNTESTGB	Salmonella enterica in	1.63e+03
419	16	1.1	1944 14	MUSGLRECB	Butanobeta histolytica	4.15e+02
420	15	1.1	1950 19	SE043247	A.tumefaciens attache	1.63e+03
421	15	1.1	1950 19	SE043248	Rattus norvegicus orph	1.63e+03
422	15	1.1	1958 17	EH078319	S.cerevisiae chromosom	4.15e+02
423	16	1.1	1969 19	ATUCOVA	S.cerevisiae chromosom	4.15e+02
424	15	1.1	1996 14	R0115660	Carassius auratus red	4.15e+02
425	15	1.1	2008 18	SCYGL208M	D.melanogaster mRNA fo	4.15e+02
426	16	1.1	2020 18	SCYR011C	Saccharomyces cerevisi	4.15e+02
427	16	1.1	2031 18	YSPB	Avian erythroblastosis	4.15e+02
428	16	1.1	2032 16	CRARED	Yeast gene for RNA pol	4.15e+02
429	15	1.1	2043 15	S82652	biglycan core protein	1.63e+03
430	16	1.1	2046 17	DM01FF6	D.melanogaster mRNA fo	4.15e+02
431	16	1.1	2061 18	YSCDPRHA	Saccharomyces cerevisi	4.15e+02
432	16	1.1	2061 21	ACGBRBBH	Saccharomyces cerevisi	4.15e+02
433	15	1.1	2094 21	S78506	Avian erythroblastosis	4.15e+02
434	16	1.1	2096 17	AF031414	Orl1 region, R-fragme	1.63e+03
435	16	1.1	2116 14	S75952	Caenorhabditis elegans	4.15e+02
436	15	1.1	2118 17	HCY14233	glucagon-like peptide	4.15e+02
437	16	1.1	2127 25	I05724	Haemonchus contortus m	1.63e+03
438	15	1.1	2134 16	XLCCTG	Sequence 12 from Paten	4.15e+02
439	16	1.1	2147 25	I08174	X.laevis Cctg mRNA.	4.15e+02
440	16	1.1	2178 17	DROSEPIHP	Sequence 1 from Patent	4.15e+02
441	16	1.1	2189 25	AI9048	Drosophila melanogaste	4.15e+02
442	16	1.1	2194 15	BOYPAF	H.sapiens mRNA for thr	4.15e+02
443	16	1.1	2200 14	MUSPIM1K	Bovine mRNA for paf ac	4.15e+02
444	16	1.1	2208 21	S69372	Mouse mRNA for Prplgamm	4.15e+02
445	16	1.1	2209 17	LB094966	Leishmania braziliensi	4.15e+02
446	16	1.1	2220 18	ZMBIAA	Z.mays B-I gene for B	4.15e+02
447	16	1.1	2224 14	RATPIG1	Rat PP-1 gene for ca	4.15e+02
448	16	1.1	2269 14	MMT90267	Mus musculus CDK5 acti	4.15e+02
449	15	1.1	2278 14	MUSPKT	Mus musculus inhibitor	1.63e+03
450	16	1.1	2294 14	MM053456	Mus musculus protein p	4.15e+02
451	15	1.1	2327 18	AF030290	Arabidopsis thaliana p	1.63e+03
452	15	1.1	2334 25	I57970	Sequence 1 from patent	1.63e+03
453	16	1.1	2348 19	ECUBI	E.coli genes ubiC and	4.15e+02
454	15	1.1	2362 21	BR053923	Bovine rotavirus spike	1.63e+03
455	15	1.1	2408 18	MMINSING	Mouse preproinsulin ge	1.63e+03
456	16	1.1	2409 18	SCYSL191W	S.cerevisiae chromosom	4.15e+02
457	15	1.1	2409 19	E11341	Cellulase gene	1.63e+03
458	16	1.1	2431 19	S57688	SIR operon: rpsG-ribos	4.15e+02
459	15	1.1	2437 16	GG015665	Gallus gallus retinal	1.63e+03
460	15	1.1	2466 17	DRODORSAL	D.melanogaster embryon	4.15e+02
461	16	1.1	2471 17	TRANKRBL	Trypanosoma brucei pro	1.63e+03
462	15	1.1	2486 14	MM044731	Mus musculus stop gene	1.63e+03
463	15	1.1	2490 16	AB008225	Mus musculus putative	4.15e+02
464	15	1.1	2493 19	PDCCGBA4	Xenopus laevis mRNA fo	1.63e+03
465	16	1.1	2502 15	DSEPM2	Xenopus laevis mRNA fo	4.15e+02
466	15	1.1	2521 18	YSCPRPMUQ	Dama sp. mRNA for bone	1.63e+03
467	15	1.1	2533 18	SPU88525	Saccharomyces cerevisi	1.63e+03
468	15	1.1	2537 18	YSATYRPHOS	Schizosaccharomyces po	1.63e+03
469	15	1.1	2555 14	MMRAD54	Candida albicans prote	4.15e+02
470	16	1.1	2571 19	SMNASP	M.musculus mRNA homo	1.63e+03
471	15	1.1	2615 19	BJH0PDGNA	S.marcescens haef gene	1.63e+03
472	15	1.1	2629 14	CG017362	B.japonicum huPC, hupD	4.15e+02
473	15	1.1	2647 17	PFHDPKDS	Cricetulus griseus elo	1.63e+03
474	15	1.1	2684 14	MM043892	P.falciparum gene for	1.63e+03
475	15	1.1	2699 16	XLRPCAD	Mus musculus ABC trans	4.15e+02
476	15	1.1	2715 15	MUSRARA	X.laevis mRNA for EP-C	1.63e+03
477	16	1.1	2732 14	MMHFK1	Mouse retinoid acid re	4.15e+02
478	15	1.1	2753 14	MUSCGMP	M.musculus mRNA for se	4.15e+02
479	16	1.1	2751 19	AF026811	Mouse cyclic GMP-depen	1.63e+03
480	16	1.1	2784 17	GLT04875	Butyrylcholinesterase	4.15e+02
481	15	1.1	2797 18	SCMET3	Giardia lamblia Portia	4.15e+02
482	15	1.1	2824 26	AC002848	Yeast MPT3 gene for AT	1.63e+03
483	15	1.1	2826 14	MKATGAT	*** SEQUENCING IN PROG	1.63e+03
484	15	1.1	2833 19	MUSSCCB	M.fortuitum KatGII gen	4.15e+02
485	15	1.1	2836 14	VP066708	Mus musculus TNFR2-TRA	1.63e+03
486	16	1.1	2879 18	RICRTH	Vibrio parahaemolyticu	4.15e+02
487	15	1.1	2906 19	STU1SN789	Rice gene for thiodio	1.63e+03
488	15	1.1	2911 18	CRUEP2	S.tuberculosis UlsRNA va	1.63e+03
489	15	1.1	2933 14	PMFGR2	Hamster elongation fac	1.63e+03
490	15	1.1	2967 16	RNTHYR02	P.waltl mRNA for fibro	1.63e+03
491	15	1.1	3018 14	S68687	Rat mRNA fragment for	1.63e+03
492	15	1.1	3022 15	CIP6RS	aminopeptidase N (rab	1.63e+03
493	15	1.1	3024 18	AC003779	Mesembryanthemum crys	1.63e+03
494	15	1.1	3027 26	AC003779	*** SEQUENCING IN PROG	1.63e+03
495	16	1.1	3053 18	SCYRN044W	S.cerevisiae chromosom	4.15e+02
496	16	1.1	3066 14	RATGLRCP	Rat mRNA sequence.	4.15e+02
497	16	1.1	3066 25	I66445	Sequence 1 from patent	4.15e+02
498	15	1.1	3080 17	DEMAC000621	Drosophila melanogaste	1.63e+03
499	16	1.1	3110 21	AEVVER	Avian erythroblastosis	4.15e+02
500	16	1.1	3113 21	HY086772	HIV-1 clone ZM174-2 f	4.15e+02
501	16	1.1	3137 18	YSCAGACS	S.cerevisiae aaggluti	4.15e+02
502	16	1.1	3153 16	CHRT054B	Chicken beta-4-tubulin	4.15e+02
503	16	1.1	3166 14	RNAJ1929	Rattus norvegicus mRNA	1.63e+03
504	15	1.1	3206 14	D78303	Rattus norvegicus brai	1.63e+03
505	15	1.1	3226 14	RATANC18HA	Rat Munc18-1 mRNA, com	1.63e+03
506	16	1.1	3231 6	AC002696	*** SEQUENCING IN PROG	4.15e+02
507	15	1.1	3251 18	SCPM2	S.cerevisiae pwp2 gene	4.15e+02
508	15	1.1	3263 17	D76445	Mouse mfr-1 mRNA, comp	1.63e+03
509	15	1.1	3279 7	HS1841750	Home sapiens (subclone	4.15e+02
510	16	1.1	3298 18	ABRSCP2	Abadilha zychae scp2 ge	4.15e+02
511	16	1.1	3322 14	RHBFR4	Bradylizibolum japoni	4.15e+02
512	15	1.1	3332 14	MM043187	Mus musculus MEK kins	1.63e+03
513	16	1.1	3370 14	S80679	IRS-1-insulin receptor	4.15e+02
514	15	1.1	3387 15	SSAMPNDN	S.scrofa mRNA for amin	1.63e+03
515	15	1.1	3392 14	YSPGAP1	Schizosaccharomyces po	1.63e+03
516	15	1.1	3414 14	MMCYLGRM	M.musculus ORF1 and OR	1.63e+03
517	15	1.1	3428 18	XLR04707	Xenopus laevis C-gadde	4.15e+02
518	16	1.1	3450 16	AP044255	Dicystostellum discoide	1.63e+03
519	15	1.1	3454 17	DMAC001911	O.cuniculus melanogaste	4.15e+02
520	16	1.1	3456 15	OCATPRNA	O.cuniculus mRNA for A	4.15e+02
521	16	1.1	3504 17	DSCHBRBP	D.suboscina chromosom	4.15e+02
522	16	1.1	3505 19	TRNTN21CAS	Transposon Tn2426 (fif	4.15e+02
523	16	1.1	3527 14	MMHVA59	Murine hepatitis virus	1.63e+03
524	15	1.1	3533 18	SC035411	Saccharomyces cerevisi	4.15e+02

526	15	1.1	3537	26	AC003306	*** SEQUENCING IN PROC	1.63e+03
527	15	1.1	3558	16	CG051DNA	G.gallus USFL-1 DNA se	4.15e+02
528	15	1.1	3615	16	D83273	Cyprinus carpio mRNA f	1.63e+03
529	15	1.1	3658	14	AF035045	Mus musculus Maxix pot	1.63e+03
530	15	1.1	3682	21	PVVAVIN83	Pumila virus M-segmen	1.63e+03
531	15	1.1	3730	25	I34014	Sequence 8 from paten	1.63e+03
532	15	1.1	3733	14	RAPTR3D	Rattus norvegicus tyro	1.63e+03
533	15	1.1	3750	19	U93704	Riftia pachyptilla endo	1.63e+03
534	15	1.1	3763	17	CEBPA2G	Caenorhabditis elegans	1.63e+03
535	15	1.1	3840	19	PCBPI	P. denitrificans bol g	1.63e+03
536	15	1.1	3865	19	ECOPISB	E.coli plsb and dck ge	4.15e+02
537	15	1.1	3874	19	RCFBC	Rhodospseudomonas sphe	1.63e+03
538	15	1.1	3876	17	BMOSP2	Slkxorm (B.mori) stor	1.63e+03
539	15	1.1	3911	18	SCYTL62C	S.cerevisiae chromosom	1.63e+03
540	15	1.1	3920	17	DRO25DC97Z	Drosophila melanogaste	1.63e+03
541	15	1.1	3923	14	MUSB14GT1	Mouse N-acetylglucosam	1.63e+03
542	15	1.1	3947	19	MBU77466	Myobacterium bovis BC	1.63e+03
543	15	1.1	3955	18	SCYRAD25A	Saccharomyces cerevisi	1.63e+03
544	15	1.1	3959	18	SCYTR010W	S.cerevisiae chromosom	4.15e+02
545	15	1.1	3969	14	MUSMHD2D	Mouse Mrc class I D-re	1.63e+03
546	15	1.1	3980	19	ALIDPAGA	A.haioiplanktis D-alani	1.63e+03
547	15	1.1	3983	17	CEIFDR3	C.elegans IPA4 gene fo	1.63e+03
548	15	1.1	4007	19	RCPEMG	Rhodospseudomonas capsu	1.63e+03
549	15	1.1	4023	14	MMU41282	Mus musculus galactose	1.63e+03
550	15	1.1	4028	15	OCATG11	Rabbit alpha-1-globin	4.15e+02
551	15	1.1	4029	17	IOU10338	Ilyanassa obsoleta RNA	1.63e+03
552	15	1.1	4031	15	RABHAPT	Rabbit alpha-globin ge	4.15e+02
553	15	1.1	4079	15	AF023128	Cryptosporidium cuniculu	1.63e+03
554	15	1.1	4080	18	SCYTL108C	S.cerevisiae chromosom	1.63e+03
555	15	1.1	4146	25	IS7017	Sequence 15 from paten	1.63e+03
556	15	1.1	4147	18	ATU50400	Arabidopsis thaliana p	1.63e+03
557	15	1.1	4182	18	SCYOR162C	S.cerevisiae chromosom	1.63e+03
558	15	1.1	4200	25	I34008	Sequence 1 from patent	1.63e+03
559	15	1.1	4239	25	I26663	Sequence 1 from patent	1.63e+03
560	15	1.1	4368	14	RNU76717	Rattus norvegicus PG10	4.15e+02
561	15	1.1	4374	18	ATU53856	Arabidopsis thaliana g	1.63e+03
562	15	1.1	4415	17	DROKCHAN	Drosophila melanogaste	1.63e+03
563	15	1.1	4469	14	RNU17096	Rattus norvegicus gamm	1.63e+03
564	15	1.1	4497	17	AF016854	Caenorhabditis elegans	4.15e+02
565	15	1.1	4534	19	BBBVAS	B.bronchiseptica bvg 1	4.15e+02
566	15	1.1	4535	17	DDY10159	D.bronchiseptica racGAP ge	1.63e+03
567	15	1.1	4546	17	PVAT4G	P.vulgaris alpha-tubuli	4.15e+02
568	15	1.1	4595	14	RNU10096	Rattus norvegicus Spira	4.15e+02
569	15	1.1	4605	14	MUS04518	Mus musculus strain CD	4.15e+02
570	15	1.1	4655	14	MMU20974	Mus musculus kidney-sp	4.15e+02
571	15	1.1	4655	14	MMU20975	Mus musculus kidney-sp	4.15e+02
572	15	1.1	4655	14	MMU20973	Mus musculus kidney-sp	4.15e+02
573	15	1.1	4700	18	AF014502	Glycine max seed coat	1.63e+03
574	15	1.1	4707	14	MUSMHR2DK	Mouse MRC class I H-2D	1.63e+03
575	15	1.1	4718	14	MUSC45DPI	Mouse C4/SIP hybrid 1	1.63e+03
576	15	1.1	4739	14	MUSC45DE2	Mouse C4/SIP hybrid 2	1.63e+03
577	15	1.1	4750	15	OCNKC2B	Oryctolagus cuniculus	4.15e+02
578	15	1.1	4750	15	OCNKC2A	Oryctolagus cuniculus	4.15e+02
579	15	1.1	4750	15	OCNKC2F	Oryctolagus cuniculus	4.15e+02
580	15	1.1	4758	14	DDU23478	Dicotylestium discoidi	1.63e+03
581	15	1.1	4763	14	MUSMHO85DB	Mouse MRC qa-2/3 class	1.63e+03
582	15	1.1	4768	16	CHKTR0SS04	Chicken tropomyosin be	1.63e+03
583	15	1.1	4785	18	M1PCURAP	P.chrysogenum mtocoon	1.63e+03
584	15	1.1	4819	18	AF001273	Emeriaella nidulans hy	4.15e+02
585	15	1.1	4821	23	XXU02429	Cloning vector pEUR-cl	4.15e+02
586	15	1.1	4866	23	XXU13868	PSV cloning vector, c	4.15e+02
587	15	1.1	4896	16	STRG1FC	S.mutans glucosyltrans	4.15e+02
588	15	1.1	4937	14	D87117	House mouse; Musculus	1.63e+03
589	15	1.1	4993	19	MA2PMA2	Microcyctis aeruginosa	4.15e+02
590	15	1.1	5051	19	D88825	Aeromonas caviae phac	1.63e+03
591	15	1.1	5071	15	SSSDCBRS	M.s.scrofa mraA for Na/D	1.63e+03
592	15	1.1	5110	14	MMPOGRRE	Mouse pte-PDGF recepto	4.15e+02
593	15	1.1	5125	14	RNANANT	Rat anti gene for aden	1.63e+03
594	15	1.1	5147	21	AF038616	Simian virus 40 strain	4.15e+02
595	15	1.1	5187	14	MUSMELA	Mouse MHC class I T3-d	4.15e+02
596	15	1.1	5243	21	SV40XX	SV40 genome.	4.15e+02
597	15	1.1	5243	21	SV40G	Simian virus 40 comple	4.15e+02
598	15	1.1	5264	14	RNU51261	Rattus norvegicus lam1	1.63e+03

599	16	1.1	5291	19	MUSTR0A	M.luteus str operon en	4.15e+02
600	16	1.1	5326	14	MUSGDU8CA	Mus musculus glucagon	4.15e+02
601	16	1.1	5350	14	MMTAM37A2	Mus musculus laminin b	4.15e+02
602	15	1.1	5371	14	MUSMHS1PC	Mouse MHC sex-limited	1.63e+03
603	15	1.1	5382	14	MMG91967	Mus musculus platelet	1.63e+03
604	16	1.1	5425	14	RATINNSI	Rat insulin-I (ins-1)	4.15e+02
605	15	1.1	5479	15	MMH2KK	Mouse H-2K(k) gene of	1.63e+03
606	15	1.1	5491	18	ATAIKI	A.thaliana AtK-1 gene.	1.63e+03
607	15	1.1	5552	17	DROPI2C1A	D.melanogaster phospho	4.15e+02
608	15	1.1	5559	14	RNGREX2	Rattus norvegicus gluc	4.15e+02
609	15	1.1	5562	17	CEVITEEA	C.elegans gene for vit	1.63e+03
610	15	1.1	5565	14	MMLSA3A	M.musculus mRNA for la	1.63e+03
611	16	1.1	5581	14	RNS1AM	Rat s-laminin mRNA.	4.15e+02
612	15	1.1	5591	15	RABAMYA	Rabbit serum amyloid A	1.63e+03
613	15	1.1	5702	14	RNMAP2	Rat map2 gene for micr	4.15e+02
614	15	1.1	5731	14	RNMAP2	Rat mRNA for microtubu	4.15e+02
615	15	1.1	5736	14	RNMAP2R	Rat mRNA for microtubu	4.15e+02
616	15	1.1	5746	15	STPNP	S.scrofa mRNA for tena	1.63e+03
617	15	1.1	5794	15	WZ014952	Weeksella zoonelium AC	1.63e+03
618	15	1.1	5799	18	TYDNALBGT	T.versicolor Lpg 1 and	4.15e+02
619	15	1.1	5831	18	SOYMOD26A	Glycine max cv. Dare n	1.63e+03
620	15	1.1	5850	16	GGU62026A	Gallus gallus cardiac	1.63e+03
621	15	1.1	5900	19	AF034514	Zymomonas mobilis carb	1.63e+03
622	15	1.1	6008	25	TI8304	Sequence 5 from patent	1.63e+03
623	15	1.1	6008	18	ISCOBPEIT	Saccharomyces cerevisi	1.63e+03
624	15	1.1	6014	14	AF000938	Mus musculus RNA polym	4.15e+02
625	15	1.1	6018	14	AF025425	Rattus norvegicus RNA	4.15e+02
626	15	1.1	6027	19	MKY14428	Methanopyrus kandleri	4.15e+02
627	15	1.1	6161	14	MMU57393	Mus musculus class Ib	1.63e+03
628	15	1.1	6175	21	HSV11TP	Feline herpesvirus typ	1.63e+03
629	15	1.1	6225	18	HVCPMTI	H.vulgaris gene encodin	1.63e+03
630	15	1.1	6331	14	MMR200KP	M.musculus mRNA for 20	4.15e+02
631	15	1.1	6373	21	AEVDPDA	Avian erythroblastosis	1.63e+03
632	15	1.1	6466	14	D8694A	Mouse mRNA for plexin	4.15e+02
633	15	1.1	6553	16	NPOCAPA	O.pseudotubercula multie	4.15e+02
634	15	1.1	6563	16	CHKRBBF	Chicken c-erbB oncogen	1.63e+03
635	15	1.1	6642	25	I64799	Sequence 5 from patent	1.63e+03
636	15	1.1	6730	14	D8694X	Mouse mRNA for plexin	1.63e+03
637	15	1.1	6831	14	MTEENASC	Mouse mRNA for tenasci	1.63e+03
638	15	1.1	6843	25	I64800	Sequence 6 from patent	1.63e+03
639	15	1.1	6900	19	BPGAVAS	B.paraperituss bvg 10	4.15e+02
640	15	1.1	6914	18	SCCACL3R	S.cerevisiae DPH2, YCN	4.15e+02
641	15	1.1	7129	18	ZMU77346	Zea mays lethal leaf-8	1.63e+03
642	15	1.1	7350	25	I14735	Sequence 14 from paten	4.15e+02
643	15	1.1	7573	14	GPCDNPO	Guinea pig Cytochrome p	4.15e+02
644	15	1.1	7687	21	MRU01834	Multinmate rat papil	1.63e+03
645	15	1.1	7769	15	BPU55042	Bos taurus myosin X, c	1.63e+03
646	15	1.1	7872	19	BAAWYA	B.acidocaldarius any g	4.15e+02
647	15	1.1	7878	14	MMABCI	M.musculus abcl mRNA.	4.15e+02
648	15	1.1	7909	15	PFSC04059	Plasmodium falciparum	1.63e+03
649	15	1.1	7933	17	BOVCMPR	Bovine catlion-independ	1.63e+03
650	15	1.1	7942	21	HPV52	Human papillomavirus t	1.63e+03
651	15	1.1	8014	14	RNPS26	R.norvegicus (Sprague	1.63e+03
652	15	1.1	8017	18	ATU76670	Arabidopsis thaliana r	4.15e+02
653	15	1.1	8089	17	STMDAUXBC5	Streptomyces sp. alaly	4.15e+02
654	15	1.1	8809	17	DRODISABLE	Drosophila melanogaste	1.63e+03
655	15	1.1	9000	21	HIYV05942	Human immunodeficiency	4.15e+02
656	15	1.1	9022	21	HIYV059C	Human immunodeficiency	4.15e+02
657	15	1.1	9201	23	SYNVPHP	Cloning vector cosmid	4.15e+02
658	15	1.1	9623	21	STVAGMA	Simian immunodeficienc	4.15e+02
659	15	1.1	9623	21	STVAGM677A	Simian (African green	4.15e+02
660	15	1.1	9698	21	PVU09509	Potato virus Y common	4.15e+02
661	15	1.1	9709	21	HIYV143	Human immunodeficiency	4.15e+02
662	15	1.1	9811	21	CIYVG	Chimpanzee immunofic	1.63e+03
663	15	1.1	9901	19	U67530	Methanococcus jannasch	1.63e+03
664	15	1.1	10028	19	U67503	Methanococcus jannasch	1.63e+03
665	15	1.1	10039	19	STRGTEPC	S.mutans glucosyltrans	4.15e+02
666	15	1.1	10035	21	AF024514	Acyrtosiphon pisum vl	1.63e+03
667	15	1.1	10105	19	AE000946	Archaeoglobus fulgidus	4.15e+02
668	15	1.1	10145	15	GOTGLOBE	Coat beta globin locus	4.15e+02
669	15	1.1	10199	18	AF009516	Pectunia x hybrida tran	1.63e+03
670	15	1.1	10338	18	U67464	Methanococcus jannasch	4.15e+02
671	15	1.1	10512	19	HPA000639	Helicobacter pylori se	4.15e+02

672	1.1	10621	15	RABGROBIN	Rabbit zeta-1 globin (4.15e+02	745	16	32365	17	CELR26E4	Caenorhabditis elegans	4.15e+02
673	1.1	10669	19	U67584	Methanococcus jannasch	4.15e+02	746	16	32509	17	CEK07C5	Caenorhabditis elegans	4.15e+02
674	1.1	10666	15	PIGAPOLP	Sus scrofa apolipoprot	4.15e+02	747	16	32661	18	SC8010	S.cerevisiae chromosom	4.15e+02
675	1.1	10688	19	AE000889	Methanobacterium therm	4.15e+02	748	16	32679	17	CEJ20D3	Caenorhabditis elegans	4.15e+02
676	1.1	10702	19	ECAE000247	Escherichia coli K-12	4.15e+02	749	15	32719	17	CEIR13D1	Caenorhabditis elegans	1.63e+03
677	1.1	11096	14	MMY12229	M.musculus mRNA for ut	4.15e+02	750	16	33066	16	PRU82608	Pingu rubripes lymphoid	4.15e+02
678	1.1	11107	19	AE000890	Methanobacterium therm	4.15e+02	751	15	33120	17	CELR06A10	Caenorhabditis elegans	4.15e+02
679	1.1	11215	19	YERRBNGN	X.enteroocollitica rkb-2	1.63e+03	752	15	33210	17	CELR06A10	Caenorhabditis elegans	4.15e+02
680	1.1	11314	19	ECAE000477	Escherichia coli K-12	1.63e+03	753	15	33274	17	CELR52B5	Caenorhabditis elegans	4.15e+02
681	1.1	11367	19	AE001031	Archaeoglobus fulgidus	1.63e+03	754	16	33359	17	CELR55C7	Caenorhabditis elegans	4.15e+02
682	1.1	11605	14	MUSEMP2A	Mus musculus bone morph	1.63e+03	755	16	33440	17	CELR36A2	Caenorhabditis elegans	4.15e+02
683	1.1	11663	19	ECAE000242	Escherichia coli K-12	1.63e+03	756	15	33490	17	CELRK20	Caenorhabditis elegans	4.15e+02
684	1.1	11725	19	AE001106	Archaeoglobus fulgidus	1.63e+03	757	15	33545	17	CELR37E2	Caenorhabditis elegans	1.63e+03
685	1.1	11837	19	AE001172	Borrelia burgdorferi (1.63e+03	758	15	33702	17	CELR37E2	Caenorhabditis elegans	1.63e+03
686	1.1	12194	19	HTU32687	Haemophilus influenzae	1.63e+03	759	15	33762	17	CELR7D12	Caenorhabditis elegans	1.63e+03
687	1.1	12494	19	ECAE000243	Escherichia coli K-12	1.63e+03	760	15	34073	17	CELR09E11	Caenorhabditis elegans	1.63e+03
688	1.1	12710	17	PFSC03030	Plasmodium falciparum	1.63e+03	761	15	34073	17	CELR11D1	Caenorhabditis elegans	1.63e+03
689	1.1	13058	19	AF032884	Thiobacillus ferrooxid	1.63e+03	762	15	34596	26	AC000077	*** SEQUENCING IN PROG	1.63e+03
690	1.1	13242	19	AE000858	Methanobacterium therm	1.63e+03	763	15	34727	17	SPBC16C6	S.pombe chromosome II	1.63e+03
691	1.1	13242	19	HVBARE1	Methanobacterium therm	1.63e+03	764	16	35296	17	CELR12E12	Caenorhabditis elegans	1.63e+03
692	1.1	13271	18	AVIHOXHP	H.vulgaris DNA for BARE	1.63e+03	765	16	35348	17	CELR13A2	Caenorhabditis elegans	1.63e+03
693	1.1	13914	19	AVIHOXHP	Acetobacter vinelandii	1.63e+03	766	15	35383	18	SCDNAIV	S.cerevisiae DNA for O	1.63e+02
694	1.1	14009	18	CRU15303	Chlamydomonas reinhard	1.63e+03	767	16	35409	17	CEC44C10	Caenorhabditis elegans	1.63e+02
695	1.1	14198	19	AE001162	Borrelia burgdorferi (1.63e+03	768	15	35452	18	SC354CHY	S.cerevisiae 35.4kb DN	4.15e+02
696	1.1	14278	19	U39680	Mycoplasma genitalium	1.63e+03	769	16	35728	17	CELRK08B5	Caenorhabditis elegans	4.15e+02
697	1.1	14993	18	U81044	Gillardia theta plast	1.63e+03	770	15	35820	17	CELR21E12	Caenorhabditis elegans	4.15e+02
698	1.1	15359	19	D90792	E.coli genomic DNA, Ko	4.15e+02	771	16	35855	17	CELR38C3	Caenorhabditis elegans	1.63e+03
699	1.1	15471	18	SPAC1B1	S.pombe chromosome I c	1.63e+03	772	15	35950	17	CELR30G4	Caenorhabditis elegans	4.15e+02
700	1.1	15541	15	OCRYARA	O.cuniculus mRNA for r	1.63e+03	773	15	36049	17	CELR31F6	Caenorhabditis elegans	1.63e+03
701	1.1	16033	19	CEKX795	Caenorhabditis elegans	1.63e+03	774	15	36180	17	CELR05G5	Caenorhabditis elegans	1.63e+03
702	1.1	16382	13	E11392	E.coli genomic DNA, Ko	1.63e+03	775	15	36189	17	CELR08G9	Caenorhabditis elegans	1.63e+03
703	1.1	17913	13	D90848	Human cDNA encoding FC	1.63e+03	776	16	36362	17	HSAD823	Homo sapiens DNA from	4.15e+02
704	1.1	17970	19	D90838	E.coli genomic DNA, Ko	1.63e+03	777	16	36709	17	CELR0507	Caenorhabditis elegans	4.15e+02
705	1.1	18757	15	AB010579	E.coli genomic DNA, Ko	1.63e+03	778	16	36811	17	CELR20B12	Caenorhabditis elegans	4.15e+02
706	1.1	19001	17	CEM01A8	Caenorhabditis elegans	1.63e+03	779	15	36880	17	CELR35D10	Caenorhabditis elegans	4.15e+02
707	1.1	19108	18	SPAC1B9	S.pombe chromosome I c	1.63e+03	780	16	37049	19	MLACEA	M.leptae aceA gene for	4.15e+02
708	1.1	19541	17	DMAC001647	Drosophila melanogaste	1.63e+03	781	15	37434	18	SC81128	Caenorhabditis elegans	4.15e+02
709	1.1	19929	19	D90791	E.coli genomic DNA, Ko	4.15e+02	782	16	37516	17	CELR49H3	S.cerevisiae chromosom	1.63e+03
710	1.1	20258	18	CRU02963	Chlamydomonas reinhard	1.63e+03	783	16	37532	17	CEC41G6	Caenorhabditis elegans	4.15e+02
711	1.1	20303	25	I40904	Sequence 6 from patent	1.63e+03	784	16	37665	17	CELR24D5	Caenorhabditis elegans	4.15e+02
712	1.1	20343	16	GGVIT1IG	Human coronavirus RNA	4.15e+02	785	16	37689	17	CELR18C12	Caenorhabditis elegans	4.15e+02
713	1.1	20580	21	HCYORFIAB	Chicken vitellogenin I	4.15e+02	786	16	38000	17	CELR58A4	Caenorhabditis elegans	4.15e+02
714	1.1	21732	18	YSCU9324	Saccharomyces cerevisi	1.63e+03	787	15	38060	17	CELR13F2	Caenorhabditis elegans	1.63e+03
715	1.1	22847	18	SPAC18B11	S.pombe chromosome I c	1.63e+03	788	15	38070	17	CELR58H12	Caenorhabditis elegans	1.63e+03
716	1.1	23753	17	CELM09C3	Caenorhabditis elegans	1.63e+03	789	16	38259	17	CELR04G2	Caenorhabditis elegans	4.15e+02
717	1.1	23787	19	BS16823KB	Bacillus subtilis geno	1.63e+03	790	16	38477	18	SPAC23C4	S.pombe chromosome I c	4.15e+02
718	1.1	23897	17	SCU55021	Pseudomonas cerevisi	1.63e+03	791	16	38477	18	SCPEKGA	Human DNA sequence ***	4.15e+02
719	1.1	24937	18	PTU24215	Pseudomonas putida p-c	4.15e+02	792	16	38889	26	HSCE33B10	Caenorhabditis elegans	4.15e+02
720	1.1	25550	17	CEFA6P6	Caenorhabditis elegans	4.15e+02	793	15	38967	17	CELR25G6	Caenorhabditis elegans	1.63e+03
721	1.1	25934	17	CELM05B11	Caenorhabditis elegans	4.15e+02	794	15	39228	19	MLC517E8	Caenorhabditis elegans	1.63e+03
722	1.1	26054	17	CELC46A5	Caenorhabditis elegans	1.63e+03	795	15	39320	17	CELR13E6	Caenorhabditis elegans	1.63e+03
723	1.1	26054	17	CELC46A5	Caenorhabditis elegans	1.63e+03	796	15	39478	17	CELR3EFL	Caenorhabditis elegans	1.63e+03
724	1.1	26210	17	CELC46A5	Caenorhabditis elegans	1.63e+03	797	15	39580	17	CELR45H7	Caenorhabditis elegans	1.63e+03
725	1.1	26764	25	I40899	Sequence 1 from patent	1.63e+03	798	15	39621	7	HSAD827	Homo sapiens DNA from	4.15e+02
726	1.1	26764	25	I40899	Sequence 1 from patent	1.63e+03	799	15	40014	17	CELR48B9	Caenorhabditis elegans	1.63e+03
727	1.1	26959	17	CELR07F10	Caenorhabditis elegans	4.15e+02	800	15	40265	17	CELR03A8	Caenorhabditis elegans	1.63e+03
728	1.1	27068	17	CEC15A7	Caenorhabditis elegans	4.15e+02	801	15	40475	17	CELRD1009	Caenorhabditis elegans	1.63e+03
729	1.1	27248	17	CEK08E4	Caenorhabditis elegans	4.15e+02	802	15	40481	17	CEC82D4	Caenorhabditis elegans	1.63e+03
730	1.1	27298	26	CEH26P12	Caenorhabditis elegans	4.15e+02	803	15	41087	17	CELR09G2	Caenorhabditis elegans	1.63e+03
731	1.1	27559	18	SC8339	S.cerevisiae chromosom	1.63e+03	804	16	41313	26	CELR13C10	Caenorhabditis elegans	4.15e+02
732	1.1	27598	17	CEFA5A11	Caenorhabditis elegans	4.15e+02	805	15	41313	26	CELR13C10	Caenorhabditis elegans	1.63e+03
733	1.1	27608	21	IBACG8	Avian infectious bronc	1.63e+03	806	16	42018	26	AC000002	*** SEQUENCING IN PROG	4.15e+02
734	1.1	27613	17	CEK08G2	Caenorhabditis elegans	1.63e+03	807	15	42056	17	CEC33D6	Caenorhabditis elegans	4.15e+02
735	1.1	27797	17	CEP23B12	Caenorhabditis elegans	4.15e+02	808	16	42730	17	CEC33H4	Caenorhabditis elegans	4.15e+02
736	1.1	28573	17	CELM151	Caenorhabditis elegans	1.63e+03	809	16	42769	18	CELR47E1	Caenorhabditis elegans	4.15e+02
737	1.1	28698	18	SC9375	S.cerevisiae chromosom	4.15e+02	810	16	42808	19	MTY13E12	Mycobacterium tubercul	4.15e+02
738	1.1	28932	18	SC9375	S.cerevisiae chromosom	4.15e+02	811	15	43441	18	CEP2005	Caenorhabditis elegans	1.63e+03
739	1.1	29807	14	MMU73107	Mus musculus adenosine	1.63e+03	812	15	43468	18	SC8358	S.cerevisiae chromosom	4.15e+02
740	1.1	30061	17	CEC30D11	Caenorhabditis elegans	1.63e+03	813	16	43661	18	SCXOOSM83	S.cerevisiae chromosom	4.15e+02
741	1.1	30794	17	CELR28F3	Caenorhabditis elegans	1.63e+03	814	15	43776	18	SC9499X	S.cerevisiae chromosom	1.63e+03
742	1.1	31364	17	CELR25A11	Caenorhabditis elegans	4.15e+02	815	15	45022	17	CEC34D1	Caenorhabditis elegans	1.63e+03
743	1.1	31664	17	CELR10A3	Caenorhabditis elegans	1.63e+03	816	15	45164	26	AC002360	Homo sapiens: HTGS pha	1.63e+03
744	1.1	32215	17	CEM02B9	Caenorhabditis elegans	4.15e+02	817	15	45389	17	CELR32E12	Caenorhabditis elegans	1.63e+03

818	16	1.1	46105	17	CEIC055C3	Caenorhabditis elegans	4.15e+02	881	16	1.1	120781	26	HS506	Human DNA sequence ***	4.15e+02
819	15	1.1	46462	17	CEIC335F10	Caenorhabditis elegans	1.63e+03	882	16	1.1	120787	14	AC002282	Genomic sequence of Ar	4.15e+02
820	15	1.1	47368	26	AC000090	*** SEQUENCING IN PROG	1.63e+03	883	16	1.1	122176	14	AC003997	Mouse BAC mbac20 from	1.63e+03
821	15	1.1	47512	26	CEIR03E1	Caenorhabditis elegans	1.63e+03	884	16	1.1	123080	26	HS510H16	Human DNA sequence ***	1.63e+03
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825	15	1.1	50994	18	SCAYORS	S.cerevisiae DNA of 51	1.63e+03	888	16	1.1	128200	26	AC003040	*** SEQUENCING IN PROG	4.15e+02
826	16	1.1	51776	26	HSN91G8	*** SEQUENCING IN PROG	4.15e+02	889	16	1.1	128393	26	HS146H21	Human DNA sequence ***	4.15e+02
827	16	1.1	53419	14	MMU05333	Mus musculus H2-M alpha	4.15e+02	890	16	1.1	128607	26	HS1334	Human DNA sequence ***	4.15e+02
828	16	1.1	53517	26	AC002405	Homo sapiens: HTGS pha	4.15e+02	891	16	1.1	131047	26	AC002421	*** SEQUENCING IN PROG	4.15e+02
829	16	1.1	53533	26	BSY09476	B.subtilis 54kb genom	4.15e+02	892	16	1.1	131193	26	HS510D11	Human DNA sequence ***	4.15e+02
830	16	1.1	54606	26	AC000053	*** SEQUENCING IN PROG	4.15e+02	893	16	1.1	131936	26	AC003063	*** SEQUENCING IN PROG	4.15e+02
831	16	1.1	55786	26	SCILACHYI	S.cerevisiae chromosome	4.15e+02	894	16	1.1	131960	21	OP075930	Oryza pseudoturgata n	4.15e+02
832	15	1.1	57677	26	HSU151E3	Human DNA sequence ***	1.63e+03	895	16	1.1	132697	26	AC002365	*** SEQUENCING IN PROG	1.63e+03
833	15	1.1	57892	18	AB005241	Arabidopsis thaliana g	1.63e+03	896	16	1.1	133661	21	U93872	Kaposi's sarcoma-asso	1.63e+03
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837	16	1.1	68302	18	SCB8781	Saccharomyces cerevisi	4.15e+02	900	16	1.1	136294	26	EC00W82	E. coli: the region fr	1.63e+03
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843	16	1.1	78616	14	AC000398	Genomic sequence from	4.15e+02	906	16	1.1	139467	19	D90905	Synechocystis sp. PCC	1.63e+03
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854	15	1.1	89350	18	ATT12H17	Arabidopsis thaliana D	1.63e+03	917	16	1.1	146505	18	P21M12	Sequence of BAC P21M12	4.15e+02
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864	16	1.1	95456	26	CEH002092	*** SEQUENCING IN PROG	4.15e+02	927	16	1.1	157684	14	AC004093	Mus musculus (129SV) D	1.63e+03
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C	985	15	1.1	233780	19	BSUB0010	Bacillus subtilis comp	1.65e+03
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C	987	16	1.1	247085	26	AC003037	Homo sapiens; HTGS pha	4.15e+02
C	988	16	1.1	251364	14	MMAR000664	Mus musculus; TCR beta	4.15e+02
C	989	15	1.1	252128	26	CER1BD10	Caenorhabditis elegans	1.65e+03
C	990	15	1.1	257948	26	HS21265	Human DNA sequence ***	4.15e+02
C	991	15	1.1	266831	26	AC003684	Homo sapiens; HTGS pha	1.65e+03
C	992	15	1.1	276361	26	HSAC004046	*** SEQUENCING IN PROG	4.15e+02
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C	995	16	1.1	315339	18	SCCHRI11	S.cerevisiae chromosome	4.15e+02
C	996	16	1.1	320751	26	AC003978	Homo sapiens; HTGS pha	4.15e+02
C	997	15	1.1	330740	21	PBU42580	Paramecium bursaria Ch	1.65e+03
C	998	15	1.1	332000	20	CERY102A5	Caenorhabditis elegans	1.65e+03
C	999	15	1.1	338534	19	EC00983	Escherichia coli K-12	1.65e+03
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ALIGNMENTS

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RESULT	2		
LOCUS	S81111	1288 bp	ROD 02-AUG-1996
DEFINITION	kappa-opioid receptor [alternatively spliced] [mice, C58/J, R1.1		
ACCESSION	S81111	thymoma cells, mRNA Partial, 1288 nt].	
NID	G1478285		
KEYWORDS			
SOURCE	Mus sp.	C58/J R1.1 thymoma cells.	
ORGANISM	Mus sp.	Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;	
REFERENCE	1 (bases 1 to 1288)		
AUTHORS	Belkowsky, S.M., Zhu, J., Liu-Chen, L.Y., Eisenstein, T.K., Adler, M.W. and Rogers, T.J.		
TITLE	Sequence of kappa-opioid receptor cDNA in the R1.1 thymoma cell line		
JOURNAL	J Neuroimmunol. 62 (1), 113-117 (1995)		
MEDLINE	96084989		
REMARK	GenBank staff at the National Library of Medicine created this entry [NCBI gisb3 175931] from the original journal article. This sequence comes from Fig. 3.		
COMMENT	longer of two transcripts.		
FEATURES	location/Qualifiers		
Source	1..1288		
gene	/organism="Mus sp."		
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	CHPKRALDPRTPKAKIINICITWLASVGSIAVLGTYREVDYIECSLPDDE		
	YSWMDLEMKTCVFAFVIVPLIITVCTYMLILDKSVRLSSREDNRIRITKIV		
	LVYAVVITICMTPIHIFILVLAUSISHTASLSYFICNLIGTNSLNVPLAFILD		
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BASE COUNT	283	a	336	c	305	g	364	t
Query Match								
Best Local Similarity			85.7%					
Matches 1208;			Conservative		0;		Mismatches	0;
							Indels	0;
							Gaps	
Db	81	AGCTGACGAGCGCTACACATGAGAGTCCCGCCCACTTGAAGATCTTCCGAGAGAGATCCAGCGCTTAC	140					
QY	170	AGCTGACGAGCGCTACACATGAGAGTCCCGCCCACTTGAAGATCTTCCGAGAGAGATCCAGCGCTTAC	229					
Db	141	CTGCTCTCCCAAGTGTGCTTCCCTTCCCAAGCAAGCAAGCTTTGGTCCCACTGGAGCA	200					
QY	230	CTGCTCTCCCAAGTGTGCTTCCCTTCCCAAGCAAGCAAGCTTTGGTCCCACTGGAGCA	289					
Db	201	ATCCGACAGTAATGAGCAGTGTGGGCTCAGAGAGATGAGCAGAGTGGAGTCCCGACATCTC	260					
QY	290	ATCCGACAGTAATGAGCAGTGTGGGCTCAGAGAGATGAGCAGAGTGGAGTCCCGACATCTC	349					
Db	261	TCCGGCCATCCCTGTATATCAACCGCTGTCTACTGTGTGATTTTGTGTGGGCTTGT	320					
QY	350	TCCGGCCATCCCTGTATATCAACCGCTGTCTACTGTGTGATTTTGTGTGGGCTTGT	409					
Db	321	GGGGAATTCCTGGTATGTTTGTCTATCTCCGATACAGAGATGAGAGACCGACACCA	380					
QY	410	GGGGAATTCCTGGTATGTTTGTCTATCTCCGATACAGAGATGAGAGACCGACACCA	469					
Db	381	CATCTACATATTTAACTGGGCTTTGGCAAGTGGCTTGTGTTATACACTATGCCCTTTCA	440					
QY	470	CATCTACATATTTAACTGGGCTTTGGCAAGTGGCTTGTGTTATACACTATGCCCTTTCA	529					
Db	441	GAGTGTCTGTACTTGATGTAATTCCTGGCTTTGGAGATGTCTATSCAAGATTTGTAT	500					
QY	530	GAGTGTCTGTACTTGATGTAATTCCTGGCTTTGGAGATGTCTATSCAAGATTTGTAT	589					
Db	501	TTCCATTTGACTACTACAAATGTTTACCAAGCATTCACCTTGACCAATGATGAGGTGTGA	560					
QY	590	TTCCATTTGACTACTACAAATGTTTACCAAGCATTCACCTTGACCAATGATGAGGTGTGA	649					
Db	561	CCGCTACATTTGCTGTGTGGCCACCCTGTGAAGTTTGGACTCCGCAACACCTTGAAGC	620					
QY	650	CCGCTACATTTGCTGTGTGGCCACCCTGTGAAGTTTGGACTCCGCAACACCTTGAAGC	709					
Db	621	AAAGATCATCAACATCTGCATTTTGGCTCTGGCATCATCTGTGGTATATCAGGATAGT	680					
QY	710	AAAGATCATCAACATCTGCATTTTGGCTCTGGCATCATCTGTGGTATATCAGGATAGT	769					
Db	661	CTTTGGAGGACCAAGCTCAGGGAAGATGTGATGTCAATGATCTCTTGCAGTTTCC	740					
QY	770	CTTTGGAGGACCAAGCTCAGGGAAGATGTGATGTCAATGATCTCTTGCAGTTTCC	829					
Db	741	TGATGATGAATATCCGATGGGATCTCTCATGGAAGATCTGTGCTCTGGCTTGGCTT	800					
QY	830	TGATGATGAATATCTCTGTGGGATCTCTCATGGAAGATCTGTGCTCTGGCTTGGCTT	889					
Db	801	TGTATCCCACTCTCATCATCTATTGTCTGCTACACCCATGATGATCTGGGCTGAAAG	860					
QY	890	TGTATCCCACTCTCATCATCTATTGTCTGCTACACCCATGATGATCTGGGCTGAAAG	949					
Db	861	TGTCCGGCTCTGTCTGGCTTCCGAGAGAGAACGAAATCTCCGGCCGATCACCAGCT	920					
QY	950	TGTCCGGCTCTGTCTGGCTTCCGAGAGAGAACGAAATCTCCGGCCGATCACCAGCT	1009					
Db	921	GGTGTGGTATGATTTGACATCTTTCATCAATCTGATGAGTGGGACCCCATTCACATTTTATCT	980					
QY	1010	GGTGTGGTATGATTTGACATCTTTCATCAATCTGATGAGTGGGACCCCATTCACATTTTATCT	1068					
Db	981	GATGAGAGCTCTGTGGAAGCAAGCTTCCACAGCAAGTGTGCTCTCAGATATATTCTTG	1048					
QY	1070	GATGAGAGCTCTGTGGAAGCAAGCTTCCACAGCAAGTGTGCTCTCAGATATATTCTTG	1129					
Db	1041	TATTGCTTGGGTTATACCAACAGAGCTGAATCTGTTCCTATAGCTTTCTGGATGA	1100					

RESULT 5
 LOCUS 577868S2 1109 bp DNA ROD 26-SEP-1995
 DEFINITION kappa opioid receptor [mice, genomic, 1109 nt, segment 2 of 3].
 ACCESSION 577869
 NID 9998530
 KEYWORDS
 SEGMENT 2 of 3
 SOURCE Mus sp.
 ORGANISM Mus sp.
 Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 1109)
 AUTHORS Liu,H.C., Lu,S., Augustin,L.B., Felsheim,R.F., Chen,H.C., Ioh,H.H. and Wei,L.N.
 TITLE Cloning and promoter mapping of mouse kappa opioid receptor gene
 JOURNAL Biochem. Biophys. Res. Commun. 209 (2), 639-647 (1995)
 MEDLINE 95251663
 REMARK GenBank staff at the National Library of Medicine created this entry [NCBI gibsseq 166534] from the original journal article.
 This sequence comes from Fig. 2.
 FEATURES
 source Location/Qualifiers
 1..1109
 /organism="Mus sp."
 /db_xref="taxon:10095"
 BASE COUNT 331 a 213 c 204 g 361 t
 ORIGIN
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 Best Local Similarity 100.0%; Pred. No. 0.00e+00;
 Matches 354; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 370 GATACAGAGATGAGAGACCGCACACATCTACATATTTAACCTGGCTTGGCAGATG 429
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 Qy 442 GATACAGAGATGAGAGACCGCACACATCTACATATTTAACCTGGCTTGGCAGATG 501
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 Db 430 CTTTGACTCTACCACTATGCCCCCTTACAGAGTGCTGTCTACTGATGAAATTTGGCCTT 489
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 Qy 502 CTTTGACTCTACCACTATGCCCCCTTACAGAGTGCTGTCTACTGATGAAATTTGGCCTT 561
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 Db 490 TTGGAGATGCTATGACAGATGTCATTCATTCATGACAGTACAAACATGTTACAGCA 549
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 Db 550 TATTCACCTTGACCATGATGAGTGTGACCGCTACATTCCTGTGTGCCACCTGTGAAG 609
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 Qy 622 TATTCACCTTGACCATGATGAGTGTGACCGCTACATTCCTGTGTGCCACCTGTGAAG 681
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 Db 610 CTTTGACTCTCGAAGACCTTTGAAAGCAAGATCATCAACATCTGCATTGGCTCTCTG 669
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 Qy 682 CTTTGACTCTCGAAGACCTTTGAAAGCAAGATCATCAACATCTGCATTGGCTCTCTG 741
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 Db 670 CATCATCTTTGGTATATGACGATATGCTCTTGAGAGCCACCAAGCAGGGAAG 723
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 Qy 742 CATCATCTTTGGTATATGACGATATGCTCTTGAGAGCCACCAAGTCAAGGGAAG 795
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 RESULT 7
 LOCUS MMU16998 432 bp DNA ROD 07-DEC-1994
 DEFINITION Mus musculus kappa opioid receptor (oprk1) gene, partial cds.
 ACCESSION U16998
 NID 9595936
 KEYWORDS
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 432)
 AUTHORS Murandy,D.K.
 TITLE Mapping of the human kappa opioid receptor gene to chromosome

JOURNAL 8q11.2-q12: no evidence for multiple kappa opioid receptor genes
 REFERENCE 2 (bases 1 to 432)
 AUTHORS Murandy,D.K.
 TITLE Direct Submission
 JOURNAL Submitted (07-NOV-1994) David K. Murandy, Vollum Institute, Oregon Health Sciences, University, 3181 S.W. Sam Jackson Park Road, Portland, OR 97201, USA
 FEATURES
 source Location/Qualifiers
 1..432
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 /clone="R21mg1"
 /clone_lib="Scratagene lambda FIX"
 /sex="male"
 /dev_stage="adult"
 14..366
 /gene="oprk1"
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 /note="encodes putative transmembrane domains II, III and IV"
 /codon_start=2
 /evidence="experimental"
 /product="kappa opioid receptor"
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 BASE COUNT 114 a 92 c 85 g 141 t
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 Query Match 19.5%; Score 275; DB 14; Length 432;
 Best Local Similarity 99.7%; Pred. No. 0.00e+00;
 Matches 305; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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 Qy 490 CTTTGAGAGTCTTTGGTACTACCACTANGCCCTTTCAGAGTCTGTCTACATGATGCA 549
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 Db 121 ATTCTTGCGCTTTGAGAGTGTGCTATGCAAGATGTGCAATTCATTTGGCTCTCAACA 180
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 Qy 550 ATTCTTGCGCTTTGAGAGTGTGCTATGCAAGATGTGCAATTCATTTGGCTCTCAACA 609
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 Db 181 TGTTTACAGCATATTACCTGACCATGATGAGTGTGAGCCGCTACATCTGCTGTGCC 240
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 Qy 610 TGTTTACAGCATATTACCTGACCATGATGAGTGTGAGCCGCTACATCTGCTGTGCC 669
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 Db 361 GGGAG 366
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 Qy 790 GGGAG 795
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 RESULT 8
 LOCUS MUSMORGDPI 423 bp DNA ROD 12-APR-1996
 DEFINITION Mouse MORF gene for kappa-opioid receptor, exon 1.
 ACCESSION D31653
 NID 9643592
 KEYWORDS
 SEGMENT 1 of 3
 SOURCE Mus musculus DNA, clone_lib:phage lambda fixII.
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 423)
 AUTHORS Nishi, M., Takeshima, H., Mori, M., Nakagawara, K. and Takeuchi, T.
 TITLE Structure and chromosomal mapping of genes for the mouse
 +kappa-opioid receptor and an opioid receptor homolog (MOR-C)
 JOURNAL Biochemical and Biophysical Research Communication 205, 1353-1357
 (1994)

REFERENCE 2 (bases 1 to 423)
 AUTHORS Takeshima, H.
 TITLE Direct Submission
 JOURNAL Submitted (28-MAY-1994) to the DDBJ/EMBL/GenBank databases. Hiroshi
 Takeshima, Tokyo Institute of Psychiatry, Department of
 Neuropsychiatry, 2-1-8 Kamikitazawa, Setagaya-ku, Tokyo 156, Japan
 (Tel:03-3304-5701(ex.312), Fax:03-3329-8035)
 COMMENT Submitted (28-May-1994) to DDBJ by:
 Hiroshi Takeshima
 Department of Neuropsychiatry
 Tokyo Institute of Psychiatry
 2-1-8 Kamikitazawa, Setagaya-ku
 Tokyo 156
 Japan
 Phone: 03-3304-5701 x312
 Fax: 03-3329-8035.

FEATURES
 source Location/Qualifiers
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 /db_xref="taxon:10090"
 /clone_lib="phage lambda fixit"
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 /note="first protein coding sequence (P1)"
 exon /number=1
 BASE COUNT 64 a 126 c 116 g 117 t
 ORIGIN Chromosome 1 A2-3.

Query Match 19.4%; Score 273; DB 14; Length 423;
 Best Local Similarity 100.0%; Pred. No. 0.00e+00;
 Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 QY 170 AGCTGAGGCGTCACCATGAGTCCCATTCAGATCTCCAGAGATCCAGGCCCTAC 229
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 Db 155 CTGCTCTCCAGTGTCTTGCCTTCTCCCAACAGACAGCTCTGTTCCCACTGGGCGAGA 214
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 QY 230 CTGCTCTCCAGTGTCTTGCCTTCTCCCAACAGACAGCTCTGTTCCCACTGGGCGAGA 289
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 QY 290 ATCCGACATATAGGAGTGTGGGCTCAGAGATCAGCAGCTGGAGTCCGCGACATCTC 349
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 Db 275 TCCGGCCATCCCTGTATATCATCAGCGCTGTACTCTGTGTATTTGGTGGGCTTACT 334
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 QY 350 TCCGGCCATCCCTGTATATCATCAGCGCTGTACTCTGTGTATTTGGTGGGCTTACT 409
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 Db 335 GGGCAATTCCTGGTCAATTTGTTCATATCCG 367
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 QY 410 GGGCAATTCCTGGTCAATTTGTTCATATCCG 442
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RESULT 9
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 DEFINITION kappa opioid receptor [mouse, genomic, 2074 nt, segment 1 of 3].
 ACCESSION S77868
 NID 9998529
 KEYWORDS
 SEGMENT 1 of 3
 SOURCE Mus sp.
 ORGANISM Mus sp.
 Eukaryotes; Mitochondrial eukaryotes; Metazoa; Chordata;
 Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Mus.

REFERENCE 1 (bases 1 to 2074)
 AUTHORS Liu, H.C., Lu, S., Augustin, L.B., Felsheim, R.F., Chen, H.C., Loh, H.H.
 TITLE Cloning and promoter mapping of mouse kappa opioid receptor gene
 JOURNAL Biochem. Biophys. Res. Commun. 209 (2), 639-647 (1995)
 MEDLINE 95251663
 REMARK Genbank staff at the National Library of Medicine created this
 entry [NCBI gisbseq 165350] from the original journal article.
 This sequence comes from Fig. 2.

FEATURES
 source Location/Qualifiers
 1..2074
 /organism="Mus sp."
 /db_xref="taxon:10095"
 BASE COUNT 492 a 485 c 564 g 533 t
 ORIGIN

Query Match 19.4%; Score 273; DB 14; Length 2074;
 Best Local Similarity 100.0%; Pred. No. 0.00e+00;
 Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1622 AGCTGAGGCGTCACCATGAGTCCCATTCAGATCTCCAGAGATCCAGGCCCTAC 1681
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 QY 170 AGCTGAGGCGTCACCATGAGTCCCATTCAGATCTCCAGAGATCCAGGCCCTAC 229
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 Db 1682 CTGCTCTCCAGTGTCTTGCCTTCTCCCAACAGACAGCTCTTGTCCCACTGGGCGAGA 1741
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 QY 230 CTGCTCTCCAGTGTCTTGCCTTCTCCCAACAGACAGCTCTTGTCCCACTGGGCGAGA 289
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 Db 1742 ATCCGACATATAGGAGTGTGGGCTCAGAGATCAGCAGCTGGAGTCCGCGACATCTC 1801
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 QY 290 ATCCGACATATAGGAGTGTGGGCTCAGAGATCAGCAGCTGGAGTCCGCGACATCTC 349
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 Db 1802 TCCGGCCATCCCTGTATATCATCAGCGCTGTACTCTGTGTATTTGGTGGGCTTACT 1861
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 QY 350 TCCGGCCATCCCTGTATATCATCAGCGCTGTACTCTGTGTATTTGGTGGGCTTACT 409
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 Db 1862 GGGCAATTCCTGGTCAATTTGTTCATATCCG 1894
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 QY 410 GGGCAATTCCTGGTCAATTTGTTCATATCCG 442
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RESULT 10
 LOCUS R4TRORD 1273 bp mRNA ROD 21-DEC-1993
 DEFINITION Rat mRNA for opioid receptor, complete cds.
 ACCESSION D16534
 NID 9409390
 KEYWORDS
 SOURCE G-protein coupled receptor; opioid receptor; transmembrane protein.
 Rattus norvegicus (strain Wistar) adult brain cDNA to mRNA, clone
 pROR2.

ORGANISM Rattus norvegicus
 Eukaryotes; Mitochondrial eukaryotes; Metazoa; Chordata;
 Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
 Murinae; Rattus.

REFERENCE 1 (bases 1 to 1273)
 AUTHORS Nishi, M., Takeshima, H., Fukuda, K., Kato, S. and Mori, K.
 TITLE CDNA cloning and pharmacological characterization of an opioid
 receptor with high affinities for kappa-subtype-selective ligands
 JOURNAL FEBS Lett. 330 (1), 77-80 (1993)
 MEDLINE 93380575
 REFERENCE 2 (bases 1 to 1273)
 AUTHORS Takeshima, H.
 TITLE Direct Submission
 JOURNAL Submitted (19-JUN-1993) to the DDBJ/EMBL/GenBank databases. Hiroshi
 Takeshima, International Institute for Advanced Studies, C/O
 Shimadzu Corporation N-80, 1 Nishinokyo-Kuwahara-cho, Kyoto 604,
 Japan (Tel.:075-823-1208, Fax:075-811-8186)
 COMMENT Submitted (19-JUN-1993) to DDBJ by:
 Hiroshi Takeshima
 International Institute
 for Advanced Studies
 C/O Shimadzu Corporation
 N-80
 1 Nishinokyo-Kuwahara-cho


```

RESULT 12
LOCUS RAKOR1B 2094 bp mRNA
DEFINITION Rattus norvegicus kappa opiod receptor (KOR-1) mRNA, complete cds.
ACCESSION L22536
NID 9425188
KEYWORDS G-protein coupled receptor; kappa opiod receptor; transmembrane protein.
SOURCE Rattus norvegicus (strain Sprague-Dawley) (library: lambda gt10)
ORGANISM Rattus norvegicus
Eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 2094)
AUTHORS Li,S., Zhu,J., Chen,C., Chen,Y.-W., de Riel,J.K., Ashby,B. and Liu-Chen,L.-Y.
TITLE Molecular cloning and expression of a rat k opiod receptor
JOURNAL Biochem. J. 295, 629-633 (1993)
MEDLINE 94059009
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                     /gene_1kb="lambda gt10"
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                     /product="kappa opiod receptor"
                     /db_xref="PID:9425189"
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                     CHVKALDPRTPLEAKILINICIMLASVGSALVIGTVREVDYIECSLQPDDE
                     YSWWDLFMKICVFARFIVLITVCTYMLILKSVRLSGSREKDRNLRRTKIV
                     LVVAVAFIICWPIFIPIVLEALGSTSHSTAVLSVYECALAGYNSLNPVLAFLD
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BASE COUNT      520 a      519 c      488 g      567 t
ORIGIN
Query Match      16.2%; Score 229; DB 14; Length 2094;
Best Local Similarity 98.1%; Pred. No. 1,90e-252;
Matches 529; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Db 391 GCCATCCCTGTTATCATCACCGCTGTCTACTCTGCTGTTGGTGGGCTTAGTGGGC 450
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QY 354 GCCATCCCTGTTATCATCACCGCTGTCTACTCTGCTGTTGGTGGGCTTAGTGGGC 413
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Db 451 AATTCCTGCTCATGTTTGTATCATCCGATACACAAAGATGAAGACCGCAACCAATC 510
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QY 414 AATTCCTGCTCATGTTTGTATCATCCGATACACAAAGATGAAGACCGCAACCAATC 473
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Db 511 TACATATTAACTGGCTTGGAGATGCTTGGTACTATACCATATGCTTCCAGAGT 570
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QY 474 TACATATTAACTGGCTTGGAGATGCTTGGTACTATACCATATGCTTCCAGAGT 533
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Db 571 GCGTCTACTTGAAGTATCTTGGCTTTGGAGATGCTTGGTCAAGATGTGATTTCC 630
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QY 534 GCGTCTACTTGAAGTATCTTGGCTTTGGAGATGCTTGGTCAAGATGTGATTTCC 593
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Db 631 ATTGACTACTACAAGATGTTTACCAAGATATTCACCTTGACCAAGATGATGGACGC 690
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QY 594 ATTGACTACTACAAGATGTTTACCAAGATATTCACCTTGACCAAGATGATGGACGC 653
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Db 691 TACATGCTGCTGTCACCGCTGTGAAGCTTTGATTCGGAACACTTTGAAGCAAG 750
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QY 654 TACATGCTGCTGTCACCGCTGTGAAGCTTTGACTTCCGAACACTTTGAAGCAAG 713
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Db 871 GATGATATATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 929
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RESULT 13
LOCUS E08874 2481 bp RNA
DEFINITION cdna coding rat kappa-opioid receptor.
ACCESSION E08874
NID 52176978
KEYWORDS JP 1995070191-A/1.
SOURCE Rattus sp.
ORGANISM Rattus sp.
Eukaryotes; Mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 2481)
AUTHORS Kimimichi,S.
TITLE RECEPTOR PROTEIN, ITS PRODUCTION AND USE INHEROF
JOURNAL Patent: JP 1995070191-A 1 14-MAR-1995;
TAKEDA CHEM IND LTD
OS Rattus sp. (rat)
PN JP 1995070191-A/1
PD 14-MAR-1995
PF 30-JUL-1993 JP 1993190261
PR 09-JUL-1993 JP 93P 170591
PI SATO KIMIMICHI
PC C07K14/47, C12N1/21, C12N5/09, C12P21/02//A61K38/00, A61K38/00,
PC C12N1/21, C12P21/02, C12R1/19, C07K99:00;
PC C12R1:19; (C12P21/02, C12R1:19), C07K99:00;
CC strandedness: Double;
CC topology: linear;
CC key
FH key
FH source
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FT /organism="Rattus sp."
FT /db_xref="taxon:10118"
FT CDS 111..1253
FT /product="rat kappa-opioid receptor".
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BASE COUNT      629 a      588 c      544 g      720 t
ORIGIN
Query Match      16.2%; Score 229; DB 25; Length 2481;
Best Local Similarity 98.1%; Pred. No. 1,90e-252;
Matches 529; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Db 279 GCCATCCCTGTTATCATCACCGCTGTCTACTCTGCTGTTGGTGGGCTTAGTGGGC 338
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QY 354 GCCATCCCTGTTATCATCACCGCTGTCTACTCTGCTGTTGGTGGGCTTAGTGGGC 413
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Db 339 AATTCCTGCTCATGTTTGTATCATCCGATACACAAAGATGAAGACCGCAACCAATC 398
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QY 414 AATTCCTGCTCATGTTTGTATCATCCGATACACAAAGATGAAGACCGCAACCAATC 473
    |||||||

Db 399 TACATATTAACTGGCTTGGAGATGCTTGGTACTATACCATATGCTTCCAGAGT 458
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DEFINITION Rattus norvegicus mRNA for kappa opiod receptor, complete cds.
ACCESSION D16829
NID 5404115
KEYWORDS kappa opiod receptor.
SOURCE Rattus norvegicus CDNA to mRNA.
ORGANISM Rattus norvegicus
Eukaryotes; Mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
Murinae; Rattus.
REFERENCE 1 (bases 1 to 2481)
AUTHORS Minami, M., Toya, T., Katao, Y., Maekawa, K., Nakamura, S., Onogi, T.,
Kaneho, S. and Satoh, M.
Cloning and expression of a cDNA for the rat kappa-opioid receptor
FEBS Lett. 329 (3), 291-295 (1993)
93374033
2 (bases 1 to 2481)
AUTHORS Minami, M.
Direct Submission
Submitted (21-JUL-1993) to the DDBJ/EMBL/GenBank databases.
Masabumi Minami, Faculty of Pharmaceutical Sciences, Kyoto
University, Department of Pharmacology, Kyoto, 606-01, Japan
(E-mail: f51230@sakura.kudpc.kyoto-u.ac.jp, Tel: 075-753-4546,
Fax: 075-753-4586)
Submitted (21-JUL-1993) to DDBJ by:
COMMENT
Masabumi Minami
Department of Pharmacology
Faculty of Pharmaceutical Sciences
Kyoto University
Kyoto, Kyoto 606-01
Japan
Phone: 075-753-4546
Fax: 075-753-4586.
FEATURES
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Best Local Similarity 98.1%; Pred. No. 1,90e-252;
Matches 529; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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Db 699 GGAGGACCAACAGTCAGGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 758
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QY 774 GGAGGACCAACAGTCAGGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 833
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QY 834 GATGAATATCTGCTGGTGGGACCTCTTCATGAAGATCTGTGCTTCTGCTTTGCTTTGT 892
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RESULT 15
LOCUS RNU00442 4742 bp mRNA ROD 25-MAR-1994
DEFINITION Rattus norvegicus kappa1 opiod receptor mRNA, complete cds.
ACCESSION U00442
NID 9403486
KEYWORDS
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryotes; Mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
Murinae; Rattus.
REFERENCE 1 (bases 1 to 4742)
AUTHORS Meng, F., Xie, G.-X., Thompson, R.C., Mansour, A., Goldstein, A.,
Watson, S.J. and Akil, H.
Cloning and pharmacological characterization of a rat kappa opiod
receptor
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 90, 9954-9958 (1993)
MEDLINE 94052210
REFERENCE 2 (bases 1 to 4742)
AUTHORS Meng, F.
Direct Submission
Submitted (05-AUG-1993) Fan Meng, Mental Health Research Institute,
University of Michigan, 205 Zina Pitcher Place, Ann Arbor, Michigan
48109, USA
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Matches 528; Conservative	0;	Mismatches 11;	Indels 0;	Gaps 0;

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Search completed: Tue Apr 21 00:27:03 1998
Job time : 1432 secs.

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1. 2. 3. 4. 5. 6.

 (\mathbb{M}_i)

Release 3.0.4A John F. Collins, Biocomputing Research Unit
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Distribution rights by Oxford Molecular Ltd

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MPSrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm
Run on: Tue Apr 21 00:47:28 1998; MasPar time 195.35 Seconds
Tabular output not generated. 832.932 Million cell updates/sec

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Description: (1-1410) from US08292694A.seq
Perfect Score: 1410
N.A. Sequence:
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CGCGTGGACCACTGATAGGCTT.....TTGGGTCTAATGTTGACGTC

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Scoring table: TABLE jmetric
Gap 60

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Searched: 159651 seqs, 57698962 bases x 2
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Statistics: Mean 7.967; Variance 2.921; scale 2.727

SUMMARIES						
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2	229	16.2	2481	15	Q68725	Mammalian kappa opioid re
3	32	2.3	1000	13	Q75931	Human kappa opioid re
4	32	2.3	1142	20	T12550	Human kappa opioid re
5	31	2.2	2447	10	Q56702	Partial sequence of t
6	29	2.1	822	5	Q29156	Brain somatostatin re
7	25	1.8	1330	13	Q75928	Mouse opiomorphin receptor
8	25	1.8	1567	14	Q88233	Rat opioid receptor
9	25	1.8	2600	14	Q90096	Mouse kappa3 opioid
10	25	1.8	2706	15	Q92972	Rat opiorph receptor
11	23	1.6	1821	10	Q56700	Sequence of murine de
12	23	1.6	2216	11	Q66556	Murine delta opioid r
13	23	1.6	2372	13	Q75927	Mouse delta opioid re
14	20	1.4	36	20	T12551	Human kappa opioid re
15	20	1.4	39	20	T12554	Human kappa opioid re

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C	17	20	1.4	0.89223	Transcription regulat	4.66e-02
C	18	20	1.4	1.618 14	Rat mu opioid recepto	4.66e-02
C	19	20	1.4	0.79199	Rat mu-subtype opioid	4.66e-02
C	20	20	1.4	2.070 12	Human mu opiate recep	4.66e-02
C	21	18	1.3	0.93102	Human mu opiate recep	4.66e-02
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C 90	15	1.1	741	8	Q45080	Human glucokinase gen	1.23e+02	163	16	1.1	2167	21	T31553	Human Irf-3 homol	2.90e+01
C 91	15	1.1	754	2	N60072	Sequence encoding hum	1.23e+02	164	16	1.1	2174	14	Q79972	Human Interleukin-1 b	2.90e+01
C 92	15	1.1	754	1	Q04263	Encodes Colon Cancer	1.23e+02	165	16	1.1	2189	3	Q20349	Thrombopoietin clone	2.90e+01
C 93	16	1.1	801	1	Q06637	Coat protein gene of	2.90e+01	166	15	1.1	2242	28	T58403	Human heat shock prot	1.23e+02
C 94	16	1.1	801	6	Q36838	Potato virus Y coat p	2.90e+01	167	16	1.1	2254	11	Q66167	Seven transmembrane r	2.90e+01
C 95	15	1.1	847	15	Q86972	Clone contg. yeast p	1.23e+02	168	15	1.1	2319	29	T60489	Chicken liver alpha-N	1.23e+02
C 96	15	1.1	847	2	Q10546	Yeast peptidyl prol	1.23e+02	169	15	1.1	2319	29	Q73728	Chicken liver alpha-N	1.23e+02
C 97	15	1.1	847	15	Q86965	Clone contg. yeast p	1.23e+02	170	15	1.1	2334	29	T66121	Chicken alpha-N-acety	1.23e+02
C 98	15	1.1	854	1	Q03296	Sequence of clone c21	1.23e+02	171	15	1.1	2340	9	Q51427	Human FACC cDNA clone	1.23e+02
C 99	15	1.1	858	13	Q80340	DNA fragment function	1.23e+02	172	15	1.1	2380	3	Q14982	Alpha-1,6-glucan-6-g1	1.23e+02
C 100	15	1.1	877	10	Q56738	Sequence of CC49 sng	2.90e+01	173	15	1.1	2400	28	T59642	Human prostaglandin H	1.23e+02
C 101	16	1.1	885	10	Q62008	SSO2 gene.	1.23e+02	174	15	1.1	2421	31	Q54621	Mammalian vesicle mem	1.23e+02
C 102	15	1.1	892	10	N60706	Sequence encoding hum	1.23e+02	175	15	1.1	2475	27	T49003	Tumour necrosis facto	1.23e+02
C 103	15	1.1	897	27	N49878	Porcine trypsinogen c	1.23e+02	176	16	1.1	2485	14	Q79971	Human Interleukin-1 b	2.90e+01
C 104	15	1.1	914	2	N60076	Sequence encoding hum	1.23e+02	177	16	1.1	2491	14	Q79968	Human Interleukin-1 b	2.90e+01
C 105	15	1.1	1039	14	Q26960	Human platelet activa	1.23e+02	178	15	1.1	2521	3	Q20542	Mouse retinoic acid r	1.23e+02
C 106	16	1.1	1125	11	Q65603	Pre-huPpV cDNA.	2.90e+01	179	16	1.1	2580	8	Q49166	84 kD ISGF-3alpha gen	2.90e+01
C 107	15	1.1	1164	2	Q12871	Polyhedrin-soluble IA	1.23e+02	180	16	1.1	2607	14	Q89337	Human Stat3a cDNA	2.90e+01
C 108	15	1.1	1200	17	Q99494	Recombinant high affi	1.23e+02	181	16	1.1	2607	22	T31277	Human STAT1-beta cDNA	2.90e+01
C 109	15	1.1	1200	5	Q30011	Sequence encoding a h	1.23e+02	182	15	1.1	2617	5	Q29153	DNA sequence encoding	1.23e+02
C 110	15	1.1	1259	11	Q63919	Interleukin 8 (IL-8)	1.23e+02	183	15	1.1	2629	24	T35903	Sequence encoding tob	1.23e+02
C 111	15	1.1	1321	23	T51049	Human adipocyte comp1	1.23e+02	184	15	1.1	2740	3	Q20541	Mouse retinoic acid r	1.23e+02
C 112	15	1.1	1321	23	T29035	Endoglucanase (60 kDa	1.23e+02	185	15	1.1	2749	11	Q63492	S-Locus receptor (ser	1.23e+02
C 113	15	1.1	1323	2	N60363	Sequence encoding hum	1.23e+02	186	15	1.1	2862	30	T61592	Marine c-IAP.	1.23e+02
C 114	15	1.1	1331	10	Q58207	Sequence of CC49 sng	1.23e+02	187	15	1.1	2923	31	T76529	DNA encoding macropha	1.23e+02
C 115	15	1.1	1346	10	Q58208	Sequence of CC49 sng	1.23e+02	188	15	1.1	2943	2	N70160	Sequence encoding a v	1.23e+02
C 116	15	1.1	1347	33	T86173	Human hD53 O1 nucleot	1.23e+02	189	15	1.1	2943	2	N70159	Sequence encoding elo	1.23e+02
C 117	16	1.1	1352	12	Q70299	Mutant human tissue f	2.90e+01	190	15	1.1	2944	1	N80253	Insert of lambda 3 en	1.23e+02
C 118	16	1.1	1352	12	Q84924	Human Ice-ced-3 homol	2.90e+01	191	15	1.1	2967	14	Q87171	Natural resistance a	1.23e+02
C 119	16	1.1	1352	28	T61373	Mutant tissue factor	2.90e+01	192	16	1.1	3069	8	Q48985	Rat glucagon-Like pep	2.90e+01
C 120	15	1.1	1352	10	Q56737	Sequence of CC49 sng	1.23e+02	193	15	1.1	3099	17	T05572	MEK3 cDNA.	1.23e+02
C 121	15	1.1	1373	15	Q30013	Sequence encoding a h	1.23e+02	194	15	1.1	3150	9	Q51428	Human FACC cDNA clone	1.23e+02
C 122	15	1.1	1373	17	Q99951	Recombinant high affi	1.23e+02	195	15	1.1	3247	38	T63080	Active clone XI of Ig	1.23e+02
C 123	16	1.1	1430	17	T15579	ICE-like apoptosis pr	2.90e+01	196	16	1.1	3261	33	T80100	Mouse Kp-1 gene.	1.23e+02
C 124	16	1.1	1456	21	T31552	Human Ice-ced-3 homol	2.90e+01	197	15	1.1	3373	4	Q24433	Rak B3 gene.	1.23e+02
C 125	16	1.1	1473	30	T68622	HiV integrase-LexA (I	2.90e+01	198	15	1.1	3373	4	Q12239	Ad41 E3 region.	1.23e+02
C 126	15	1.1	1476	16	Q86542	Wilson disease exon 1	1.23e+02	199	15	1.1	3451	26	T28492	P. aeruginosa detecti	1.23e+02
C 127	15	1.1	1480	13	N30040	Sequence encoding bov	1.23e+02	200	15	1.1	3466	29	T47757	Pathogenic Staphyloco	1.23e+02
C 128	16	1.1	1500	13	Q76311	Plasmid pRF271 encode	2.90e+01	201	16	1.1	3561	1	Q30849	Human TYR2 kinase cod	1.23e+02
C 129	15	1.1	1515	12	Q77721	Human glucagon-like 1	2.90e+01	202	15	1.1	3690	5	T03195	Type III procollagen	1.23e+02
C 130	16	1.1	1567	14	Q81505	Rat cardiac alpha myo	1.23e+02	203	15	1.1	3730	18	Q30395	Group B Streptococcal	1.23e+02
C 131	15	1.1	1588	21	T31005	Human p58 cDNA clone.	1.23e+02	204	15	1.1	3848	24	T45417	P. suis leukotoxin ge	1.23e+02
C 132	15	1.1	1623	6	Q38253	HCV CxS-NS5F recombin	1.23e+02	205	15	1.1	3923	14	Q03463	cDNA encoding N-acety	2.90e+01
C 133	15	1.1	1623	6	Q38268	HCV CxS-NS5F fusion g	1.23e+02	206	16	1.1	3943	22	T31276	Human Stat91 cDNA.	2.90e+01
C 134	15	1.1	1626	3	Q38238	HCV CxS-NS5F recombin	1.23e+02	207	16	1.1	3973	8	T31276	Human STAT1-alpha cDN	2.90e+01
C 135	15	1.1	1626	3	Q21680	PCMV-48 - recombinant	1.23e+02	208	16	1.1	4146	20	T09026	91 kD ISGF-3alpha gen	1.23e+02
C 136	16	1.1	1660	5	Q32869	Human PMP-22 cDNA.	2.90e+01	209	15	1.1	4163	31	T72214	Arabidopsis thaliana	1.23e+02
C 137	16	1.1	1731	33	T84446	Rat SCCH chaperone pr	2.90e+01	210	15	1.1	4200	18	T03190	Grapevine laeifrol vi	1.23e+02
C 138	15	1.1	1736	5	Q32870	Rat PMP cDNA.	1.23e+02	211	15	1.1	4203	2	Q14000	Group B Streptococcal	1.23e+02
C 139	15	1.1	1748	26	T49319	Wnt-10b-delta gene.	1.23e+02	212	15	1.1	4346	24	T45897	Leukotoxin genes.	1.23e+02
C 140	15	1.1	1828	21	T34367	Plasmid pJC265 (AtrC	1.23e+02	213	15	1.1	4362	24	T45897	Serine kinase SHKX1 c	1.23e+02
C 141	15	1.1	1828	3	Q14637	Human Glioblastoma c1	1.23e+02	214	15	1.1	4392	20	T10166	Feline infectious per	1.23e+02
C 142	15	1.1	1828	14	Q86998	Human cathepsin O12 cl	1.23e+02	215	15	1.1	4455	6	Q39177	PXY ORF1 encoding a r	1.23e+02
C 143	15	1.1	1871	2	Q12869	Lymphocyte Activation	1.23e+02	216	15	1.1	4488	8	Q51426	Human FACC cDNA clone	1.23e+02
C 144	15	1.1	1872	11	Q66176	Seven transmembrane r	1.23e+02	217	15	1.1	4529	8	Q46121	Human FACC cDNA clone	1.23e+02
C 145	16	1.1	1875	10	Q58758	Rat glucagon receptor	2.90e+01	218	15	1.1	4708	3	N50415	Human acetyl choline	1.23e+02
C 146	15	1.1	1878	28	T63079	Active clone Y1 of Ig	1.23e+02	219	15	1.1	4756	16	Q86541	Human disease gene.	1.23e+02
C 147	15	1.1	1881	33	T59892	Coding sequence for t	1.23e+02	220	15	1.1	4975	12	Q73445	Wnt3 cDNA.	1.23e+02
C 148	15	1.1	1905	8	Q47835	Murine interleukin 9	1.23e+02	221	15	1.1	4989	20	T29608	IGF-1 receptor gene.	1.23e+02
C 149	16	1.1	1909	8	Q48986	Human glucagon-like p	2.90e+01	222	15	1.1	4989	20	T13329	Human type I insulin-	1.23e+02
C 150	15	1.1	1912	2	Q10388	Encodes skin-specific	1.23e+02	223	15	1.1	4989	24	Q99245	Insulin like growth f	1.23e+02
C 151	15	1.1	1913	18	T05282	Murine retinoic acid	1.23e+02	224	15	1.1	4989	24	Q99245	Human Irf-1 receptor.	1.23e+02
C 152	15	1.1	1924	12	Q77964	Heavy subunit of rat	1.23e+02	225	15	1.1	5187	19	T14218	Mouse patched gene.	1.23e+02
C 153	15	1.1	2052	33	T80101	Murine Kp-1 gene open	1.23e+02	226	15	1.1	5288	19	T14220	Human patched gene.	1.23e+02
C 154	15	1.1	2097	27	T49006	Tumour necrosis facto	1.23e+02	227	15	1.1	5421	14	Q85678	Wilson's disease gene	1.23e+02
C 155	15	1.1	2111	21	T12940	RPL1 transcripional	1.23e+02	228	16	1.1	5437	13	Q76185	Mutant tissue factor.	2.90e+01
C 156	15	1.1	2122	26	T49318	Wnt-10b gene.	1.23e+02	229	16	1.1	5437	10	Q64219	Human tissue factor.	2.90e+01
C 157	16	1.1	2127	1	N61104	Sequence of human tis	2.90e+01	230	15	1.1	5460	20	T16508	Vector pAC3al contg.	1.23e+02
C 158	16	1.1	2141	33	T68488	Human tissue factor c	2.90e+01	231	15	1.1	6008	7	Q41289	Ubiquitin-specific pr	1.23e+02
C 159	16	1.1	2147	1	N92782	cDNA of entire human	2.90e+01	232	15	1.1	6843	33	T84509	Human LDL receptor an	1.23e+02
C 160	16	1.1	2147	1	N81953	Encodes human tissue	2.90e+01	233	15	1.1	7183	1	Q06074	Sequence encoding the	1.23e+02
C 161	15	1.1	2165	11	Q68659	CC49 VL-L-VH-L-L-V	1.23e+02	234	15	1.1	7184	11	Q70050	pkx gene of Pasteurel	1.23e+02

235	16	1.1	7350	17	O98955	Complete B-g gene enc	2.93e+01	308	14	1.0	283	13	O78988	Human immunoglobulin	4.79e+02
236	15	1.1	7360	24	T43072	Wheat acetyl-CoA carb	1.23e+02	309	14	1.0	291	22	T25886	Human gene signature	4.79e+02
237	16	1.1	7399	5	O38479	HDPACK1.	2.90e+01	310	14	1.0	295	22	T26677	Human gene signature	4.79e+02
238	15	1.1	7824	28	T63073	7.8 kb fragment of pN	1.23e+02	311	14	1.0	297	11	N92584	CEM kappa promoter of	4.79e+02
239	15	1.1	8301	20	T12170	pUG4-5-CDK-BP cDNA cl	1.23e+02	312	14	1.0	302	19	T09832	Tomato genomic DNA, D	4.79e+02
240	15	1.1	8738	31	T72327	Lactobacillus bacteri	1.23e+02	313	14	1.0	303	20	T23565	Human gene signature	4.79e+02
241	15	1.1	8791	23	T37090	Human T cell thositol	1.23e+02	314	14	1.0	303	8	O61356	Human brain signature	4.79e+02
242	15	1.1	9071	3	O23891	U266-Lambda gene and	1.23e+02	315	14	1.0	308	8	O60888	Human brain Expressed	4.79e+02
243	15	1.1	9071	3	O22491	Human U266 Lambda gen	1.23e+02	316	14	1.0	317	2	O10903	Synthetic HIV-2 gp 36	4.79e+02
244	15	1.1	9192	2	O11943	Nucleotide sequence o	1.23e+02	317	14	1.0	318	8	O59588	Human brain Expressed	4.79e+02
245	16	1.1	9709	16	O96140	HIV-1 proviral clone	2.90e+01	318	14	1.0	319	19	T21953	Human gene signature	4.79e+02
246	15	1.1	9709	3	O22488	Mouse bone morphogene	1.23e+02	319	14	1.0	322	8	O61160	Human brain Expressed	4.79e+02
247	15	1.1	15144	29	T47715	Human gene signature	1.23e+02	320	14	1.0	330	27	T35302	Human immunodeficienc	4.79e+02
248	15	1.1	15382	28	T63074	Ugc-Fc binding protei	1.23e+02	321	14	1.0	333	22	T26687	Human gene signature	4.79e+02
249	15	1.1	20383	30	T71699	Human deoxycytidylate	1.23e+02	322	14	1.0	333	8	O59791	Human brain Expressed	4.79e+02
250	15	1.1	26764	30	T71696	Human deoxycytidylate	1.23e+02	323	14	1.0	341	20	T23290	Human gene signature	4.79e+02
251	15	1.1	133894	17	T13635	AcNPV genomic DNA clo	1.23e+02	324	14	1.0	342	7	O43695	Sequence of intron 46	4.79e+02
252	15	1.1	580073	27	T58840	Mycoplasma genitalium	1.23e+02	325	14	1.0	349	8	O60437	Human brain Expressed	4.79e+02
253	14	1.0	15	24	T49727	Human CEMP HH ribozym	4.79e+02	326	14	1.0	357	29	T39996	Alphafetl variable hea	4.79e+02
254	14	1.0	18	13	O78329	crvA(c) terminator p	4.79e+02	327	14	1.0	363	33	T67327	Human gamma-signalin	4.79e+02
255	14	1.0	20	10	O57790	Primer pair 5B MTC de	4.79e+02	328	14	1.0	365	8	O56887	Human brain Expressed	4.79e+02
256	14	1.0	21	14	O83684	Epsilon oploid recept	4.79e+02	329	14	1.0	368	15	O87447	Varicella major virus s	4.79e+02
257	14	1.0	24	4	O24949	PCR primer vput for a	4.79e+02	330	14	1.0	369	18	T19957	Human gene signature	4.79e+02
258	14	1.0	24	12	O72200	Human PACAP receptor	4.79e+02	331	14	1.0	374	18	T19100	Human gene signature	4.79e+02
259	14	1.0	25	28	T59305	Primer for 5'-end of	4.79e+02	332	14	1.0	377	1	O03265	DNA probe for the det	4.79e+02
260	14	1.0	26	23	T38625	Chimaeric human/murin	4.79e+02	333	14	1.0	377	8	O61026	Human brain Expressed	4.79e+02
261	14	1.0	26	15	O94511	Human/murine chimeric	4.79e+02	334	14	1.0	379	15	O94521	Human/murine chimeric	4.79e+02
262	14	1.0	26	15	O94512	Human/murine chimeric	4.79e+02	335	14	1.0	379	15	O94514	Human/murine chimeric	4.79e+02
263	14	1.0	26	23	T38626	Chimaeric human/murin	4.79e+02	336	14	1.0	379	15	O94520	Human/murine chimeric	4.79e+02
264	14	1.0	28	16	O99509	Mouse Fas ligand gene	4.79e+02	337	14	1.0	379	23	T38635	Chimaeric human/murin	4.79e+02
265	14	1.0	28	7	O43669	Sequence of 146F an a	4.79e+02	338	14	1.0	379	23	T38627	Chimaeric human/murin	4.79e+02
266	14	1.0	30	2	O13759	D2 receptor probe.	4.79e+02	339	14	1.0	379	23	T38631	Chimaeric human/murin	4.79e+02
267	14	1.0	30	20	T18355	G-protein coupled rec	4.79e+02	340	14	1.0	379	23	T38634	Chimaeric human/murin	4.79e+02
268	14	1.0	31	12	O78156	BatMY capsid protein	4.79e+02	341	14	1.0	379	15	O94513	Human/murine chimeric	4.79e+02
269	14	1.0	33	33	T91668	Mistletoe lectin RMJ.	4.79e+02	342	14	1.0	379	15	O94517	Human/murine chimeric	4.79e+02
270	14	1.0	33	32	T17818	Primer #5 for secreto	4.79e+02	343	14	1.0	379	23	T38628	Chimaeric human/murin	4.79e+02
271	14	1.0	37	5	O28820	Anti-tumour ribozyme	4.79e+02	344	14	1.0	403	11	O45439	KK641 J chain variabl	4.79e+02
272	14	1.0	37	5	O28822	Ribozyme.	4.79e+02	345	14	1.0	403	14	O83709	Human beta-globin reg	4.79e+02
273	14	1.0	37	11	O68654	CC49 V-light primer 3	4.79e+02	346	14	1.0	403	6	O37057	Rat immunoglobulin H	4.79e+02
274	14	1.0	38	9	O55262	Stable hairpin ribozy	4.79e+02	347	14	1.0	412	8	O60101	Human brain Expressed	4.79e+02
275	14	1.0	40	9	O88038	U6-type RNA polymera	4.79e+02	348	14	1.0	415	14	O86052	MLV modified LTR.	4.79e+02
276	14	1.0	40	9	O50717	ERM HIV target sequen	4.79e+02	349	14	1.0	415	1	N90383	Synthetic gene for hu	4.79e+02
277	14	1.0	40	14	O83090	HIVPC12 No.13 enzym	4.79e+02	350	14	1.0	415	1	N90274	Synthetic human grenu	4.79e+02
278	14	1.0	42	5	O28821	Anti-tumour ribozyme	4.79e+02	351	14	1.0	417	3	N40018	DNA encoding fusion p	4.79e+02
279	14	1.0	42	26	T45962	24-Hydroxylase gene p	4.79e+02	352	14	1.0	423	33	T80665	Type II topoisomerase	4.79e+02
280	14	1.0	45	17	T00676	Primer 259 for human	4.79e+02	353	14	1.0	429	23	T37122	GM-CSF (N- and O-link	4.79e+02
281	14	1.0	45	18	T07608	RT-PCR primer/probe 2	4.79e+02	354	14	1.0	432	4	O24294	Ovine GM-CSF gene.	4.79e+02
282	14	1.0	48	2	O11524	Probe S3 complementar	4.79e+02	355	14	1.0	434	24	T38480	Rat peltin cDNA clone	4.79e+02
283	14	1.0	55	4	O25727	N-terminal extracellu	4.79e+02	356	14	1.0	435	23	T37123	GM-CSF (N-linked site	4.79e+02
284	14	1.0	56	5	O28623	Anti-tumour ribozyme	4.79e+02	357	14	1.0	435	23	T37121	GM-CSF (N-linked site	4.79e+02
285	14	1.0	83	10	O45281	Sequence of a D10 RNA	4.79e+02	358	14	1.0	459	1	O04737	Sequence encoding pol	4.79e+02
286	14	1.0	87	10	O77150	Human genome fragment	4.79e+02	359	14	1.0	459	18	T19065	Human gene signature	4.79e+02
287	14	1.0	90	7	O47048	GM-CSF oligomer, sens	4.79e+02	360	14	1.0	459	18	T19065	Human gene signature	4.79e+02
288	14	1.0	99	24	T30893	Primer 23 for 95 kb p	4.79e+02	361	14	1.0	477	32	T60777	Mabillin MR111 cDNA	4.79e+02
289	14	1.0	103	5	O33960	Downstream sequence o	4.79e+02	362	14	1.0	479	24	T38482	Mabillin MB11 cDNA fir	4.79e+02
290	14	1.0	105	23	T13519	PVLBS2p67120 fragmen	4.79e+02	363	14	1.0	479	24	T38482	Rat peltin cDNA clone	4.79e+02
291	14	1.0	107	31	T60683	Beta chain of Class I	4.79e+02	364	14	1.0	479	24	O56261	Brevibacterium deriva	4.79e+02
292	14	1.0	111	31	T47135	Beta chain of Class I	4.79e+02	365	14	1.0	484	27	T61384	Human fibrocin cDNA.	4.79e+02
293	14	1.0	119	16	T01088	Vilins-gp160IIIB const	4.79e+02	366	14	1.0	484	27	T33599	Human fibrocin cDNA.	4.79e+02
294	14	1.0	121	10	O45279	Sequence of a D10 DNA	4.79e+02	367	14	1.0	485	15	O86357	Human granulocyte mac	4.79e+02
295	14	1.0	121	10	O45279	Human gene signature	4.79e+02	368	14	1.0	485	15	O86357	DNA sequence of wild	4.79e+02
296	14	1.0	121	10	O45279	Human gene signature	4.79e+02	369	14	1.0	485	12	O67878	Vaccinia E3L promoter	4.79e+02
297	14	1.0	121	10	O45279	Human gene signature	4.79e+02	370	14	1.0	488	2	N70929	Sequence encoding pro	4.79e+02
298	14	1.0	121	10	O45279	Human gene signature	4.79e+02	371	14	1.0	514	15	O86358	Human granulocyte mac	4.79e+02
299	14	1.0	121	10	O45279	Human gene signature	4.79e+02	372	14	1.0	514	2	O12781	hbm-CSF1enz3asp276lu	4.79e+02
300	14	1.0	121	10	O45279	Human gene signature	4.79e+02	373	14	1.0	522	2	O11771	Sequence encoding rec	4.79e+02
301	14	1.0	121	10	O45279	Human gene signature	4.79e+02	374	14	1.0	534	30	T71702	Human deoxycytidylate	4.79e+02
302	14	1.0	121	10	O45279	Human gene signature	4.79e+02	375	14	1.0	534	30	T71702	Human deoxycytidylate	4.79e+02
303	14	1.0	121	10	O45279	Human gene signature	4.79e+02	376	14	1.0	552	17	O94247	pUG4-5-CDK-BP cDNA cl	4.79e+02
304	14	1.0	121	10	O45279	Human gene signature	4.79e+02	377	14	1.0	552	16	O89755	Cystelmid PAR6 partiel	4.79e+02
305	14	1.0	121	10	O45279	Human gene signature	4.79e+02	378	14	1.0	555	2	O87557	Human I cell lymphotr	4.79e+02
306	14	1.0	121	10	O45279	Human gene signature	4.79e+02	379	14	1.0	565	15	N70930	Sequence encoding pro	4.79e+02
307	14	1.0	121	10	O45279	Human gene signature	4.79e+02	380	14	1.0	573	29	T67537	H. pylori inner membr	4.79e+02

C	381	14	1.0	574	14	085063	Mtly modified LTR.	4.79e+02	454	14	1.0	921	12	Q74442	sacs positive regulat	4.79e+02
C	382	14	1.0	582	5	Q32239	Human NT-4, clone 4-2	4.79e+02	455	14	1.0	922	1	Q04259	Encodes Colon Cancer	4.79e+02
C	383	14	1.0	582	9	Q54717	Human NT-4 DNA isolat	4.79e+02	456	14	1.0	925	23	T27151	Human Machado-Joseph	4.79e+02
C	384	14	1.0	550	7	Q42320	EMC coagulation sequ	4.79e+02	457	14	1.0	927	28	T39062	Chimeric endoglucan	4.79e+02
C	385	14	1.0	551	13	Q78955	Human immunoglobulin	4.79e+02	458	14	1.0	935	2	N70784	Sequence encoding hum	4.79e+02
C	386	14	1.0	556	16	Q99026	Chelating peptide-HPV	4.79e+02	459	14	1.0	935	5	Q29653	HERV glycoprotein G (4.79e+02
C	387	14	1.0	556	4	Q27124	DNA encoding a Met-hg	4.79e+02	460	14	1.0	942	21	T18013	Beta-lipone 4-methyl	4.79e+02
C	388	14	1.0	606	13	Q78960	Human immunoglobulin	4.79e+02	461	14	1.0	951	30	T68792	Melanocortin-1 recept	4.79e+02
C	389	14	1.0	608	1	N90364	Rish growth hormone g	4.79e+02	462	14	1.0	953	5	Q29858	Oolant receptor clon	4.79e+02
C	390	14	1.0	627	6	Q37629	Native PIV coat prot	4.79e+02	463	14	1.0	954	33	T73913	EG-binding protein B6	4.79e+02
C	391	14	1.0	627	6	Q37630	Modified PIV coat pr	4.79e+02	464	14	1.0	957	24	T29932	Human striata A3 aden	4.79e+02
C	392	14	1.0	633	31	Q53460	PLRV integument prote	4.79e+02	465	14	1.0	957	17	T00647	Human A3 adenosine re	4.79e+02
C	393	14	1.0	633	31	Q53460	CDNA encoding soluble	4.79e+02	466	14	1.0	957	13	Q78087	Hepatitis C virus cor	4.79e+02
C	394	14	1.0	636	5	Q29867	Pheromone receptor cl	4.79e+02	467	14	1.0	957	8	Q48428	Human A3 adenosine re	4.79e+02
C	395	14	1.0	648	6	Q35444	Cysteine protease gen	4.79e+02	468	14	1.0	957	18	T07651	Human adenosine recep	4.79e+02
C	396	14	1.0	648	6	Q35446	Cysteine protease cod	4.79e+02	469	14	1.0	971	4	Q23666	Neurotrophic factor 4	4.79e+02
C	397	14	1.0	651	6	Q48029	Potato Leaf Roll Viru	4.79e+02	470	14	1.0	975	24	T39912	Mize acetyl CoA carb	4.79e+02
C	398	14	1.0	654	31	T60866	CDNA encoding soluble	4.79e+02	471	14	1.0	981	12	Q74278	Human transaldolase p	4.79e+02
C	399	14	1.0	661	2	N70561	Sequence encoding gra	4.79e+02	472	14	1.0	982	7	Q45592	Sequence of VR-alpha	4.79e+02
C	400	14	1.0	661	2	N60246	Human granulocyte mac	4.79e+02	473	14	1.0	982	1	Q04258	Sequence homologous t	4.79e+02
C	401	14	1.0	665	2	N70571	Sequence encoding hum	4.79e+02	474	14	1.0	1000	1	Q04473	Potato leaf roll viru	4.79e+02
C	402	14	1.0	667	2	N70570	Sequence encoding hum	4.79e+02	475	14	1.0	1014	6	Q38091	NS1-19857 fusion codi	4.79e+02
C	403	14	1.0	668	2	N80049	Sequence of the E.col	4.79e+02	476	14	1.0	1031	28	T39074	Chimeric endoglucan	4.79e+02
C	404	14	1.0	672	11	Q04264	HTV2(gp32)-CD4 exon	4.79e+02	477	14	1.0	1047	15	Q91109	Human ileal/renal bil	4.79e+02
C	405	14	1.0	685	1	Q04264	Encodes Colon Cancer	4.79e+02	478	14	1.0	1048	28	T39073	Chimeric endoglucan	4.79e+02
C	406	14	1.0	702	31	T60704	CDNA encoding soluble	4.79e+02	479	14	1.0	1058	4	Q26405	Human A3 adenosine re	4.79e+02
C	407	14	1.0	711	29	T62512	Primate anti-human	4.79e+02	480	14	1.0	1060	5	T10182	Alkaline endoglucan	4.79e+02
C	408	14	1.0	712	15	Q92528	N. alata arabinogalac	4.79e+02	481	14	1.0	1060	8	Q49941	Human A3 adenosine re	4.79e+02
C	409	14	1.0	712	15	Q92528	PR-1 like gene PR-1mz	4.79e+02	482	14	1.0	1060	5	Q31181	Endoglucanase enzyme	4.79e+02
C	410	14	1.0	721	18	Q98804	Sequence encoding hum	4.79e+02	483	14	1.0	1060	8	Q30067	Sequence encoding - 4	4.79e+02
C	411	14	1.0	731	18	N71049	H. pylori cytoplasmic	4.79e+02	484	14	1.0	1060	7	Q26380	Endoglucanase #1.	4.79e+02
C	412	14	1.0	759	29	T68254	Granulocyte macrophag	4.79e+02	485	14	1.0	1060	3	Q41732	Dye transfer inhibiti	4.79e+02
C	413	14	1.0	759	29	T68254	Human immunoglobulin	4.79e+02	486	14	1.0	1060	3	Q14656	Humicola insolens DSM	4.79e+02
C	414	14	1.0	757	13	Q78990	Sequence encoding hum	4.79e+02	487	14	1.0	1060	5	Q29934	Endoglucanase gene.	4.79e+02
C	415	14	1.0	773	2	N80223	Sequence encoding hum	4.79e+02	488	14	1.0	1060	5	Q30072	43KD endoglucanase ge	4.79e+02
C	416	14	1.0	773	2	N82353	Colony stimulating fa	4.79e+02	489	14	1.0	1060	5	Q25932	Cellulase contained i	4.79e+02
C	417	14	1.0	774	33	T91660	Prepro mistletoe lect	4.79e+02	490	14	1.0	1065	15	Q27449	Plasmid pSR001 alpha	4.79e+02
C	418	14	1.0	781	2	N93172	CDNA encoding human	4.79e+02	491	14	1.0	1108	8	Q48558	reca gene.	4.79e+02
C	419	14	1.0	783	2	N93066	Clone encoding bovine	4.79e+02	492	14	1.0	1111	12	Q74280	Human transaldolase p	4.79e+02
C	420	14	1.0	787	2	N60364	Human granulocyte mac	4.79e+02	493	14	1.0	1143	10	Q58820	NANBH virus gene frag	4.79e+02
C	421	14	1.0	787	14	Q84865	Clone pcd-human-GM-CS	4.79e+02	494	14	1.0	1168	23	T41942	Src SH3 binding prote	4.79e+02
C	422	14	1.0	787	14	Q84865	Partial pUC4-5-CDK-BP	4.79e+02	495	14	1.0	1173	3	Q43896	NANB hepatitis virus	4.79e+02
C	423	14	1.0	795	20	T12164	PRRS virus (Spanish s	4.79e+02	496	14	1.0	1190	4	Q23665	Neurotrophic factor 4	4.79e+02
C	424	14	1.0	798	15	Q88193	PRRS virus (Spanish s	4.79e+02	497	14	1.0	1191	27	T33600	Human fibrosin CDNA 1	4.79e+02
C	425	14	1.0	810	2	N71121	Sequence encoding ORF-3.	4.79e+02	498	14	1.0	1203	14	Q87971	Human Factor-XA CDNA.	4.79e+02
C	426	14	1.0	813	3	Q20270	Human GM-CSF/IL-3 fus	4.79e+02	499	14	1.0	1213	28	T61895	Human IL-3-3 beta or	4.79e+02
C	427	14	1.0	813	3	Q20270	GM-CSF/IL-3 fusion pr	4.79e+02	500	14	1.0	1225	22	T33325	American elm chitinase	4.79e+02
C	428	14	1.0	813	3	Q20270	Human GM-CSF/IL-3 fus	4.79e+02	501	14	1.0	1239	17	T00645	Human A2a adenosine r	4.79e+02
C	429	14	1.0	813	3	Q20270	Human GM-CSF/IL-3 fus	4.79e+02	502	14	1.0	1239	18	T07649	Human adenosine recep	4.79e+02
C	430	14	1.0	813	3	Q20270	Human GM-CSF/IL-3 fus	4.79e+02	503	14	1.0	1239	21	T29930	Human ventricicle A2a r	4.79e+02
C	431	14	1.0	815	1	Q04269	Sequence encoding CC8	4.79e+02	504	14	1.0	1239	21	Q48415	Human A2a adenosine r	4.79e+02
C	432	14	1.0	818	1	Q04268	Sequence encoding CC4	4.79e+02	505	14	1.0	1244	7	Q45656	Murine somatosatin r	4.79e+02
C	433	14	1.0	819	6	Q38089	19857 Osp A DNA.	4.79e+02	506	14	1.0	1259	13	Q75360	Gibberellin-20-oxida	4.79e+02
C	434	14	1.0	825	4	Q24525	Human IL-3/GM-CSF fus	4.79e+02	507	14	1.0	1265	7	Q45654	Murine somatosatin r	4.79e+02
C	435	14	1.0	825	4	Q24525	IL-3/GM-CSF fusion pr	4.79e+02	508	14	1.0	1265	7	Q45654	Murine somatosatin r	4.79e+02
C	436	14	1.0	825	4	Q24525	IL-3/GM-CSF fusion pr	4.79e+02	509	14	1.0	1265	31	T69550	Kat pheromone recepto	4.79e+02
C	437	14	1.0	825	2	Q10950	IL-3/GM-CSF fusion pr	4.79e+02	510	14	1.0	1270	10	Q44340	Sequence encoding a p	4.79e+02
C	438	14	1.0	825	2	Q10950	IL-3/GM-CSF fusion pr	4.79e+02	511	14	1.0	1270	10	Q44340	Human alpha(1,3)-fucos	4.79e+02
C	439	14	1.0	858	7	Q04260	Encodes Colon Cancer	4.79e+02	512	14	1.0	1316	9	Q56911	DNA encoding a glycos	4.79e+02
C	440	14	1.0	862	7	Q45595	Sequence encoding mur	4.79e+02	513	14	1.0	1333	3	Q20499	Plasmodium falciparum	4.79e+02
C	441	14	1.0	867	21	Q45594	Sequence encoding mur	4.79e+02	514	14	1.0	1333	3	Q20499	Plasmodium falciparum	4.79e+02
C	442	14	1.0	867	21	T18014	Beta-lipone 4-methyl	4.79e+02	515	14	1.0	1320	13	Q80916	Serratia gene.	4.79e+02
C	443	14	1.0	873	23	T27149	Human Machado-Joseph	4.79e+02	516	14	1.0	1320	13	Q80916	Serratia gene.	4.79e+02
C	444	14	1.0	879	4	Q24437	Mutated mature vWF 44	4.79e+02	517	14	1.0	1326	14	Q87443	Coding strand of CDNA	4.79e+02
C	445	14	1.0	882	9	Q51189	Homeotic gene 'green	4.79e+02	518	14	1.0	1333	3	Q20499	Vaccinia virus semaph	4.79e+02
C	446	14	1.0	885	28	T39075	Chimeric endoglucan	4.79e+02	519	14	1.0	1344	31	T60705	CDNA encoding soluble	4.79e+02
C	447	14	1.0	889	5	Q29700	Chimeric endoglucan	4.79e+02	520	14	1.0	1344	31	T60705	CDNA encoding soluble	4.79e+02
C	448	14	1.0	891	12	N60919	Sequence encoding por	4.79e+02	521	14	1.0	1371	23	T29383	Hamster flank organ d	4.79e+02
C	449	14	1.0	894	28	T39061	Chimeric endoglucan	4.79e+02	522	14	1.0	1380	28	T51051	Human amine receptor	4.79e+02
C	450	14	1.0	906	4	Q25910	Chimeric endoglucan	4.79e+02	523	14	1.0	1389	2	Q13751	FATA-binding protein-	4.79e+02
C	451	14	1.0	907	2	N70905	Human Kallikrein-DNA.	4.79e+02	524	14	1.0	1395	8	Q50415	Peptidylglycine alpha	4.79e+02
C	452	14	1.0	911	2	N71002	Sequence encoding a h	4.79e+02	525	14	1.0	1398	20	T03700	Human antithrombin II	4.79e+02
C	453	14	1.0	916	3	Q20375	Sequence encoding the	4.79e+02	526	14	1.0	1399	8	Q51424	Cotton UDP glucose sy	4.79e+02

C	527	14	1.0	1408	16	Q91761	Mouse Rad51 gene, enc	4.79e+02	C	600	14	1.0	1922	3	Q21172	Human CD19 antigen co	4.79e+02
C	528	14	1.0	1409	3	N50474	Sequence of brain spe	4.79e+02	C	601	14	1.0	1922	22	T14712	Human CD19 antigen CD	4.79e+02
C	529	14	1.0	1413	9	Q54885	Etherase gene.	4.79e+02	C	602	14	1.0	1928	22	T56140	Human CD19 antigen CD	4.79e+02
C	530	14	1.0	1447	10	Q58685	Human hippocampal cho	4.79e+02	C	603	14	1.0	1969	29	T64531	Glutamate dehydrogena	4.79e+02
C	531	14	1.0	1447	5	Q30002	HGNP precursor gene #	4.79e+02	C	604	14	1.0	1969	29	T64531	Glutamate dehydrogena	4.79e+02
C	532	14	1.0	1473	29	T64548	NADP-specific glutama	4.79e+02	C	605	14	1.0	1970	17	Q08751	DNA encoding murine s	4.79e+02
C	533	14	1.0	1489	2	Q10323	Antithrombin III cDNA	4.79e+02	C	606	14	1.0	1985	7	T00613	DNA encoding lucifera	4.79e+02
C	534	14	1.0	1496	4	Q28119	P-falciaparin USA gene	4.79e+02	C	607	14	1.0	1985	7	Q30687	Argylglycerol-beta-ary	4.79e+02
C	535	14	1.0	1506	29	T64547	NADP-specific glutama	4.79e+02	C	608	14	1.0	1989	16	Q29245	Dopamine transporter	4.79e+02
C	536	14	1.0	1515	19	T07072	Adhesive protein gene	4.79e+02	C	609	14	1.0	1989	16	Q29245	Schizosaccharomyces p	4.79e+02
C	537	14	1.0	1518	14	Q83682	Epsilon oploid recept	4.79e+02	C	610	14	1.0	1989	16	Q70810	Protein kinase (hnp2-	4.79e+02
C	538	14	1.0	1518	24	T73313	Aromatase acyl trans	4.79e+02	C	611	14	1.0	2009	20	T11379	Cytochrome P450 2C9 c	4.79e+02
C	539	14	1.0	1523	1	Q04757	Sequence encoding bat	4.79e+02	C	612	14	1.0	2010	12	Q71448	Intitin 1 from human f	4.79e+02
C	540	14	1.0	1523	1	N81741	Bactoxobin gene	4.79e+02	C	613	14	1.0	2012	12	Q43249	Intitin 1 from human f	4.79e+02
C	541	14	1.0	1527	29	Q67337	H. pylori cytoplasmic	4.79e+02	C	614	14	1.0	2012	17	T04755	Sequence of Atr20 mur	4.79e+02
C	542	14	1.0	1527	5	Q30974	HIV-1 SF2 gp120 precu	4.79e+02	C	615	14	1.0	2020	18	T04755	Sequence of Atr20 mur	4.79e+02
C	543	14	1.0	1533	13	Q81497	HIV-1 SF2 gp120 precu	4.79e+02	C	616	14	1.0	2020	18	T04755	Sequence of Atr20 mur	4.79e+02
C	544	14	1.0	1557	5	Q30973	HIV gp160-RF precursor	4.79e+02	C	617	14	1.0	2028	18	T04755	Sequence of Atr20 mur	4.79e+02
C	545	14	1.0	1575	12	Q72192	Human PACAP receptor	4.79e+02	C	618	14	1.0	2032	5	Q29937	ALVAC recombinant vcp	4.79e+02
C	547	14	1.0	1578	24	T79597	TATA-binding protein	4.79e+02	C	619	14	1.0	2043	8	Q51425	PEP4 gene encoding p	4.79e+02
C	548	14	1.0	1588	31	T72231	Human TARA-binding pr	4.79e+02	C	620	14	1.0	2048	14	Q85985	Rat vitamin D recepto	4.79e+02
C	549	14	1.0	1599	3	N30203	PAR-GM-CSF immunostim	4.79e+02	C	621	14	1.0	2058	2	N60759	Zea mays pPRF-ZM1 gen	4.79e+02
C	550	14	1.0	1610	31	T72724	Sequence encoding hum	4.79e+02	C	622	14	1.0	2058	11	Q62597	Sequence encoding cyc	4.79e+02
C	551	14	1.0	1620	21	T18011	Beta-ionone 4-methyl	4.79e+02	C	623	14	1.0	2060	18	T04709	Human cytoplasmic NAD	4.79e+02
C	552	14	1.0	1630	12	N60813	Sequence encoding tis	4.79e+02	C	624	14	1.0	2071	10	Q58121	COPAK recombinant vcp	4.79e+02
C	553	14	1.0	1632	12	Q71341	Human basigin I immun	4.79e+02	C	625	14	1.0	2078	30	T47598	Human cytoplasmic NAD	4.79e+02
C	554	14	1.0	1633	9	Q51237	Human MSH-R gene.	4.79e+02	C	626	14	1.0	2080	7	Q42383	pH 2.5 acid phosphata	4.79e+02
C	555	14	1.0	1648	6	Q45653	Human somatostatin re	4.79e+02	C	627	14	1.0	2095	10	Q64830	Banana polyphenol oxi	4.79e+02
C	557	14	1.0	1648	6	Q45052	Human PACAP receptor	4.79e+02	C	628	14	1.0	2095	10	Q64830	Receptor tyrosine kin	4.79e+02
C	558	14	1.0	1656	12	Q72194	Human PACAP receptor	4.79e+02	C	629	14	1.0	2096	29	T64530	NADP-specific glutama	4.79e+02
C	559	14	1.0	1657	7	Q45503	Sequence encoding an	4.79e+02	C	630	14	1.0	2099	29	T64530	NADP-specific glutama	4.79e+02
C	560	14	1.0	1659	12	Q72193	Human PACAP receptor	4.79e+02	C	631	14	1.0	2116	6	Q35987	Tomato Hsp80 cDNA seq	4.79e+02
C	561	14	1.0	1659	12	Q72195	Human PACAP receptor	4.79e+02	C	632	14	1.0	2116	6	Q35987	NADP-specific glutama	4.79e+02
C	562	14	1.0	1664	12	Q72207	Human PACAP receptor	4.79e+02	C	633	14	1.0	2140	29	T64542	NADP-specific glutama	4.79e+02
C	563	14	1.0	1680	15	Q74150	Plasmodium falciparum	4.79e+02	C	634	14	1.0	2148	12	Q73222	NADP-specific glutama	4.79e+02
C	564	14	1.0	1685	21	T30395	Borage delta-6-desatu	4.79e+02	C	635	14	1.0	2151	29	T68080	H. pylori cell envelo	4.79e+02
C	565	14	1.0	1695	22	T05877	CDNA encoding transfo	4.79e+02	C	636	14	1.0	2156	2	Q11562	Partial endothelial p	4.79e+02
C	566	14	1.0	1695	22	T36138	Guinea pig L-asparagi	4.79e+02	C	637	14	1.0	2175	5	Q29268	Fungal signal recogni	4.79e+02
C	567	14	1.0	1702	15	Q97236	Rhizodium dicta gene.	4.79e+02	C	638	14	1.0	2175	5	Q29268	Fungal signal recogni	4.79e+02
C	568	14	1.0	1738	6	Q40503	Rat ATR gene.	4.79e+02	C	639	14	1.0	2175	5	Q29268	Fungal signal recogni	4.79e+02
C	569	14	1.0	1745	12	Q72209	Human PACAP receptor	4.79e+02	C	640	14	1.0	2196	31	T45307	Nucleotide sequence o	4.79e+02
C	570	14	1.0	1747	29	T47179	Adh encoding alcohol	4.79e+02	C	641	14	1.0	2200	17	T04115	Human protein-kinase-	4.79e+02
C	571	14	1.0	1747	29	T47179	Zymomonas mobilis alc	4.79e+02	C	642	14	1.0	2206	1	Q03510	Simian-human hybrid T	4.79e+02
C	572	14	1.0	1748	12	Q72208	Human PACAP receptor	4.79e+02	C	643	14	1.0	2207	1	Q03511	Human transforming gr	4.79e+02
C	573	14	1.0	1748	12	Q72210	Human PACAP receptor	4.79e+02	C	644	14	1.0	2207	1	Q03512	Human TGF-beta1/TGF-B	4.79e+02
C	574	14	1.0	1755	11	Q64088	Mouse gene participat	4.79e+02	C	645	14	1.0	2208	3	Q20291	Sequence encoding hyb	4.79e+02
C	575	14	1.0	1761	8	Q46064	Sequence of tomato po	4.79e+02	C	646	14	1.0	2217	11	N90768	Sequence of human tra	4.79e+02
C	576	14	1.0	1766	6	Q37734	Cell adhesion protein	4.79e+02	C	647	14	1.0	2222	11	Q68556	Murine pro-hormone co	4.79e+02
C	577	14	1.0	1766	6	Q37734	AAMP-1 cDNA.	4.79e+02	C	648	14	1.0	2222	11	Q68556	Murine pro-hormone co	4.79e+02
C	578	14	1.0	1767	21	T26980	Aspergillus oryzae ta	4.79e+02	C	649	14	1.0	2258	20	T11380	Cytochrome P450 2C9 c	4.79e+02
C	579	14	1.0	1770	21	Q06266	Promoter region and s	4.79e+02	C	650	14	1.0	2263	15	Q08844	Hamster ileal/renal b	4.79e+02
C	580	14	1.0	1779	29	T68171	H. pylori transporter	4.79e+02	C	651	14	1.0	2263	15	Q08844	Hamster ileal/renal b	4.79e+02
C	581	14	1.0	1796	17	Q13322	PLRV Sac1-BcoRI fragm	4.79e+02	C	652	14	1.0	2291	1	N80309	Amylase gene from Str	4.79e+02
C	582	14	1.0	1796	17	Q13322	TNF-R p55IC/Par-IC-bi	4.79e+02	C	653	14	1.0	2294	28	T60957	Entire amyase gene.	4.79e+02
C	583	14	1.0	1800	21	T31542	Mouse immunoglobulin	4.79e+02	C	654	14	1.0	2324	25	T45037	Mouse chondroctin-6 s	4.79e+02
C	584	14	1.0	1804	16	Q91769	Coding sequence of PE	4.79e+02	C	655	14	1.0	2326	12	Q34582	Murine TNF-c gene.	4.79e+02
C	585	14	1.0	1809	13	T48550	Mouse tub gene.	4.79e+02	C	656	14	1.0	2376	5	Q28669	Partial sequence of a	4.79e+02
C	586	14	1.0	1830	23	T18383	Hydrogen peroxide-gen	4.79e+02	C	657	14	1.0	2376	5	Q28669	Partial sequence of a	4.79e+02
C	587	14	1.0	1830	23	T18383	Human Fas-associated	4.79e+02	C	658	14	1.0	2376	20	T66998	N. meningitidis serot	4.79e+02
C	588	14	1.0	1833	16	Q98988	TNF-R p55IC-binding p	4.79e+02	C	659	14	1.0	2379	20	T66998	N. meningitidis serot	4.79e+02
C	589	14	1.0	1835	24	T62654	Clone 3-2 cDNA.	4.79e+02	C	660	14	1.0	2385	31	T72725	He2-GM-CSF immunost	4.79e+02
C	590	14	1.0	1836	24	T62654	DNA encoding protein	4.79e+02	C	661	14	1.0	2389	28	T62793	Mouse khes cDNA.	4.79e+02
C	591	14	1.0	1854	3	T16842	Rat p65 oncogene	4.79e+02	C	662	14	1.0	2397	2	N70599	Sequence encoding the	4.79e+02
C	592	14	1.0	1855	30	T16842	B. laurus endol core d	4.79e+02	C	663	14	1.0	2403	18	T11061	V. harveyi luxAB genes	4.79e+02
C	593	14	1.0	1876	28	T29743	Human adrenal gland c	4.79e+02	C	664	14	1.0	2418	17	T15598	Murine TNF-c K3 isofor	4.79e+02
C	594	14	1.0	1886	6	Q37488	gry-1 coding sequence	4.79e+02	C	665	14	1.0	2434	21	T17044	Laccase-LCC1 gene.	4.79e+02
C	595	14	1.0	1890	6	Q37488	gry-1 coding sequence	4.79e+02	C	666	14	1.0	2439	31	T63354	Bacillus subtilis epr	4.79e+02
C	596	14	1.0	1898	9	N91471	1.9 kb Ro (Ro/SSA) an	4.79e+02	C	667	14	1.0	2439	31	T63354	Bacillus subtilis epr	4.79e+02
C	597	14	1.0	1919	8	Q54624	Mammalian vesicle mem	4.79e+02	C	668	14	1.0	2439	31	T63354	Bacillus subtilis epr	4.79e+02
C	598	14	1.0	1921	1	N90612	CD19 cDNA.	4.79e+02	C	669	14	1.0	2452	9	T59381	Extracellular protease	4.79e+02
C	599	14	1.0	1922	24	T38356	Human CD19 cDNA.	4.79e+02	C	670	14	1.0	2452	9	T59381	Extracellular protease	4.79e+02
C	600	14	1.0	1922	24	T38356	Human CD19 cDNA.	4.79e+02	C	671	14	1.0	2452	9	T59381	Extracellular protease	4.79e+02
C	601	14	1.0	1922	24	T38356	Human CD19 cDNA.	4.79e+02	C	672	14	1.0	2452	9	T59381	Extracellular protease	4.79e+02
C	602	14	1.0	1922	24	T38356	Human CD19 cDNA.	4.79e+02	C	673	14	1.0	2452	9	T59381	Extracellular protease	4.79e+02
C	603	14	1.0	1922	24	T38356	Human CD19 cDNA.	4.79e+02	C	674	14	1.0	2452	9	T59381	Extracellular protease	4.79e+02
C	604	14	1.0	1922	24	T38356	Human CD19 cDNA.	4.79e+02									

[illegible]

C	819	14	1.0	6971	24	T38740	Moraxella outer membr	4.79e+02	892	14	1.0	31122	7	040706	Bacillus subtilis str	4.79e+02
C	820	14	1.0	7032	15	Q84662	Human neuronal calciu	4.79e+02	893	14	1.0	53577	28	T18551	Human polykystic kidn	4.79e+02
C	821	14	1.0	7089	15	Q84663	Human neuronal calciu	4.79e+02	894	14	1.0	133894	17	T18633	AcNPV genomic DNA clo	4.79e+02
C	822	14	1.0	7158	23	T27394	Hepatitis B virus str	4.79e+02	895	14	1.0	58073	27	T18640	Mycoplasma genitalium	4.79e+02
C	823	14	1.0	7168	10	Q45197	HEV strain SAR-55 cDN	4.79e+02	C	896	13	38	33	T87255	IL-4 2'f/3' RNA lig	1.70e+03
C	824	14	1.0	7171	2	Q14413	Composite sequence fir	4.79e+02	C	897	13	39	32	T87185	Interleukin-4 2'f RNA	1.70e+03
C	825	14	1.0	7195	2	Q14412	Forward strand of Bur	4.79e+02	C	898	13	39	32	T87180	Interleukin-4 2'f RNA	1.70e+03
C	826	14	1.0	7470	24	T39905	Maize acetyl CoA carb	4.79e+02	C	899	13	42	32	T87206	Interleukin-4 2'f RNA	1.70e+03
C	827	14	1.0	7608	16	Q74118	DNA encoding mouse ce	4.79e+02	C	900	13	42	32	T87206	Interleukin-4 2'f RNA	1.70e+03
C	828	14	1.0	7625	31	T71323	Hydral activation vec	4.79e+02	C	901	13	42	32	T87206	Interleukin-4 2'f RNA	1.70e+03
C	829	14	1.0	7726	2	T70834	L-Tryptophan producti	4.79e+02	C	902	13	216	33	T12136	Bispecific tetraalen	1.70e+03
C	830	14	1.0	7742	32	T84745	Bordetella pertussis	4.79e+02	C	903	13	234	33	T60425	Rabbit CCRP hairpin r	1.70e+03
C	831	14	1.0	8043	14	Q85924	Human protein tyrosin	4.79e+02	C	904	13	242	32	T73781	Vector pC19MCH frag	1.70e+03
C	832	14	1.0	8075	24	T31981	Invertebrate calciu	4.79e+02	C	905	13	294	27	T47917	Light chain VL leader	1.70e+03
C	833	14	1.0	8115	12	Q74450	Neuronal Invertebrate	4.79e+02	C	906	13	299	27	T47918	Porcine starch branch	1.70e+03
C	834	14	1.0	8316	24	T35524	Myod retroviral expre	4.79e+02	C	907	13	302	24	T47918	Human mature interfe	1.70e+03
C	835	14	1.0	8355	24	T35524	Human interferon-beta	4.79e+02	C	908	13	302	24	T31590	Human mature interfe	1.70e+03
C	836	14	1.0	8654	14	Q55138	Staphylococcus epide	4.79e+02	C	909	13	484	1	N95402	Probe (BLU82) for Alu	1.70e+03
C	837	14	1.0	9046	15	T02792	Transcription factor	4.79e+02	C	910	13	499	1	N95402	Plasmid pcgla insert	1.70e+03
C	838	14	1.0	9088	3	Q15132	Zucchini ACC synthase	4.79e+02	C	911	13	558	33	T65463	Sequence of new sigma	1.70e+03
C	839	14	1.0	9088	3	Q15132	Zucchini ACC synthase	4.79e+02	C	912	13	576	32	T75083	Mouse thymus and acti	1.70e+03
C	840	14	1.0	9115	12	Q74449	Sequence of lymphaden	4.79e+02	C	913	13	580	32	T75094	Human mature growth h	1.70e+03
C	841	14	1.0	9193	2	M60365	myod retroviral expre	4.79e+02	C	914	13	612	32	T58248	Sinapis alba flowerin	1.70e+03
C	842	14	1.0	9213	2	M60288	Sequence of LAV virus	4.79e+02	C	915	13	647	13	Q73017	5' end of CH14-2a16-1	1.70e+03
C	843	14	1.0	9229	29	T47716	Sequence of the HTIV-	4.79e+02	C	916	13	660	31	T58531	Hepatitis Type-C viru	1.70e+03
C	844	14	1.0	9239	29	T47716	Mouse bone morphogene	4.79e+02	C	917	13	774	24	T43312	Nucleotide sequence o	1.70e+03
C	845	14	1.0	9326	4	Q25051	DNA complementary to	4.79e+02	C	918	13	808	24	T38531	CsPpA variant #1 codin	1.70e+03
C	846	14	1.0	9360	1	Q02830	CDNA to HIV-2 RNA.	4.79e+02	C	919	13	820	14	Q24034	CH14pYla trichromatis	1.70e+03
C	847	14	1.0	9425	7	Q45921	HTIV-III DNA (Clone	4.79e+02	C	920	13	840	14	T58122	HvH8 gene promoter re	1.70e+03
C	848	14	1.0	9425	7	Q45921	HTIV-III DNA (Clone	4.79e+02	C	921	13	929	31	T58123	Human CD40L mutetr c	1.70e+03
C	849	14	1.0	9425	7	Q45921	HTIV-III DNA (Clone	4.79e+02	C	922	13	1056	31	T42665	CDNA encoding yeast G	1.70e+03
C	850	14	1.0	9425	7	Q45921	HTIV-III DNA (Clone	4.79e+02	C	923	13	1095	29	T73693	Histidine tagged yea	1.70e+03
C	851	14	1.0	9427	7	Q45920	HTIV-III DNA (Clone	4.79e+02	C	924	13	1176	31	T74024	DNA encoding phenylal	1.70e+03
C	852	14	1.0	9427	7	Q45920	HTIV-III DNA (Clone	4.79e+02	C	925	13	1205	32	Q25060	Fusion peptide #3 hav	1.70e+03
C	853	14	1.0	9473	1	N62768	HTIV-2 variant HIV-D19	4.79e+02	C	926	13	1275	32	T74888	Ethylene synthase enc	1.70e+03
C	854	14	1.0	9515	14	Q55145	Pseudomonas aeruginos	4.79e+02	C	927	13	1313	17	T74888	psaApha-318 clone.	1.70e+03
C	855	14	1.0	9534	17	T17419	Merosin cDNA.	4.79e+02	C	928	13	1323	9	Q50561	Xenopus neurogenic di	1.70e+03
C	856	14	1.0	9589	6	Q38218	NANBH virus strain HC	4.79e+02	C	929	13	1340	33	T85003	Asparagilylendopeptid	1.70e+03
C	857	14	1.0	9629	18	T14600	PXCTI-hgM-GST express	4.79e+02	C	930	13	1340	33	T85003	Matze 5-enolpyruvylsh	1.70e+03
C	858	14	1.0	9633	1	N80890	Sequence of cDNA clon	4.79e+02	C	931	13	1340	33	T85003	Matze 5-enolpyruvylsh	1.70e+03
C	859	14	1.0	9636	12	Q67190	P. falciparum transmi	4.79e+02	C	932	13	1340	33	T85003	Matze 5-enolpyruvylsh	1.70e+03
C	860	14	1.0	9693	1	N92119	Sequence of clone HIV	4.79e+02	C	933	13	1340	33	T85003	Matze 5-enolpyruvylsh	1.70e+03
C	861	14	1.0	9718	19	T14180	Attenuated HIV-1 stra	4.79e+02	C	934	13	1602	31	T72215	Malze 5-enolpyruvylsh	1.70e+03
C	862	14	1.0	9737	23	T33898	HIV-1 SF2 genome.	4.79e+02	C	935	13	1610	2	Q11190	Grapevine leafroll vi	1.70e+03
C	863	14	1.0	9737	23	T33898	ARV-2 proviral DNA fr	4.79e+02	C	936	13	1713	33	T85993	Immunoglobulin gamma	1.70e+03
C	864	14	1.0	9745	2	N60240	HTLV-III virus (HIV v	4.79e+02	C	937	13	1713	33	T85993	Matze 5-enolpyruvylsh	1.70e+03
C	865	14	1.0	9745	2	N60240	HTLV-III virus (HIV v	4.79e+02	C	938	13	1764	10	T68000	Matze 5-enolpyruvylsh	1.70e+03
C	866	14	1.0	9746	26	T58550	Human Immunodeficienc	4.79e+02	C	939	13	1767	31	T75076	Matze 5-enolpyruvylsh	1.70e+03
C	867	14	1.0	9746	26	T58550	Human Immunodeficienc	4.79e+02	C	940	13	1921	31	T58786	Matze 5-enolpyruvylsh	1.70e+03
C	868	14	1.0	9749	7	Q45922	HTLV-III DNA (Clone	4.79e+02	C	941	13	2082	33	T59528	Human growth hormone	1.70e+03
C	869	14	1.0	9749	7	Q45922	HTLV-III DNA (Clone	4.79e+02	C	942	13	2082	33	T59528	Human growth hormone	1.70e+03
C	870	14	1.0	10163	32	T61085	Full-length HIV-2KR p	4.79e+02	C	943	13	2173	8	Q51345	Human growth hormone	1.70e+03
C	871	14	1.0	10614	15	Q89555	Hamster cholesteryl 7	4.79e+02	C	944	13	2173	8	Q51345	Human growth hormone	1.70e+03
C	872	14	1.0	10660	14	Q84793	Spirocerbellar ataxi	4.79e+02	C	945	13	2198	31	T73117	Human Auroara-2 cDNA.	1.70e+03
C	873	14	1.0	10723	31	T49304	CDNA encoding polypro	4.79e+02	C	946	13	2394	31	T49305	Human Auroara-2 cDNA.	1.70e+03
C	874	14	1.0	10723	31	T49304	CDNA encoding polypro	4.79e+02	C	947	13	2394	31	T49305	Human Auroara-2 cDNA.	1.70e+03
C	875	14	1.0	10723	31	T49304	CDNA encoding polypro	4.79e+02	C	948	13	2404	31	T73282	Human Auroara-2 cDNA.	1.70e+03
C	876	14	1.0	11478	32	T79784	Full length potato st	4.79e+02	C	949	13	2418	32	T58629	Human Auroara-2 cDNA.	1.70e+03
C	877	14	1.0	11478	32	T79784	Full length potato st	4.79e+02	C	950	13	2418	32	T58629	Human Auroara-2 cDNA.	1.70e+03
C	878	14	1.0	12492	1	N70543	Complete sequence of	4.79e+02	C	951	13	2476	31	T67234	Human Auroara-2 cDNA.	1.70e+03
C	879	14	1.0	12923	3	N90338	VAC-beta (genomic - p	4.79e+02	C	952	13	2550	32	T85402	Human Auroara-2 cDNA.	1.70e+03
C	880	14	1.0	13633	3	Q40862	Swinepox virus HindIII	4.79e+02	C	953	13	2550	32	T85402	Human Auroara-2 cDNA.	1.70e+03
C	881	14	1.0	14176	33	T84564	Swinepox virus HindIII	4.79e+02	C	954	13	2550	32	T85402	Human Auroara-2 cDNA.	1.70e+03
C	882	14	1.0	15101	17	T16239	Leiystad virus genom	4.79e+02	C	955	13	2631	31	T75433	Human Auroara-2 cDNA.	1.70e+03
C	883	14	1.0	15101	17	T16239	Leiystad virus genom	4.79e+02	C	956	13	2631	31	T75433	Human Auroara-2 cDNA.	1.70e+03
C	884	14	1.0	15108	5	Q32002	Leiystad Agent genome	4.79e+02	C	957	13	2631	31	T75433	Human Auroara-2 cDNA.	1.70e+03
C	885	14	1.0	15223	29	T63430	Respiratory syncytial	4.79e+02	C	958	13	2809	31	T75280	Human Auroara-2 cDNA.	1.70e+03
C	886	14	1.0	15223	29	T63430	Respiratory syncytial	4.79e+02	C	959	13	2809	31	T75280	Human Auroara-2 cDNA.	1.70e+03
C	887	14	1.0	16079	7	N70753	Sequence of segment o	4.79e+02	C	960	13	2879	33	T63318	Xenopus beta-signalin	1.70e+03
C	888	14	1.0	17327	7	Q44278	Serilycin - proteogly	4.79e+02	C	961	13	2894	24	T31792	Human kidney inward r	1.70e+03
C	889	14	1.0	21126	2	N60970	TL-DNA region of A.rh	4.79e+02	C	962	13	2894	24	T31792	Human kidney inward r	1.70e+03
C	890	14	1.0	21126	2	N60970	TL-DNA region of A.rh	4.79e+02	C	963	13	2923	31	T76529	DNA encoding macropha	1.70e+03
C	891	14	1.0	22481	24	T11658	PEDE full length sequ	4.79e+02	C	964	13	2968	10	Q58740	MEP2.	1.70e+03

C	965	13	0.9	2392.32	T67285	Soluble starch synthase	1.70e+03
C	966	13	0.9	3135.32	T85406	Rat full length cadherin	1.70e+03
C	967	13	0.9	3164.32	T85401	Human cadherin-5 codd	1.70e+03
C	968	13	0.9	3182.4	Q25799	HLIF-R.	1.70e+03
C	969	13	0.9	3192.17	T08222	X region antisense he	1.70e+03
C	970	13	0.9	3225.32	T78402	Feline immunodeficient	1.70e+03
C	971	13	0.9	3225.32	T49091	Feline immunodeficient	1.70e+03
C	972	13	0.9	3349.32	T51256	Human alpha 4 gene genom	1.70e+03
C	973	13	0.9	3373.31	T76768	Human alpha 1,2 fucos	1.70e+03
C	974	13	0.9	3394.33	T84484	Human alpha-1 collagen	1.70e+03
C	975	13	0.9	3561.31	T77277	Bacillus thuringiensis	1.70e+03
C	976	13	0.9	3780.29	T61864	c-abl gene.	1.70e+03
C	977	13	0.9	4004.32	T51260	Human A04 gene genom	1.70e+03
C	978	13	0.9	4049.2	N70682	Sequence of cry-1-1.1 g	1.70e+03
C	979	13	0.9	4173.31	T72214	Grapevine leafroll vi	1.70e+03
C	980	13	0.9	4320.32	T73388	DNA encoding HSP72 an	1.70e+03
C	981	13	0.9	4360.32	T36284	DNA encoding crystal	1.70e+03
C	982	13	0.9	4373.31	T72719	Pyruvate:flavodoxin o	1.70e+03
C	983	13	0.9	4438.2	Q13073	Modified CRYIA(b) gen	1.70e+03
C	984	13	0.9	4579.33	T78203	Physiologically activ	1.70e+03
C	985	13	0.9	4739.32	T78303	Mouse SP76 cDNA.	1.70e+03
C	986	13	0.9	5274.2	N70579	Human homologue of ye	1.70e+03
C	987	13	0.9	5376.33	T84444	Sequence encoding pse	1.70e+03
C	988	13	0.9	5836.33	Q96296	Human prostate-specif	1.70e+03
C	989	13	0.9	5836.15	T72812	Human prostate-speci	1.70e+03
C	990	13	0.9	5864.33	T79596	Human SP76 cDNA.	1.70e+03
C	991	13	0.9	5962.32	T77803	RTA-binding protein	1.70e+03
C	992	13	0.9	6524.32	T77803	cDNA encoding wild ty	1.70e+03
C	993	13	0.9	6527.32	T77806	cDNA encoding variant	1.70e+03
C	994	13	0.9	6538.33	T79882	Tomato immunity 2 gen	1.70e+03
C	995	13	0.9	6843.33	T84509	Human LDL receptor an	1.70e+03
C	996	13	0.9	7052.32	T77805	cDNA encoding variant	1.70e+03
C	997	13	0.9	9880.31	T68647	Halobacterium halobiu	1.70e+03
C	998	13	0.9	10380.31	T67164	Human alpha-N-acetyl	1.70e+03
C	999	13	0.9	12687.32	T70125	Equine arteritis viru	1.70e+03
C	1000	13	0.9	40875.32	T80043	Insert from cosmid 10	1.70e+03

ALIGNMENTS

RESULT 1
ID Q75926 standard; DNA; 1410 bp.

AC Q75926;
DE Mouse kappa oploid receptor MOR1 cDNA.
KW Mouse; kappa; delta; mu; oploid receptor; brain; primer; PCR; amplify;
KW transmembrane domain; somatostatin; receptor; human; expression vector;
KW truncate; chimeric; assay; probe; ss.
OS Mus musculus.
FH Key Location/Qualifiers
FT CDS 185..1328
FT /*tag- a
FT /product- mouse kappa oploid receptor
PN MO9428132-A.
PD 08-DEC-1994; U05747.
PE 20-MAY-1994; US-066296.
PR 30-JUL-1993; US-100694.
PR 05-NOV-1993; US-147592.
PA (ARCH-) ARCH DEV CORP.
PI Bell GI, Reisine T, Yasuda K;
PI WPI; 55-022804/03.
DR P-RED; R67669.
PT Polynucleotides and peptides derived from oploid receptor
PT polypeptides - for use in therapeutic compositions and in
PT screening assays for useful drug substances.
PI Claim 10; Page 207-211; 300pp; English.
CC The nucleotide sequence of the novel mouse kappa oploid receptor gene
CC MOR1. The gene was isolated from a mouse brain cDNA library using a
CC fragment (amplified from the cDNA library with primers Q75929-30) as a
CC probe. The primers are based on the conserved sequences present in the
CC second and third transmembrane domains of somatostatin (SSTR) receptor
CC subtypes SSTR1, SSTR2 and SSTR3. The 1.2 kb pStI fragment from the mouse

CC	kappa oploid receptor clone, lambda ms1-1, was subcloned into the CMV	
CC	promoter-based expression vector pCMV-6b. The resultant construct	
CC	pCMV-ms1-1 was transfected into COS-1 cells for protein production. The	
CC	gene encoding the oploid receptor can be used to produce complete,	
CC	truncated or chimeric oploid receptor proteins. The oploid receptors	
CC	thus produced are useful for the development of novel assays designed to	
CC	select or improve substances, capable of interacting with the oploid	
CC	receptor proteins, for use in diagnosis, drug design and therapeutic	
CC	applications.	
CC	Sequence 1410 bp; 322 A; 360 C; 337 G; 391 T;	
SQ		
Query Match	100.0%; Score 1410; DB 13; Length 1410;	
Best Local Similarity 100.0%; Pred. No. 0.00e+00;		
Matches 1410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
D	1 ggcacaccttgcgtatcccaaacagcagagctctctccagctttggaagcaaatga	60
Q	1 GGCACCTTGTGATGCCAAMACAGCAGAGCTTCCAGTCTTGGAAGCAAAATTA	60
D	61 gatacagagctgagccatcagcagctgaacagctacacagctacacgaatgagtt	120
Q	61 GATACAGAGAGCTGACCCATCAGGCTGACAGCTACACAGATTAAGTGGTACT	120
D	121 ggaagctgacggtgacttgggaagggaggtgcacatcagatctgagctgcagcc	180
Q	121 GGAAGCTGACGCTGACTGGGAGAGAGGAGGTCACATCAGCATTTGAGCTGAC	180
D	181 tcaacatgagatcccccattcagatcttcgagagatcagccctacatgctccca	240
Q	181 TCACCATGAGATCCCCATTCAATCTCCAGAGAGATCCAGGCTTACCTGCTCC	240
D	241 gtcttcgctctccccaacagcagcttggtcccaacttggagagaatccagagta	300
Q	241 GTCTTGCCTCTCCCCACAGAGAGCTTGTTCCCACTGGGAGATCCGACAGTA	300
D	301 atggcagctgaggctcagagatcagcagctgagctgcagacatctcccgccatcc	360
Q	301 ATGCCAGCTGGGCTCAGAGATCAGCAGCTGAGCTGCGGACATCTCCGGCATCC	360
D	361 ctgtatcaccacccgctgttactctgtgtattgtgtgaggtgagtaattctc	420
Q	361 CTGTATCATCACCGCTGTACTCTGTGATTTGGATTTGGTGGGCAATTCCTC	420
D	421 tggcatgcttgcgtatcattcgatcgaatcgaatgagagccgcaacacatcaca	480
Q	421 TGGCATGCTTGTGATCATCGATCGAATGAGAGAGAGCCGCAACACATCAAT	480
D	481 ttaacctgcttggcagatgcttggttactaccactatgccccttcagagtgct	540
Q	481 TTAACCTGGCTTGGCAGATGCTTGGTTACTACACATACCCCTTCAGAGTGTCT	540
D	541 actgatgaattcttgagctttgagagtggtgatgagatgacattcattcattg	600
Q	541 AACTGATGAATTTGGCTTTGGAGATGCTGATGCAATGATGCTTCAATTGACT	600
D	601 actacaacatgtaacacagcatatcaccattgacacatgagtgagtgacogctac	660
Q	601 ACTACAACATGTTACCAAGCATATCACCTTGACCATGATGAGTGAGACCGCTAC	660
D	661 ctgtgtgcaacctgtgaagcttggagcttcggaacacattggaagcaagacatca	720
Q	661 CMTGTGCAACCTGTGAAGCTTGGAGCTTCCGAAACCTTGAAGGAAGATCACTA	720
D	721 acatctgatttggtccctcgatcatctgttggtatcatcagcagatgacctgag	780
Q	721 ACATCTGATTTGGCTCCCTCGCATCTGTTGGTATCATCAGCATAGCTTGAAGGA	780
D	781 ccaagtcaggaagatgagatgcatatgagtgatgagtgatgagttccatgagat	840
Q	781 CCAAGTCAAGGAAGATGAGATGATGATGATGATGATGATGATGATGATGATGAT	840
D	841 attcctgtgagatctctcatgagatgctgtgcttgccttgccttgccttgcct	900


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QY 841 ATTCCTGGTGGATCTCTCATGAGATCTGTCTGCTTTCCTTTGCTTGTATCCAG 900
Db 901 tccatcaatcattgtctctctacacccctgatgagtcctgagagatgtctcctc 960
QY 901 TCCATCAATCAATGTCTCTCATGAGATCTGTCTGCTTTCCTTTGCTTGTATCCAG 960
Db 961 tctctgctcccgagagagagacccgaatctcgcgcgcacacacacacacacacac 960
QY 961 TCTCTGCTCCCGAGAGAGAGACCCGAATCTCGCGCATCACACACACACACACAC 960
Db 1021 tagttgaactcttcaatcattgtctctgagcccatcacaatcttctctgtgagagctc 1020
QY 1021 TAGTTGCACTCTTCATCAATCTGTGAGACCCCATTCACATCTTTATTCCTGAGAGCTC 1080
Db 1081 tggagagacccctccacacacacacacacacacacacacacacacacacacacac 1140
QY 1081 TGGAGAGACCCCTCCACACACACACACACACACACACACACACACACACACACAC 1140
Db 1141 gttatacaacagacgacctgactctgtctctctctctctctctctctctctctct 1200
QY 1141 GTTATACCAACAGACGACCTGAACTCTGTCTCTCTCTCTCTCTCTCTCTCTCTCT 1200
Db 1201 ggtgttttagggactcttgccttccctctctctctctctctctctctctctctct 1260
QY 1201 GGTGTTTAGGACTCTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1260
Db 1261 gagttagaacaacagcttcaagatctctctctctctctctctctctctctctctct 1320
QY 1261 GAGTTAGAAACAGCTTCAAGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1320
Db 1321 cagctatgactagtcgttgaatgtctctctctctctctctctctctctctctctct 1380
QY 1321 CAGTATGACTAGTCGTGAATGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1380
Db 1381 atcttggttaacccaatctacactgcag 1410
QY 1381 ATCTTGTTTAAACCAGATTACACTCAG 1410

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RESULT 2
ID 086725 standard; cDNA, 2481 BP.
AC 086725;
DT 01-DEC-1995 (first entry)
DE Mammalian kappa opiod receptor protein cDNA.
KW Mammalian kappa opiod receptor; mouse delta opiod receptor; analgesic;
OS Rattus rattus.
FH Key Location/Qualifiers
FT CDS 111..1253
FT /tag= a
FT /product= kappa opiod receptor
PN J07070191-A.
PD 14-MAR-1995.
PF 30-JUL-1993; 190261.
PR 09-JUL-1993; JP-170591.
PA (TAKE) TAKEDA CHEM IND LTD.
DR WPI; 95-144857/19.
DR P-PSDB; R72591.
PT Kappa opiod receptor protein and cells expressing it - useful
PI for the screening of compounds for analgesic and hypnotic
PS properties
PS Claim 2; Page 9-10; 15pp; Japanese.
CC The nucleotide sequence of the novel mammalian kappa opiod receptor
CC cDNA. The gene was isolated by amplifying a fragment from rat brain mRNA
CC by reverse transcriptase-PCR (RT-PCR) using primers 086726-7 derived from
CC the mouse delta opiod receptor gene. This fragment was cloned into the
CC plasmid pCRIT to produce pRIT. The plasmid pRIT was used to probe a rat
CC brain DNA library in lambda ZapII to obtain a clone of the rat kappa
CC opiod receptor gene, designated pKOR2. This clone was introduced into
CC E.coli JM109 for production of the receptor protein. The receptor protein
CC is useful for screening of analgesic and hypnotic compounds including
CC peptides and proteins.
SO Sequence 2481 BP; 629 A; 588 C; 544 G; 720 T;

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Query Match 16.2%; Score 229; DB 15; Length 2481;
Best Local Similarity 98.1%; Pred. No. 8,006-228;
Matches 529; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
Db 279 gccatccctgttatcatcacccctgtctactctgtgaggttgggtggttaattgagc 338
QY 354 GCCATCCCTGTATCATCACCCCTCTTACCTGTGAGATTTGTGTGGCTTACGTGGCC 413
Db 339 aattccctgttattgttgcataccgatacaaaaatgaagacccgaacacacac 398
QY 414 AATCTCTGTCATCTTTGTATCATCCGATACAGAGATAAACCCGACACACATC 473
Db 399 taacatttaacctgtcttggcagatgcttgattactacacatgacctccagagt 458
QY 474 TACATTTTAACTGGCTTGGCAATGCTTTGTTACTACACTATGCCCTTTAGAGT 533
Db 459 gctgtactatgaataatcttggccttggagatgtctgtgcaaatgttcaatcc 518
QY 534 GCTGTACTCTGATGATGATTTCTTGCCCTTTTGAAGATGTGTATGCAATTTTC 593
Db 519 atttactactaacaatgtttaccagatatccacttgaccatgatgagtgtagccgc 578
QY 594 ATTGACTACTTCAACATGTTTACACGATATTCACTTACCATGATGATGATGAT 653
Db 579 taacttccctgtgtccacacctgtgaagcttggattccgaacaccttgaagcaag 638
QY 654 TACTTCTGTGTGCCACCCCTGTGAAGCTTGGACTTCCGAACACTTTGAAGCAAG 713
Db 639 atcaatacatcttcatattgtctactgscatactctgttggatatacagatagctt 698
QY 714 ATCATCAACATCTGCATTTGGCTCTGCACTCATCTTGTGATATCAGAGATAGTCT 773
Db 699 ggaagcaacaaagcaagagagagatgtgatgtcaatgaatgctctctgagttccgat 758
QY 774 GGAGGCACCAAGCAAGGAGAGATGTGATGATCATTAAGCTCTCTGAGATTCGAT 833
Db 759 gatgaatatccctgtgtgagacaccttcaatgaagatctgttcttcccttgcctgt 817
QY 834 GATGAATATTCGAGTGGAGATCTCTCATGAGATCTGTCTGCTTTCCTTTGCTTGT 892

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RESULT 3
ID 075931 standard; DNA, 1000 BP.
AC 075931;
DT 18-AUG-1995 (first entry)
DE Human kappa opiod receptor partial cDNA fragment.
KW Mouse; kappa; delta; mu; opiod receptor; brain; primer; PCR; amplify;
KW transmembrane domain; somatostatin; receptor; human; expression vector;
KW truncate; chimeric; assay; probe; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 102..989
FT /tag= a
FT /product= partial human kappa opiod receptor
PN W09428132-A.
PD 08-DEC-1994.
PF 20-MAY-1994; 005747.
PR 30-JUL-1993; US-066296.
PR 05-NOV-1993; US-100694.
PA (ARCH-) ARCH DEV CORP.
PI Bell GI, Reisine T, Yasuda K;
DR WPI; 95-022804/03.
DR P-PSDB; R67672.
FT Polynucleotides and peptides derived from opiod receptor
FT polypeptides - for use in therapeutic compositions and in
FT screening assays for useful drug substances.
PS Claim 10; Page 236-239; 300pp; English.
CC The partial nucleotide sequence of the novel human kappa opiod receptor
CC gene. The gene was isolated from a human brain hippocampus cDNA library
CC using a probe from the mouse kappa opiod receptor gene (075926). The
CC gene is missing the N-terminal sequence. The C-terminal sequence is

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CC very similar to the mouse kappa opioid receptor sequence. Of the
CC C-terminal 293 amino acids, 281 residues are identical and 6 residues
CC have conservative substitutions. The gene encoding the human opioid
CC receptor can be placed in a suitable expression vector for production of
CC the protein in a cell. The opioid receptors thus produced are useful for
CC the development of novel assays designed to select or improve substances,
CC capable of interacting with the opioid receptor proteins, for use in
CC diagnosis, drug design and therapeutic applications.
SQ Sequence 1000 BP; 238 A; 253 C; 225 G; 278 T;

Query Match 2.3%; Score 32; DB 13; Length 1000;
Best Local Similarity 100.0%; Pred. No. 4,01e-12;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 132 tacatatttaacctgcttgccagatgctt 163
|||||
Qy 474 TACATATTTAACCTGCTTGCCAGATGCTTT 505

RESULT 4
ID T12550 standard; cDNA; 1142 BP.
AC T12550.
DE 03-SEP-1996 (first entry)
KW Human kappa opioid receptor cDNA.
KW Human; kappa opioid receptor; psychiatric disorder; cardiovascular;
KW neurology; diagnosis; ds.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 1..1142
FT /tag= a
FT /product= kappa-opioid-receptor
FT /note= "incomplete termination codon"
FT WO9601898-21.
PD 25-JUN-1996.
PE 07-JUL-1995; F00912.
PR 11-JUL-1994; FR-008531.
PA (USTR-) UNIV PASTEUR STRASBOURG LODIS.
PI Kieffer B, Simonin F;
PI WPI: 96-097628/10.
DR P-PSDB; R88722.
DE New nucleic acid encoding the human kappa opioid receptor - useful
PT in diagnosis and therapy, and for isolating receptor ligands and
PT modulators
PS Claim 3: Page 13-15; 30pp; French.
CC This sequence codes for the human kappa opioid receptor and was
CC obtained from two overlapping cDNA fragments isolated from a
CC human placental cDNA library. The fragments were amplified from
CC the library using PCR primers based on the sequence of human
CC genomic clones which hybridised with a murine delta receptor cDNA
CC probe. Nucleotide probes derived from the kappa opioid receptor
CC coding sequence are useful for diagnosis of neurological, cardio-
CC vascular and psychiatric disorders associated with opioid
CC receptors.
SQ Sequence 1142 BP; 236 A; 337 C; 283 G; 286 T;

Query Match 2.3%; Score 32; DB 20; Length 1142;
Best Local Similarity 100.0%; Pred. No. 4,01e-12;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 289 tacatatttaacctgcttgccagatgctt 320
|||||
Qy 474 TACATATTTAACCTGCTTGCCAGATGCTTT 505

RESULT 5
ID Q56702 standard; DNA; 2447 BP.
AC Q56702.
DE 15-SEP-1994 (first entry)
DE Partial sequence of the human kappa opioid receptor
DE genomic clone H14 (KORa).
OS Opioid receptor; morphine; opiate; ss.
OS Homo sapiens.
PN WO9404552-A.

PD 03-MAR-1994.
PF 13-AUG-1993; U07665.
PR 13-AUG-1992; US-928200.
PA (REGC) UNIV CALIFORNIA.
PI Edwards RH, Evans CJ, Kaufman D, Keith DE;
PI WPI: 94-083099/10.
DR DNA encoding opioid receptors and antibodies against this
PT receptor - used to express and locate these receptors, and screen
PT cpds. for opioid (antagonist) activity
PS Example; Fig 8b; 74pp; English.
CC To isolate opiate receptor genomic clones, 300,000 human genomic
CC clones and a similar number of mouse genomic clones were probed
CC with the 1.1 kb mouse delta opioid receptor clone DOR-1 pSL/XbaI
CC fragment. One mouse clone and three human genomic clones were
CC isolated. The 3 human clones had very different EcoRI patterns
CC which indicated that three different genes were represented by the
CC human genomic clones which were designated H3, H4 and H20. H14 maps
CC to chromosome 8. It encodes the human kappa opioid receptor.
SQ Sequence 2447 BP; 683 A; 512 C; 498 G; 747 T;

Query Match 2.2%; Score 31; DB 10; Length 2447;
Best Local Similarity 100.0%; Pred. No. 3,20e-11;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 213 atagtccttgagagccacaaagtcaggaag 243
|||||
Qy 765 ATAGTCCTTGAGAGCCACCAAGTCAGGAAG 795

RESULT 6
ID Q29156 standard; DNA; 822 BP.
AC Q29156.
DE 08-MAR-1993 (first entry)
DE Brain somatostatin receptor 5' DNA.
KW SR; antibodies; tumours; glycoprotein; pancreatic somatostatinoma;
KW rat; ss.
OS Rattus rattus.
FH Key Location/Qualifiers
FT CDS 1..822
FT /tag= a
FT BP-508221-A.
PD 14-OCT-1992.
PE 25-MAR-1992; 105164.
PR 28-MAR-1991; US-677009.
PR 07-JUN-1992; US-817821.
PA (AMCY) AMERICAN CYANAMID CO.
PI Corbett MJ, Eppler CM, Hadcock J, Holmes JD, Shieh H;
PI Strnad J, Zyskijr, Cecil ME;
PI WPI: 92-341551/42.
DR P-PSDB; R27605.
DE New somatostatin receptor, active fragments and antibodies -
PT prevents somatostatin binding to its receptor, useful for
PT treating and detecting tumours e.g. pancreatic somatostatinoma
PS Claim 18; Fig 10; 50pp; English.
CC A partial clone of purified pituitary somatostatin was used to design
CC PCR primers for amplification of somatostatin receptor DNA 1.e.
CC primers ICI and TM VII. Rat genomic DNA was subjected to PCR and
CC from the deduced location of the receptor cDNA was chld. This sequence
CC was used in PCR to obtain the 5' rat brain SR sequence (some bases
CC undefined and having a gap in the sequence). The receptor may be
CC used to raise antibodies for detection and treatment of tumours in
CC patients, and to treat e.g. pancreatic somatostatinoma, and to
CC regulate the action of somatostatin in vivo.
SQ Sequence 822 BP; 158 A; 245 C; 220 G; 194 T;

Query Match 2.1%; Score 29; DB 5; Length 822;
Best Local Similarity 100.0%; Pred. No. 1,92e-09;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 262 aagatgaagaccgcaaccacacatctacat 290
|||||

OY 450 AAGATGAGACCGACACACATCTACAT 478

RESULT 7

ID 075928 standard; DNA; 1330 BP.

AC 075928;

DT 17-AUG-1995 (first entry)

DE Mouse opioioid receptor-like receptor MOP2 cDNA.

KW Mouse; kappa; delta; mu; opioioid receptor; brain; primer: PCR; amplify;

KW transmembrane domain; somatostatin; receptor; human; expression vector;

OS Mus musculus.

PH key

FI CDS Location/Qualifiers

FT 161..1264

FT /*tag= a

FT /product= mouse opioioid receptor-like receptor

PN MO9428132-A.

PD 08-DEC-1994.

PF 20-MAY-1994; U05747.

PR 20-MAY-1993; US-066296.

PR 30-JUL-1993; US-100694.

PR 05-NOV-1993; US-147592.

PA (ARCH-) ARCH DEV CORP.

PI Bell GI, Reisine T, Yasuda K;

DR WPI; 95-022804/03.

DR P-PSDB; R67671.

PT Polynucleotides and peptides derived from opioioid receptor

PT screening assays for useful drug substances.

PS Claim 28, page 225-229; 300pp; English.

CC The nucleotide sequence of the novel mouse opioioid receptor-like receptor

CC gene MOP2. MOP2 is a mouse receptor with pharmacological properties which

CC are dissimilar to the properties of classic opioioid receptors such kappa,

CC delta, mu or sigma. It has been found that drug of high abuse potential

CC or analgesic potency bind selectively to this receptor. This suggests

CC that this receptor could be important in the development of drugs to

CC treat addiction. Other opioioid receptors isolated and produced such as the

CC novel mouse kappa and delta opioioid receptors (075926-7) are useful for

CC the development of novel assays designed to select or improve substances,

CC capable of interacting with the opioioid receptor proteins, for use in

CC diagnosis, drug design and therapeutic applications.

CC Sequence 1330 BP; 230 A; 368 C; 350 G; 362 T;

SEQ

Query Match 1.8%; Score 25; DB 13; Length 1330;

Best Local Similarity 100.0%; Pred. No. 5,12e-06;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 539 gactactacacacgtttaccagca 563

OY 597 GACTACTACACATGTTTACCAGCA 621

RESULT 8

ID 089233 standard; cDNA; 1567 BP.

AC 089233;

DT 20-OCT-1995 (first entry)

DE Rat opioioid receptor cDNA.

KW Opioioid receptor; MOR-1; gene therapy; diagnostic; ss.

OS Rattus sp.

PH key

FI CDS Location/Qualifiers

FT 173..1276

FT /*tag= a

FT /product= mouse opioioid receptor-like receptor

PN MO9507983-A.

PD 23-MAR-1995.

PF 13-SEP-1994; U10356.

PR 13-SEP-1993; US-120601.

PA (INDV) UNIV INDIANA FOUND.

PI Yu L;

DR WPI; 95-131351/17.

DR P-PSDB; R71968.

PT New nucleic acid encoding new human mu opioioid receptor - and

PT related vectors, transformed cells, antibodies etc., useful in

PT diagnosis, treatment and drug screening.

PS Example 9; Page 218-222; 265pp; English.

CC The cDNA given in 089233 was isolated from a rat brain library by

CC low stringency hybridization with rat mu opioioid receptor cDNA

CC (089222). The clone encoded a 367-amino acid protein (R71968)

CC that showed high homology with mu, kappa and delta opioioid receptors

CC but lacked affinity for their ligands, suggesting it to be

CC a novel member of the opioioid receptor family.

CC Sequence 1567 BP; 313 A; 440 C; 402 G; 412 T;

SEQ

Query Match 1.8%; Score 25; DB 14; Length 1567;

Best Local Similarity 100.0%; Pred. No. 5,12e-06;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 551 gactactacacacgtttaccagca 575

OY 597 GACTACTACACATGTTTACCAGCA 621

RESULT 9

ID 090096 standard; cDNA; 2600 BP.

AC 090096;

DT 03-NOV-1995 (first entry)

DE Mouse kappa-3 opioioid receptor.

KW Kappa-3 opioioid receptor; analgesia; ss.

OS Mus sp.

PH key

FI CDS Location/Qualifiers

FT 299..1402

FT /*tag= a

FT /product= mouse kappa-3 opioioid receptor

PN MO9512616-A.

PD 11-MAY-1995.

PF 03-NOV-1994; U12728.

PR 05-NOV-1993; US-147949.

PA (SLOK) SLOAN KETTERING INST CANCER RES.

PI Pan Y, Pasternak GW;

DR WPI; 95-193814/25.

DR P-PSDB; R74298.

PT Nucleic acid molecule(s) encoding a kappa-3 opioioid receptor, and

PT antibody against the receptor - used to detect the receptor, and to

PT image cell membrane-bound receptor in a subject

PS Disclosure; Fig.1; 68pp; English.

CC Degenerate primers based on conserved sequences of the mouse delta

CC opioioid receptor were used in PCR to amplify mouse kappa-3 opioioid

CC receptor cDNA from a mouse brain lambda ZAP cDNA library

CC Sequence 2600 BP; 536 A; 680 C; 663 G; 721 T;

SEQ

Query Match 1.8%; Score 25; DB 14; Length 2600;

Best Local Similarity 100.0%; Pred. No. 5,12e-06;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 677 gactactacacacgtttaccagca 701

OY 597 GACTACTACACATGTTTACCAGCA 621

RESULT 10

ID 092972 standard; DNA; 2706 BP.

AC 092972;

DT 22-DEC-1995 (first entry)

DE Rat opioioid receptor OR7 DNA.

KW Opioioid receptor; opioioid; ss.

OS Rattus sp.

PN MO9519986-A1.

PD 27-JUL-1995.

PF 20-JAN-1995; U00939.

PR 21-JAN-1994; US-185360.

PA (AMCY) AMERICAN CYANAMID CO.

PI Eppler CM, Holmes JD, Ozenberger BA;

DR WPI; 95-269412/35.

DR P-PSDB; R76638.

PT New isolated DNA encoding an opioioid receptor - used to develop

PT probe, for identifying opioioid agonists and antagonists and for

PT detection; Fig.1; 35pp; English.

CC Primers based on rodent opiod receptors were used to amplify rat
CC genomic DNA. Products were re-amplified and subcloned into pCR-II
CC vector and amplified in E. coli. Plasmid DNAs were isolated, and
CC an unsplined sequence was obtd. (G92972) encoding the transmembrane
CC domain opioiph receptor protein OR7.
SQ Sequence 2706 BP; 569 A; 675 C; 704 G; 758 T;

Query Match 1.8%; Score 25; DB 15; Length 2706;
Best Local Similarity 100.0%; Pred. No. 5,12e-06;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 485 gactactacacatggtttaccagca 509
597 GACTACTACACATGTTTACCAGCA 621

RESULT 11
ID Q56700 standard; cDNA; 1821 BP.
AC Q56700;
DT 15-SEP-1994 (first entry)
DE Sequence of murine delta opiod receptor in the DOR-1 cDNA clone.
KW Opioiid receptor; morphine; opiate; ss.
OS Mus musculus.
FH Key Location/Qualifiers
FT CDS 29..1139
FT /tag= a
FT WO9404552-A.
PD 03-MAR-1994; 007665.
PF 13-AUG-1993; 007665.
PR 13-AUG-1992; US-929200.
PA (REGC) UNIV CALIFORNIA.
PI Edwards RH, Evans CJ, Kaufman D, Keith DE;
PI WPI: 94-083099/10.
DR P-PSDB: R48629.

PT DNA encoding opioiid receptors and antibodies against this
PT receptor - used to express and locate these receptors, and screen
PT opds. for opioiid (ant)agonist activity
PS Claim 1; Fig 5; 74pp; English.

CC A cDNA library was constructed using mRNA isolated from the NG109-15
CC cell line. A single clone, named the DOR-1 clone was isolated.
CC Comparisons with known sequences in Genbank showed highest homology
CC between DOR-1 and the G-protein-coupled somatostatin receptor. Other
CC features of the DOR-1 clone AA sequence deduced from the cDNA
CC sequence include 3 consensus glycosylation sites at residues 18 and
CC 33 (predicted to be in the extracellular N-terminal domain), and at
CC residue 310 (close to the C-terminus and predicted to be
CC intracellular). Phosphokinase C consensus sites are present within
CC predicted intracellular domains, at residues 242,255,344 & 352.
CC Seven putative membrane-spanning regions were identified. The DOR-1
CC clone produces a delta receptor with a predicted mol. wt. of 40,558
CC kaltions prior to post-translational modifications.
SQ Sequence 1821 BP; 339 A; 559 C; 541 G; 382 T;

Query Match 1.6%; Score 23; DB 10; Length 1821;
Best Local Similarity 100.0%; Pred. No. 2.20e-04;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 404 tccattgactactacacatggtt 426
591 TCCTATTGACTACTACACATGTT 613

RESULT 12
ID Q66556 standard; cDNA; 2216 BP.
AC Q66556;
DT 19-JAN-1995 (first entry)
DE Murine delta opiod receptor coding sequence.
KW delta opioiid; enkephalin; receptor; mouse; murine; analgesic; pain;
KW drug addiction; neurological disorder; psychiatric; disorder;
KW cardiovascular disorder; ds.
OS Mus musculus.
FH Key Location/Qualifiers
FT CDS 59..1174

FT /tag= a
FT /product= opioiid_receptor
PN FR2697850-A.
PD 13-MAY-1994.
PF 10-NOV-1992; 013526.
PR 10-NOV-1992; FR-013526.
PA (UYST-) UNIV PASTEUR STRASBOURG LOUIS.

PI Kieffer B;
DR WPI: 94-178255/22.
DR P-PSDB: R66503.
PT New nucleic acid encoding opioiid receptor - and related
PT polypeptide, antisense nucleic acid, probes, recombinant cells
PT and ligands, useful in diagnosis and treatment of e.g.
PT neurological disorders

PS Claim 3; Page 16-18; 29pp; French.
CC A cDNA bank constructed from hybridoma NG108-15, was used to
CC transfect COS-1 cells. The cells were tested for ability to bind
CC tritium-labelled Tyr-D-Thr-Gly-Phe-Leu-Thr. In the presence or
CC absence of the opioiid antagonist naloxone. Clone K56 was isolated
CC from a positive colony and found to contain a 2216bp insert. This
CC cDNA encodes a delta opioiid (enkephalin) receptor with apparent
CC dissociation constant 1.4nM and Bmax 3.9-6.4 pmole/mg protein.
SQ Sequence 2216 BP; 460 A; 647 C; 649 G; 460 T;

Query Match 1.6%; Score 23; DB 11; Length 2216;
Best Local Similarity 100.0%; Pred. No. 2.20e-04;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 434 tccattgactactacacatggtt 456
591 TCCTATTGACTACTACACATGTT 613

RESULT 13
ID Q75927 standard; DNA; 2272 BP.
AC Q75927;
DT 17-AUG-1995 (first entry)
DE Mouse delta opioiid receptor MOR1 cDNA.
KW Mouse; kappa; delta; mu; opioiid receptor; brain; primer; PCR; amplify;
KW transmembrane domain; somatostatin; receptor; human; expression vector;
KW truncate; chimeraic; assay; probe; ss.
OS Mus musculus.
FH Key Location/Qualifiers
FT CDS 12..1130
FT /tag= a
FT /product= mouse delta opioiid receptor

PN WO9428132-A.
PD 08-DEC-1994.
PF 20-MAY-1994; 005747.
PR 30-MAY-1993; US-066296.
PR 30-JUL-1993; US-100694.
PR 05-NOV-1993; US-147592.
PA (ARCH-) ARCH DEV CORP.
PI Bell GI, Reisine T, Yasuda K;
PI WPI: 95-022804/03.
DR P-PSDB: R67670.

PT Polynucleotides and peptides derived from opioiid receptor
PT screening assays for useful drug substances.
PS Claim 6; Page 215-221; 300pp; English.
CC The nucleotide sequence of the novel mouse delta opioiid receptor gene
CC MOR1. The gene was isolated from a mouse brain cDNA library using a
CC fragment (amplified from the cDNA library with primers Q75929-30) as a
CC probe. The primers are based on the conserved sequences present in the
CC second and third transmembrane domains of somatostatin (SSTR) receptor
CC subtypes SSTR1, SSTR2 and SSTR3. The 1.3 kb EcoRI-SacI fragment from the
CC mouse delta opioiid receptor clone, lambda ms1-2, was subcloned into the
CC CMV promoter-based expression vector pCMV-6c. The resultant construct
CC pCMV-ms1-2 was transfected into COS-1 cells for protein production. The
CC gene encoding the opioiid receptor can be used to produce complete,
CC truncated or chimeric opioiid receptor proteins. The opioiid receptors
CC thus produced are useful for the development of novel assays designed to
CC select or improve substances, capable of interacting with the opioiid


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CC receptor proteins, for use in diagnosis, drug design and therapeutic
CC applications.
SQ Sequence 2272 BP; 485 A; 665 C; 650 G; 472 T;

Query Match 1.6%; Score 23; DB 13; Length 2272;
Best Local Similarity 100.0%; Pred. No. 2.20e-04;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

D> 387 tccattgactactaacatgct 409
|||
QY 591 TCCATTGACTACTAACATGCT 613

RESULT 14
ID T12551 standard; cDNA; 36 BP.
AC T12551;
DT 04-SEP-1996 (first entry)
DE Human kappa opioid receptor partial 5'-cDNA PCR primer RP69.
KW Human; kappa opioid receptor; psychiatric disorder; cardiovascular;
KW neurology; diagnosis; polymerase chain reaction; ss.
OS Synthetic.
PN WO9601898-A1.
PD 25-JAN-1996;
PF 07-JUL-1995; F00912.
PA (USTR-) UNIV PASTEUR STRASBOURG LOUIS.
PI Kieffer B, Simonin F;
DR WPI; 96-097628/10.
PT New nucleic acid encoding the human kappa opioid receptor - useful
PT in diagnosis and therapy, and for isolating receptor ligands and
PT modulators
PS Example 2; Page 9; 30pp; French.
CC The sequence coding for the human kappa opioid receptor was
CC obtained from two overlapping cDNA fragments isolated from a
CC human placental cDNA library. The fragments were amplified from
CC the library using PCR primers based on the sequence of human
CC genomic clones which hybridised with a murine delta receptor cDNA
CC probe. Specifically, primers RP69 and RH84 (T12551 and T12552)
CC amplified a 508 bp fragment comprising the 5'-region of the coding
CC sequence; primers RM6 and RP70 (T12553 and T12554) amplified a
CC 760 bp fragment comprising the 3'-region of the coding
CC sequence. The fragments were ligated via an EcoRI site at position 365.
CC Nucleotide probes derived from the kappa opioid receptor
CC coding sequence are useful for diagnosis of neurological, cardio-
CC vascular and psychiatric disorders associated with opioid
CC receptors.
SQ Sequence 36 BP; 6 A; 13 C; 13 G; 4 T;

Query Match 1.4%; Score 20; DB 20; Length 36;
Best Local Similarity 100.0%; Pred. No. 4.66e-02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

D> 17 gagctgagcgtcaccatg 36
|||||
QY 169 GAGCTGAGCGCTCACATG 188

RESULT 15
ID T12554 standard; cDNA; 39 BP.
AC T12554;
DT 04-SEP-1996 (first entry)
DE Human kappa opioid receptor partial 3'-cDNA PCR primer RP70.
KW Human; kappa opioid receptor; psychiatric disorder; cardiovascular;
KW neurology; diagnosis; polymerase chain reaction; ss.
OS Synthetic.
PN WO9601898-A1.
PD 25-JAN-1996;
PF 07-JUL-1995; F00912.
PA (USTR-) UNIV PASTEUR STRASBOURG LOUIS.
PI Kieffer B, Simonin F;
DR WPI; 96-097628/10.
PT New nucleic acid encoding the human kappa opioid receptor - useful

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PT in diagnosis and therapy, and for isolating receptor ligands and
PT modulators
PS Example 2; Page 9; 30pp; French.
CC The sequence coding for the human kappa opioid receptor was
CC obtained from two overlapping cDNA fragments isolated from a
CC human placental cDNA library. The fragments were amplified from
CC the library using PCR primers based on the sequence of human
CC genomic clones which hybridised with a murine delta receptor cDNA
CC probe. Specifically, primers RP69 and RH84 (T12551 and T12552)
CC amplified a 508 bp fragment comprising the 5'-region of the coding
CC sequence; primers RM6 and RP70 (T12553 and T12554) amplified a
CC 760 bp fragment comprising the 3'-region of the coding
CC sequence. The fragments were ligated via an EcoRI site at position 365.
CC Nucleotide probes derived from the kappa opioid receptor
CC coding sequence are useful for diagnosis of neurological, cardio-
CC vascular and psychiatric disorders associated with opioid
CC receptors.
SQ Sequence 39 BP; 9 A; 13 C; 10 G; 7 T;

Query Match 1.4%; Score 20; DB 20; Length 39;
Best Local Similarity 100.0%; Pred. No. 4.66e-02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

D> 20 tccagcactagtcactatg 39
|||||
CP 1339 TCCAGCAGTACTGACTACTG 1320

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MPsrch_n n.a. - n.a. database search, using Smith-Waterman algorithm
Run on: Tue Apr 21 00:27:25 1998; Maspar time 994.34 Seconds
Tabular output not generated. 1194.228 Million cell updates/sec

Title: >US-08-292-694A-1
Description: (1-1410) from US08292694A.seq
Perfect Score: 1410
N.A. Sequence: 1 GCGCAGCTTGCCTGATCCGAA.....AACCCAGATTACACTGCAG 1410
Comp: CCGCTGGAACGACTAGGGTT.....TTGGGCTATATGTTGACGTC

Scoring table:
TABLE jmetric
Gap 60

Mmatch STD : Dbase 0; Query 0

Searched: 1126798 segs, 421087984 bases x 2

Post-processing: Minimum Match 0%
Listing first 1000 summaries

Database:

emb1-est
1:emb1-est1 2:emb1-est2 3:emb1-est3 4:emb1-est4 5:emb1-est5
6:emb1-est6 7:emb1-est8 8:emb1-est9
Database: genbank-est
9:gb-est1 10:gb-est2 11:gb-est3 12:gb-est4 13:gb-est5
14:gb-est6 15:gb-est7 16:gb-est8 17:gb-est9 18:gb-est10
19:gb-est11 20:gb-est12 21:gb-est13

Statistics: Mean 9.434; Variance 1.217; scale 7.749

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	26	1.8	153 10	R31984	yh62c10.r1 Homo sapien	1.8e-19
2	24	1.7	183 10	R81583	yf04b04.r1 Homo sapien	2.83e-15
3	18	1.3	206 18	AA317847	EST198409 Retina r1 Hom	5.42e-04
4	18	1.3	349 14	AA000300	mg32a09.r1 Soares mous	5.42e-04
5	18	1.3	352 10	R04688	PK27e08.r1 Caenorhabdi	5.42e-04
6	18	1.3	364 19	AA866615	EST177582 Pancreas tumo	5.42e-04
7	18	1.3	374 22	CI5712	Human fetal brain cDNA	5.42e-04
8	18	1.3	384 16	NS7941	yv61g04.r1 Soares feta	5.42e-04
9	18	1.3	414 13	NS6252	za14d10.s1 Homo sapien	5.42e-04
10	18	1.3	433 11	HA1020	yp12d11.s1 Homo sapien	5.42e-04
11	18	1.3	433 11	HA1332	yf04b04.s1 Homo sapien	5.42e-04
12	18	1.3	448 13	N78731	zb05a11.s1 Homo sapien	5.42e-04
13	18	1.3	466 17	AA18901	zq15e05.s1 Striatogene	5.42e-04
14	18	1.3	477 19	AA407460	EST100811 Mouse 7.5 dpc	5.42e-04
15	18	1.3	491 21	B35459	HS-1029-A1-E02-Mr.abi	5.42e-04

16	18	1.3	492 21	B50064	CT19788K-2206 TV CT197	5.42e-04
17	18	1.3	521 23	AA447244	zw93c04.r1 Soares tota	5.42e-04
18	18	1.3	523 22	CI5915	Human fetal brain cDNA	1.40e-04
19	18	1.3	616 21	B72960	RPc111-10M22.JP RPII1	5.42e-05
20	18	1.3	630 13	W22330	65H12 Human retina cDN	5.42e-04
21	18	1.3	643 21	B75300	RPc111-15D7 TV RPII1	5.42e-04
22	18	1.3	651 15	AA130056	z662e11.r1 Striatogene	5.42e-04
23	18	1.3	680 16	AA1965290	zp22g04.s1 Striatogene	5.42e-04
24	18	1.2	150 13	R57340	F3459 Fetal heart Homo	2.17e-02
25	17	1.2	153 16	AA024669	ze76f06.r1 Soares feta	2.17e-02
26	17	1.2	169 20	G03281	human STS WI-5445.	2.17e-02
27	17	1.2	173 23	K05G500777	Mouse 3'-directed cDN	2.17e-02
28	17	1.2	191 11	T32888	ESR53465 Homo sapiens	2.17e-02
29	17	1.2	196 11	T31750	EST38189 Homo sapiens	2.17e-02
30	17	1.2	209 20	G29153	human STS SHGC-17378.	2.17e-02
31	17	1.2	239 18	AA303018	EST13269 Thyms tumor	2.17e-02
32	17	1.2	241 13	W04435	za44h04.r1 Soares feta	2.17e-02
33	17	1.2	242 21	R37984	HS-1046-B2-A08-XR.abi	2.17e-02
34	17	1.2	245 19	AA352568	ESR60579 Activated T-c	2.17e-02
35	17	1.2	254 14	N83251	K4840F Fetal heart, La	2.17e-02
36	17	1.2	272 13	W05635	za50e02.r1 Soares feta	2.17e-02
37	17	1.2	274 19	AA354599	ESR63142 Jurkat T-cell	2.17e-02
38	17	1.2	280 19	AA377442	ESR90083 Synovial memb	2.17e-02
39	17	1.2	287 16	AA066604	ml174h04.r1 Striatogene	2.17e-02
40	17	1.2	288 19	AA355953	EST76830 Pitneal gland	2.17e-02
41	17	1.2	292 14	R10994	yf38c12.s1 Homo sapien	2.17e-02
42	17	1.2	294 23	AA038808	zn44d08.s1 Striatogene	2.17e-02
43	17	1.2	299 10	R39367	yo02h03.s1 Homo sapien	2.17e-02
44	17	1.2	300 10	R50578	yf60d04.r1 Homo sapien	2.17e-02
45	17	1.2	302 15	AA148241	z053g012.s1 Striatogene	2.17e-02
46	17	1.2	307 14	AA002486	mg42e09.r1 Soares mous	2.17e-02
47	17	1.2	308 16	AA057134	zf04h04.s1 Soares feta	2.17e-02
48	17	1.2	311 21	FR0011736	F.rubripes GSS sequenc	2.17e-02
49	17	1.2	312 11	H43643	yp24c07.r1 Homo sapien	2.17e-02
50	17	1.2	316 19	AA386021	EST99944 Pancreas tumo	2.17e-02
51	17	1.2	317 22	AA055802	z175b04.s1 Striatogene	2.17e-02
52	17	1.2	321 9	T95662	ye45e04.s1 Homo sapien	2.17e-02
53	17	1.2	322 20	G14595	human STS SHGC-11563.	2.17e-02
54	17	1.2	322 19	T85007	yb45h03.s1 Homo sapien	2.17e-02
55	17	1.2	324 15	W60490	zd25e06.s1 Soares feta	2.17e-02
56	17	1.2	326 19	AA370666	EST83365 Prostate glan	2.17e-02
57	17	1.2	327 16	AA191999	rs07b05.r1 Sommer Pils	2.17e-02
58	17	1.2	327 12	N23227	yx70h10.s1 Homo sapien	2.17e-02
59	17	1.2	330 13	H5C20A072	H. sepiens partial cDN	2.17e-02
60	17	1.2	337 19	AA361360	EST170628 T-cell lympho	2.17e-02
61	17	1.2	337 19	AA361360	EST170628 T-cell lympho	2.17e-02
62	17	1.2	338 16	N78089	yy75e02.r1 Striatogene	2.17e-02
63	17	1.2	340 16	AA068348	nm55e09.r1 Soares feta	2.17e-02
64	17	1.2	344 22	AA057756	z176d12.s1 Striatogene	2.17e-02
65	17	1.2	350 16	AA591834	rs08a03.r1 Sommer Pils	2.17e-02
66	17	1.2	351 15	AA029632	ze94c10.s1 Soares feta	2.17e-02
67	17	1.2	353 18	AA305758	EST176920 Jurkat T-cell	2.17e-02
68	17	1.2	359 14	T26986	NIB072407 Infant brai	2.17e-02
69	17	1.2	360 22	CI13142	C.elegans cDNA clone Y	2.17e-02
70	17	1.2	361 12	N48588	yy74c05.s1 Homo sapien	2.17e-02
71	17	1.2	366 17	AA38039	tm97f03.r1 Soares mous	2.17e-02
72	17	1.2	375 23	HMG504037	Human colon 3'directed	2.17e-02
73	17	1.2	378 16	AA190363	zp87b04.r1 Striatogene	2.17e-02
74	17	1.2	379 16	AA519164	r508g04.r1 Sommer Pils	2.17e-02
75	17	1.2	381 23	AA515453	vf81g06.r1 Soares mous	2.17e-02
76	17	1.2	384 14	AA016810	mh41d03.r1 Soares mous	2.17e-02
77	17	1.2	385 18	AA295532	EST100701 Pancreas tum	2.17e-02
78	17	1.2	386 11	H15927	yl12f03.s1 Homo sapien	2.17e-02
79	17	1.2	387 17	AA226981	yl19g11.s1 Striatogene	2.17e-02
80	17	1.2	389 10	R48882	yf61g05.r1 Homo sapien	2.17e-02
81	17	1.2	391 14	W59166	md7a5f0.r1 Soares mous	2.17e-02
82	17	1.2	393 14	W92171	zh48f10.r1 Soares feta	2.17e-02
83	17	1.2	395 15	W60776	z626e06.r1 Soares feta	2.17e-02
84	17	1.2	396 19	AA410146	EST101881 Mouse 7.5 dpc	2.17e-02
85	17	1.2	399 23	AA088856	ye46e04.s1 Homo sapien	2.17e-02
86	17	1.2	401 15	AA102189	z180f02.s1 Striatogene	2.17e-02
87	17	1.2	401 15	W60663	z265c06.s1 Soares feta	2.17e-02
88	17	1.2	403 10	R50362	yf59e04.s1 Homo sapien	2.17e-02

C	89	17	1.2	403 11	H02609	YJ41d06.s1 Homo sapien	2.17e-02	C	162	15	1.1	142 12	N47651	YY54e06.r1 Homo sapien	1.65e+01
C	90	17	1.2	406 15	W61054	zd29h11.r1 Soares feta	2.17e-02	C	163	15	1.1	143 16	AA066237	mm44h02.r1 Stratagene	1.65e+01
C	91	17	1.2	406 14	W76826	mez3g11.r1 Soares mous	2.17e-02	C	164	15	1.1	148 17	AA223624	zrl1g08.r1 Stratagene	1.65e+01
C	92	17	1.2	407 23	AA454617	ze36d11.s1 Soares ovar	2.17e-02	C	165	16	1.1	152 15	N97330	0019M7 gmbpFHH3.1.g.	6.84e-01
C	93	17	1.2	409 21	B72394	RPC111-8K24.TV RPC111	2.17e-02	C	166	16	1.1	154 16	AA062813	ze88b06.s1 Soares feta	1.65e+01
C	94	17	1.2	410 9	T62761	yc70h03.r1 Homo sapien	2.17e-02	C	167	16	1.1	158 14	AA013030	ze88b05.s1 Soares ret1	1.65e+01
C	95	17	1.2	413 15	H02076	YJ34f01.r1 Homo sapien	2.17e-02	C	168	15	1.1	163 14	N89052	K7549F fetal heart, La	1.65e+01
C	96	17	1.2	413 15	W60914	zd29h11.s1 Soares feta	2.17e-02	C	169	15	1.1	167 11	T34757	EST74708 Homo sapiens	6.84e-01
C	97	17	1.2	417 17	AA117889	mo65b09.r1 Stratagene	2.17e-02	C	170	16	1.1	169 14	H5897D042	H. sapiens partial cDN	6.84e-01
C	98	17	1.2	418 11	H17419	Ym40d11.s1 Homo sapien	2.17e-02	C	171	16	1.1	169 14	W98597	ng14b07.r1 Soares mous	1.65e+01
C	99	17	1.2	418 22	C18527	Human placenta cDNA 5'	2.17e-02	C	172	15	1.1	171 18	AA310414	EST181d5 Heart I Homo	1.65e+01
C	100	17	1.2	422 10	R67051	vi30b07.s1 Homo sapien	2.17e-02	C	173	15	1.1	173 21	B23155	F2503TF IGF Arabidopsi	1.65e+01
C	101	17	1.2	424 18	AA305523	BSM176509 Colon carcin	2.17e-02	C	174	15	1.1	174 20	HUMSWMS1616	human chromosome 7 STS	1.65e+01
C	102	17	1.2	424 15	W92279	ze15c03.s1 Soares feta	2.17e-02	C	175	16	1.1	176 18	AA297905	EST113467 Jurkat T-cel	6.84e-01
C	103	17	1.2	425 12	H56992	YJ07G04.r1 Homo sapien	2.17e-02	C	176	16	1.1	177 15	W89440	mF80a07.r1 Soares mous	6.84e-01
C	104	17	1.2	426 16	N71798	Yz29a10.r1 Soares mult	2.17e-02	C	177	15	1.1	185 14	N93668	zb50e03.s1 Soares feta	1.65e+01
C	105	17	1.2	429 14	AA004914	zh90h05.s1 Soares feta	2.17e-02	C	178	16	1.1	188 13	N93674	zb50f01.s1 Homo sapien	6.84e-01
C	106	17	1.2	438 15	AA130357	Zol9h12.s1 Stratagene	2.17e-02	C	179	16	1.1	190 10	R70920	Y150a08.s1 Homo sapien	6.84e-01
C	107	17	1.2	440 15	W76111	zd65c03.r1 Soares feta	2.17e-02	C	180	16	1.1	197 19	AA364691	EST747579 Pitneal gland	6.84e-01
C	108	17	1.2	440 21	B44853	HS-1060-NA1-F06-MF.ab1	2.17e-02	C	181	16	1.1	201 9	T86314	Y084d10.s1 Homo sapien	6.84e-01
C	109	17	1.2	440 14	R94445	YJ74b09.s1 Soares feta	2.17e-02	C	182	16	1.1	203 20	G07077	human STS WT-9013.	6.84e-01
C	110	17	1.2	446 11	H02711	YJ41d06.r1 Homo sapien	2.17e-02	C	183	16	1.1	203 14	N93043	zb59g02.s1 Soares feta	1.65e+01
C	111	17	1.2	446 13	W47848	mc82g09.r1 Soares mous	2.17e-02	C	184	15	1.1	204 19	W87340	zh66b09.r1 Soares feta	1.65e+01
C	112	17	1.2	448 15	W94327	zg77f03.r1 Soares feta	2.17e-02	C	185	15	1.1	204 19	AA351852	ESTJ57998 Infant brain	1.65e+01
C	113	17	1.2	452 16	H86834	zm64h08.s1 Soares feta	2.17e-02	C	186	15	1.1	204 17	AA144132	mq54d12.r1 Soares 2NbM	1.65e+01
C	114	17	1.2	454 11	H23991	Ym49c03.s1 Homo sapien	2.17e-02	C	187	15	1.1	205 12	N55949	J4535F Homo sapiens cD	1.65e+01
C	115	17	1.2	455 16	N43253	SW31C6895K Brugia mal	2.17e-02	C	188	15	1.1	205 11	H25472	Y147d08.r1 Homo sapien	1.65e+01
C	116	17	1.2	457 19	AA037803	zk38b11.s1 Soares preg	2.17e-02	C	189	15	1.1	208 11	H06683	Y182f12.s1 Homo sapien	6.84e-01
C	117	17	1.2	458 21	FR0022448	F.rubripes GSS sequenc	2.17e-02	C	190	16	1.1	209 17	AA153558	ms15b02.r1 Stratagene	1.65e+01
C	118	17	1.2	459 9	T77292	Yc95h06.r1 Homo sapien	2.17e-02	C	191	15	1.1	209 22	C03524	Human Heart cDNA, clon	1.65e+01
C	119	17	1.2	469 10	R24080	YJ33h07.s1 Homo sapien	2.17e-02	C	192	15	1.1	214 11	T34758	EST747433 Homo sapiens	1.65e+01
C	120	17	1.2	471 19	AA134117	z129f07.s1 Soares preg	2.17e-02	C	193	15	1.1	215 18	AA323179	EST25921 Cerebellum II	1.65e+01
C	121	17	1.2	473 23	R1CC05244	Rice cDNA, partial seq	2.17e-02	C	194	15	1.1	215 13	W03702	za74c03.r1 Soares feta	1.65e+01
C	122	17	1.2	477 10	R20298	Yq70g07.r1 Homo sapien	2.17e-02	C	195	15	1.1	217 16	AA019688	ze61h07.r1 Soares ret1	6.84e-01
C	123	17	1.2	477 15	W74623	zd77f03.s1 Soares feta	2.17e-02	C	196	16	1.1	218 13	H57H025	H. sapiens partial cDN	1.65e+01
C	124	17	1.2	482 15	W69263	zd45h05.s1 Soares feta	2.17e-02	C	197	15	1.1	221 15	W45227	zc33c11.r1 Soares sene	1.65e+01
C	125	17	1.2	484 17	AA152660	mr8d05.r1 Stratagene	2.17e-02	C	198	15	1.1	224 19	AA368477	EST79860 Placenta I Ho	1.65e+01
C	126	17	1.2	486 11	H38947	Yp48g10.r1 Homo sapien	2.17e-02	C	199	15	1.1	225 20	HUMSWX402	Human chromosome X STS	1.65e+01
C	127	17	1.2	487 15	W52368	zc47g06.r1 Soares sene	2.17e-02	C	200	15	1.1	227 13	HSC3E042	EST16574 Aorta endothe	1.65e+01
C	128	17	1.2	489 23	AA500746	v496g12.r1 Soares mous	2.17e-02	C	201	15	1.1	228 18	AA099947	Y1465.seg.F Fetal hea	1.65e+01
C	129	17	1.2	494 19	AA115516	z103a09.r1 Soares preg	2.17e-02	C	202	15	1.1	233 18	AA347931	ms33h04.r1 Stratagene	1.65e+01
C	130	17	1.2	498 18	AA286114	vc33h08.r1 Soares MP	2.17e-02	C	203	15	1.1	233 23	AA169010	EST54310 Fetal heart I	6.84e-01
C	131	17	1.2	502 11	H43453	Yoc4b04.r1 Homo sapien	2.17e-02	C	204	16	1.1	234 18	AA347931	EST54310 Fetal heart I	6.84e-01
C	132	17	1.2	504 14	AA1606	Yc67b02.r1 Homo sapien	2.17e-02	C	205	16	1.1	235 12	H74939	527 Brassica napus cDN	1.65e+01
C	133	17	1.2	504 12	AA017033	ze37c09.s1 Soares ret1	2.17e-02	C	206	15	1.1	236 12	N53996	YY99c05.r1 Homo sapien	6.84e-01
C	134	17	1.2	505 21	B01901	C58R-142H10-u cSNL f1c	2.17e-02	C	207	16	1.1	237 20	DM61P10T	D. melanocaster STS de	6.84e-01
C	135	17	1.2	506 14	R93265	Yf69c06.r1 Soares feta	2.17e-02	C	208	16	1.1	237 20	G05485	human STS WT-9956.	6.84e-01
C	136	17	1.2	513 21	B53657	CIT-HSP-201104.IR CIT-	2.17e-02	C	209	16	1.1	240 15	AA091515	113716.seg.F Fetal hea	6.84e-01
C	137	17	1.2	514 22	HUM421E11B	Human fetal brain cDNA	2.17e-02	C	210	16	1.1	241 19	AA350961	EST58517 Infant brain	1.65e+01
C	138	17	1.2	518 18	AA310332	EST181175 Jurkat T-cel	2.17e-02	C	211	15	1.1	246 19	AA367208	EST78285 Pancreas tumo	6.84e-01
C	139	17	1.2	533 23	AA541932	VJ58c02.r1 Knowles Sol	2.17e-02	C	212	15	1.1	246 19	AA367208	EST100316 Pancreas tumo	1.65e+01
C	140	17	1.2	533 21	FR0010690	F.rubripes GSS sequenc	2.17e-02	C	213	15	1.1	247 13	AA367208	H. sapiens partial cDN	1.65e+01
C	141	17	1.2	533 21	AA167745	zq40g03.s1 Stratagene	2.17e-02	C	214	15	1.1	248 11	AA367208	ymb7b10.r1 Homo sapien	1.65e+01
C	142	17	1.2	537 21	FR0022410	F.rubripes GSS sequenc	2.17e-02	C	215	15	1.1	249 18	AA88057	EST144201 Testis tumor	6.84e-01
C	143	17	1.2	581 23	AA445665	Vf62f03.r1 Barstead MP	2.17e-02	C	216	16	1.1	250 18	AA301155	EST14433 Testis tumor	6.84e-01
C	144	17	1.2	592 21	B64863	CIT-HSP-201104.TRB CIT	2.17e-02	C	217	16	1.1	250 20	AA301155	human STS SHGC-13575.	6.84e-01
C	145	17	1.2	604 16	AA044960	Zf52h09.r1 Soares ret1	2.17e-02	C	218	16	1.1	251 19	AA361886	EST71211 T-cell lympho	1.65e+01
C	146	17	1.2	613 16	AA191666	zq43d04.s1 Stratagene	2.17e-02	C	219	15	1.1	251 19	AA361886	H. sapiens partial cDN	6.84e-01
C	147	17	1.2	618 21	FR0022405	F.rubripes GSS sequenc	2.17e-02	C	220	16	1.1	253 21	AA361886	zn21f11.r1 Stratagene	6.84e-01
C	148	17	1.2	619 21	FR0019372	F.rubripes GSS sequenc	2.17e-02	C	221	16	1.1	254 13	HSC346112	zn21f11.r1 Stratagene	6.84e-01
C	149	17	1.2	636 22	AA195013	Zr35a07.s1 Soares NhhM	2.17e-02	C	222	16	1.1	258 15	AA081960	EST82779 Prostate glan	6.84e-01
C	150	17	1.2	672 22	AA195119	Zr35a07.r1 Soares NhhM	2.17e-02	C	223	15	1.1	258 19	AA371042	EST82779 Prostate glan	6.84e-01
C	151	17	1.2	884 16	AA203299	zx35a01.r1 Soares feta	2.17e-02	C	224	15	1.1	259 21	FR0021983	F.rubripes GSS sequenc	6.84e-01
C	152	17	1.2	925 20	G26659	human STS STS-X82240.	2.17e-02								

C	235	16	1.1	269	15	AA073507	mj98b09.r1	Soares	mous	6.84e-01	C	308	15	333	18	AA36668	EST29878	Cerebellum II	1.65e+01			
C	236	16	1.1	269	15	W08605	mb46c01.r1	Soares	mous	6.84e-01	C	309	16	334	16	AA185649	ms50c01.r1	Soares	mous	6.84e-01		
C	237	15	1.1	269	15	H28672	y168g12.s1	Homo	sapien	1.65e+01	C	310	16	336	11	M85601	EST02117	Homo sapiens	1.65e+01			
C	238	15	1.1	272	15	AA052103	tf50h01.r1	Soares	mous	1.65e+01	C	311	15	336	16	T54088	ya92d07.r1	Homo sapiens	1.65e+01			
C	239	15	1.1	273	11	T31586	EST37070	Homo	sapiens	1.65e+01	C	312	16	337	19	AA376864	BSR89338	Small Intest	1.65e+01			
C	240	16	1.1	274	13	AT154985	A. thaliana	transcribe		6.84e-01	C	313	15	337	19	AA155628	zK96c08.r1	Soares	preg	1.65e+01		
C	241	16	1.1	275	22	HUM233E05B	Human aorta	CDNA 5'-en		6.84e-01	C	314	15	339	16	AA107623	mb60c09.r1	Stratagene		6.84e-01		
C	242	15	1.1	276	19	AA366973	EST77990	Pancreas	tumo	1.65e+01	C	315	15	339	12	H84490	yy02c11.r1	Homo sapien		1.65e+01		
C	243	15	1.1	276	10	R65722	Y126b09.r1	Homo	sapien	1.65e+01	C	316	15	330	23	AA271340	wa71b07.r1	Soares	mous	1.65e+01		
C	244	15	1.1	276	9	T06372	EST04161	Homo	sapiens	1.65e+01	C	317	15	330	23	AA271340	Rice	CDNA, partial	seq	1.65e+01		
C	245	15	1.1	277	13	HSC33C052	H. sapiens	partial	CDN	1.65e+01	C	318	16	331	17	AA220928	23	Furus	radiata	somat	6.84e-01	
C	246	16	1.1	277	19	AA373670	EST8513	HSC172	cells	6.84e-01	C	319	16	331	16	AA167676	zy90e03.s1	Stratagene		6.84e-01		
C	247	16	1.1	282	22	N87727	IL3581F	Petal	heart, L	6.84e-01	C	320	15	331	12	N51131	yy95e11.r1	Homo sapien		1.65e+01		
C	248	15	1.1	282	22	C06509	z558b09.r1	Soares	retl	1.65e+01	C	321	16	332	17	AA175451	EST03981	Homo sapiens		6.84e-01		
C	249	16	1.1	283	13	N80375	z596f04.s1	Homo	sapien	6.84e-01	C	322	15	332	22	CEIK056F1R	ms87g03.r1	Soares	mous	1.65e+01		
C	250	15	1.1	283	18	AA319093	EST12258	Adrenal	gland	1.65e+01	C	323	15	332	11	R96649	C.elegans	CDNA	clone	y	1.65e+01	
C	251	16	1.1	287	9	T07937	EST05828	Homo	sapiens	6.84e-01	C	324	16	333	9	T91903	yy39e09.s1	Homo sapien		6.84e-01		
C	252	16	1.1	289	10	HSC13E041	yc13b12.r1	Homo	sapien	6.84e-01	C	325	15	333	9	T73934	yy02a05.s1	Homo sapien		6.84e-01		
C	253	16	1.1	289	13	HSC34C041	H. sapiens	partial	CDN	6.84e-01	C	326	15	333	9	T96050	yy54g12.s1	Homo sapien		1.65e+01		
C	254	16	1.1	289	16	AA057340	z558b09.r1	Soares	retl	6.84e-01	C	327	15	334	18	AA345864	yy42e10.s1	Homo sapien		1.65e+01		
C	255	16	1.1	290	16	R02410	ye82a06.r1	Homo	sapien	6.84e-01	C	328	15	334	15	AA345864	EST52203	Greater oment		1.65e+01		
C	256	16	1.1	292	18	AA325123	EST28075	Cerebellum II		6.84e-01	C	329	15	335	19	AA379676	15327.seq	F. Petal	heart	1.65e+01		
C	257	16	1.1	293	19	AA361581	EST10959	T-cell	lympho	6.84e-01	C	330	16	335	19	AA379676	EST92546	Skin	tumor	I	6.84e-01	
C	258	15	1.1	293	10	R23656	yh35g05.s1	Homo	sapien	6.84e-01	C	331	16	336	9	R00603	ye74c05.r1	Homo sapien		1.65e+01		
C	259	15	1.1	294	10	T79088	yd69g01.r1	Homo	sapien	6.84e-01	C	332	15	336	9	T06382	EST35974	Embryo, 8 wee		6.84e-01		
C	260	16	1.1	294	22	C06971	similar	to	insulin	1.65e+01	C	333	16	337	18	AA332005	me04c02.r1	Soares	mous	6.84e-01		
C	261	16	1.1	294	12	H86153	ys97g07.r1	Homo	sapien	1.65e+01	C	334	16	337	14	W64490	EST04227	Homo sapiens		1.65e+01		
C	262	15	1.1	294	9	T00683	WEST01404	Caenorhabdit		1.65e+01	C	335	15	337	15	AA097387	mx09d12.r1	Soares	mous	6.84e-01		
C	263	15	1.1	295	16	AA196658	zq59c11.r1	Stratagene		1.65e+01	C	336	16	337	22	CEIK071BYR	C.elegans	CDNA	clone	y	6.84e-01	
C	264	15	1.1	295	19	AA374651	EST6818	HSC172	cells	1.65e+01	C	337	16	337	22	C06608	similar	to	insulin	1.65e+01		
C	265	15	1.1	296	16	AA370835	EST1869	Aorta	endothe	1.65e+01	C	338	16	338	10	R35292	yy6c210.r1	Homo sapien		6.84e-01		
C	266	15	1.1	296	15	AA159039	co57e01.s1	Stratagene		1.65e+01	C	339	16	339	18	AA327941	EST91374	Embryo, 12 we		1.65e+01		
C	267	15	1.1	296	16	AA360788	EST69986	T-cell	lympho	1.65e+01	C	340	15	339	18	AA327941	rs10g11.s1	Summer	prits	1.65e+01		
C	268	15	1.1	297	13	HSC36A048	H. sapiens	partial	CDN	6.84e-01	C	341	15	339	12	H56449	yy98g10.s1	Homo sapien		1.65e+01		
C	269	15	1.1	297	18	AA333428	EST17603	Embryo, 8 wee		6.84e-01	C	342	15	339	9	T07190	EST05079	Homo sapiens		6.84e-01		
C	270	15	1.1	298	12	H84296	ys95d12.r1	Homo	sapien	6.84e-01	C	343	15	339	22	AA338069	ve48f06.r1	Beddington		1.65e+01		
C	271	16	1.1	298	18	AA298142	EST11371	Uterus	Homo	s	6.84e-01	C	344	15	340	22	AA418591	vh94h06.r1	Barstead	mo	1.65e+01	
C	272	16	1.1	298	14	W08119	mb4a07.r1	Soares	mous	6.84e-01	C	345	15	340	22	AA426500	z57f1h02.r1	Soares	test	1.65e+01		
C	273	16	1.1	300	22	C08313	C.elegans	CDNA	clone	y	6.84e-01	C	346	15	341	20	C06750	similar	to	insulin	1.65e+01	
C	274	15	1.1	300	22	C08195	C.elegans	CDNA	clone	y	1.65e+01	C	347	15	341	20	HUM8WS3352	human	chromosome	7	STS	1.65e+01
C	275	15	1.1	302	22	C08319	ye55h06.r1	Homo	sapien	6.84e-01	C	348	15	341	21	B23035	F24N87R	IGF	Arabidopsi		1.65e+01	
C	276	15	1.1	302	22	C15349	Human fetal	brain	CDNA	6.84e-01	C	349	15	343	23	RICSL18055A	Rice	CDNA, partial	seq		6.84e-01	
C	277	15	1.1	304	13	R26732	yh51f01.s1	Homo	sapien	1.65e+01	C	350	16	343	23	AA354608	EST28937	Jurkat	T-cell		1.65e+01	
C	278	15	1.1	304	13	HSH20E012	H. sapiens	partial	CDN	1.65e+01	C	351	16	344	20	G05527	human	STS	WT-6040		6.84e-01	
C	279	15	1.1	304	18	AA312960	EST18320	Pancreas	tum	1.65e+01	C	352	16	344	11	T27939	EST07070	Homo sapiens		6.84e-01		
C	280	15	1.1	304	20	HS240VF10	H. sapiens	(DI05551)	D	1.65e+01	C	353	15	344	21	T53787	ye05d07.s1	Homo sapien		1.65e+01		
C	281	15	1.1	305	11	HS1043	yp84d10.s1	Homo	sapien	1.65e+01	C	354	15	344	21	B59737	Cit-HSP-228K3	TF	CIT-H		1.65e+01	
C	282	15	1.1	305	16	AA055893	yf43h12.r1	Homo	sapien	6.84e-01	C	355	15	345	15	AA097679	mo10a02.r1	Life	Tech	m	6.84e-01	
C	283	15	1.1	306	16	AA055893	me6b09.r1	Stratagene		6.84e-01	C	356	15	347	18	AA347422	EST53717	Fetal	heart	I	6.84e-01	
C	284	16	1.1	307	14	W76723	me6b09.r1	Stratagene		6.84e-01	C	357	16	347	18	AA270513	C.elegans	CDNA	clone	y	6.84e-01	
C	285	15	1.1	307	12	N36917	yy38c07.s1	Homo	sapien	1.65e+01	C	358	16	347	18	CA2311	ve65h10.r1	Soares	mous		6.84e-01	
C	286	15	1.1	307	23	AA464189	zx83g05.s1	Soares	ovar	1.65e+01	C	359	15	347	19	R68402	Citrus	CDNA, partial	s		1.65e-01	
C	287	15	1.1	308	16	AA373501	EST85569	HSC172	cells	6.84e-01	C	360	15	348	10	HSC1PH091	H. sapiens	partial	CDN		6.84e-01	
C	288	15	1.1	308	16	AA001137	ze48a02.r1	Soares	retl	1.65e+01	C	361	15	349	16	AA057139	z5f0a07.r1	Soares	retl		1.65e-01	
C	289	15	1.1	308	17	HSC2FH072	cs90618.seq	F	Human	cdn	1.65e+01	C	362	15	350	22	AA435026	ve66b05.r1	Soares	mous		6.84e-01
C	290	15	1.1	309	13	HSC1RH011	H. sapiens	partial	CDN	1.65e+01	C	363	15	350	22	PR0021096	F. rubripes	GSS	sequenc		6.84e-01	
C	291	15	1.1	309	19	AA240853	mw23d03.r1	Soares	mous	6.84e-01	C	364	15	351	13	AT1S2521	A. thaliana	transcribe			1.65e+01	
C	292	15	1.1	310	17	AA361579	EST70954	T-cell	lympho	6.84e-01	C	365	15	352	9	R03086	pk03f11.r1	Caenorhabdi			6.84e-01	
C	293	16	1.1	311	22	AA174960	ms88d07.r1	Soares	mous	6.84e-01	C	366	15	352	12	NA4209	yy52d11.r1	Homo sapien			6.84e-01	
C	294	16	1.1	311	22	C15673	Human fetal	brain	CDNA	6.84e-01	C	367	15	353	20	G35600	STS	h14a618	5		1.65e+01	
C	295	15	1.1	315	18	AA333726	BS137843	Embryo, 3 wee		6.84e-01	C	368	16	353	20	G03535	human	STS	WT-2058		6.84e-01	
C	296	15	1.1	316	18	AA344780	EST950701	Gall	bladder	1.65e+01	C	369	15	353	16	AA057798	z115907.s1	Soares	feta		6.84e-01	
C	297	15	1.1	318	10	R06620	rice	CDNA, partial	seq	1.65e+01	C	370	15	353	17	T37407	EST10524	Saccharomyce			1.65e+01	
C	298	15	1.1	319	23	RIICC10064A	mu24f06.r1	Beddington		6.84e-01	C	371	15	354	12	W72739	z671e06.s1	Soares	feta		1.65e+01	
C	299	15	1.1	320	22	AA438188	ve63c11.r1	Beddington		6.84e-01	C	372	15	354	12	H85911	yy55b08.r1	Homo sapien			1.65e+01	
C	300	15	1.1	320	22	AA438188	H. sapiens	partial	CDN	6.84e-01	C	373	15	355	12	HUMEST2C10	ye54h07.r1	Homo sapien			6.84e-01	
C	301	15	1.1	321	13	HSC1MH031	H. sapiens	partial	CDN	6.84e-01	C	374	15	355	12	AA298266	EST114123	Prostate	gla		1.65e+01	
C	302	16	1.1	3																		

C	381	16	1.1	356 10	R76032	Yf60a07.r1 Homo sapien	6.84e-01	454	16	1.1	383 14	AA050766	m16c06.r1 Soares mus	6.84e-01
C	382	16	1.1	356 19	AA033705	ZK20a07.s1 Soares preg	6.84e-01	455	15	1.1	383 10	R49981	m16c06.r1 Homo sapien	1.65e+01
C	383	16	1.1	357 17	W33525	mc52b05.r1 Soares mus	6.84e-01	456	15	1.1	383 11	H08432	Yf96a06.r1 Homo sapien	1.65e+01
C	384	16	1.1	357 18	AA332236	ESC56146 Embryo, 8 wee	6.84e-01	457	15	1.1	384 23	AA451108	Vf67f12.r1 Soares mus	1.65e+01
C	385	15	1.1	357 11	H19765	ym56i0.r1 Homo sapien	1.65e+01	458	15	1.1	384 9	T09604	0194m3 Plasmidium falc	1.65e+01
C	386	15	1.1	357 15	AA094643	cp0942.seg.F Petal hea	1.65e+01	459	15	1.1	384 15	W47412	zc35e01.s1 Soares sene	1.65e+01
C	387	15	1.1	359 22	C06950	similar to insulin 1.	6.84e-01	460	15	1.1	384 10	R5418	y998a03.r1 Homo sapien	1.65e+01
C	388	15	1.1	359 11	W79933	EST10137 Homo sapiens	1.65e+01	461	15	1.1	385 15	W89879	m177e01.r1 Soares mus	1.65e+01
C	389	15	1.1	359 9	W79619	EST10137 Homo sapiens	1.65e+01	462	15	1.1	385 21	FR0005835	Yp06c09.s1 Homo sapien	6.84e-01
C	390	15	1.1	359 14	AA050307	m12b07.r1 Soares mus	1.65e+01	463	15	1.1	385 21	FR0005835	Yp06c09.s1 Homo sapien	1.65e+01
C	391	16	1.1	360 18	AA324493	EST12672 Cerebellum II	6.84e-01	464	15	1.1	385 11	FR0005835	Yp06c09.s1 Homo sapien	1.65e+01
C	392	15	1.1	360 18	AA302095	EST15206 Aorta endothe	1.65e+01	465	15	1.1	385 22	AA243300	Zr26h03.r1 Strati gene	1.65e+01
C	393	15	1.1	360 22	CEIK09481F	C.elegans CDNA clone Y	1.65e+01	466	15	1.1	385 22	H0M079A05A	Human fetal brain cDNA	6.84e-01
C	394	15	1.1	360 22	CEIK0518F	C.elegans CDNA clone Y	1.65e+01	467	15	1.1	386 15	AA112396	zn68h10.s1 Strati gene	6.84e-01
C	395	16	1.1	360 22	CEIK103H2F	C.elegans CDNA clone Y	6.84e-01	468	16	1.1	386 15	W83783	mfn3a03.r1 Soares mus	6.84e-01
C	396	16	1.1	360 22	CEIK090H2F	C.elegans CDNA clone Y	6.84e-01	469	16	1.1	386 11	H20456	yp61c01.r1 Homo sapien	6.84e-01
C	397	16	1.1	360 22	CEIK05286F	C.elegans CDNA clone Y	6.84e-01	470	16	1.1	387 19	AA148882	z127a09.r1 Soares preg	1.65e+01
C	398	16	1.1	360 22	CEIK116E9F	C.elegans CDNA clone Y	6.84e-01	471	15	1.1	388 15	RA0685	y179h12.s1 Homo sapien	1.65e+01
C	399	16	1.1	360 9	T60833	Yb70f06.r1 Homo sapien	6.84e-01	472	15	1.1	388 22	CEIK027C2R	m16h08.r1 Beddinglton	1.65e+01
C	400	15	1.1	360 22	CEIK103G3F	C.elegans CDNA clone Y	6.84e-01	473	16	1.1	389 22	CEIK027C2R	C.elegans CDNA clone Y	6.84e-01
C	401	15	1.1	360 22	CEIK035A4F	C.elegans CDNA clone Y	1.65e+01	474	15	1.1	389 21	RA1283	Yf85e04.s1 Homo sapien	1.65e+01
C	402	15	1.1	361 10	R80207	Y192g06.s1 Homo sapien	1.65e+01	475	15	1.1	389 21	B53168	CIT-HSP-200986.TF CIT	1.65e+01
C	403	15	1.1	361 13	N76825	zb17a01.s1 Homo sapien	1.65e+01	476	16	1.1	390 13	W33605	mc35h01.r1 Soares mus	6.84e-01
C	404	15	1.1	361 23	AA455186	zx79e02.r1 Soares ovar	1.65e+01	477	15	1.1	390 13	AA144490	m17d10.r1 Soares mus	1.65e+01
C	405	15	1.1	362 17	AA250510	mw99e01.r1 Soares mus	1.65e+01	478	15	1.1	390 12	NS1734	yz01a01.s1 Homo sapien	1.65e+01
C	406	15	1.1	362 14	AA051444	mj51a09.r1 Soares mus	1.65e+01	479	15	1.1	391 9	TS1054	yz26c04.r1 Homo sapien	1.65e+01
C	407	16	1.1	363 18	AA346307	EST152430 Greater oment	6.84e-01	480	15	1.1	391 13	W39059	zb34c02.r1 Soares para	1.65e+01
C	408	16	1.1	363 11	H42280	Yb63d01.r1 Homo sapien	6.84e-01	481	16	1.1	392 18	AA273395	ya23b07.r1 Guaywoodfor	6.84e-01
C	409	15	1.1	364 9	T83653	Yd67b09.s1 Homo sapien	1.65e+01	482	15	1.1	392 10	R30916	Yf85e03.r1 Homo sapien	1.65e+01
C	410	15	1.1	364 11	T836285	EST97924 Homo sapiens	1.65e+01	483	16	1.1	392 10	R35583	y996a06.r1 Homo sapien	1.65e+01
C	411	16	1.1	365 19	AA376939	EST9427 Small Intesti	6.84e-01	484	15	1.1	393 20	AA064541	m14e06.r1 Strati gene	6.84e-01
C	412	16	1.1	365 14	W69980	me04a06.r1 Soares mus	6.84e-01	485	16	1.1	393 12	HSR247ZD9	H.sapiens (D6S1581) DN	6.84e-01
C	413	16	1.1	365 11	R83526	Yp15h01.r1 Homo sapien	6.84e-01	486	16	1.1	393 11	W65547	zd28g06.r1 Soares feta	6.84e-01
C	414	16	1.1	367 14	W35018	mc35a06.r1 Soares mus	1.65e+01	487	16	1.1	394 15	W65547	mo27g02.r1 Life Tech m	6.84e-01
C	415	15	1.1	367 9	T836643	Yd67a07.s1 Homo sapien	1.65e+01	488	16	1.1	394 15	AA119687	ys65f12.s1 Homo sapien	1.65e+01
C	416	16	1.1	368 15	AA093070	mm0450.seg.F Fetal hea	6.84e-01	489	15	1.1	395 10	H82534	human Chromosome 7 STS	6.84e-01
C	417	16	1.1	368 9	T60780	Yb70f06.s1 Homo sapien	6.84e-01	490	16	1.1	395 22	HUMSWS3726	va67d01.r1 Soares mus	6.84e-01
C	418	15	1.1	368 23	AA530207	Vj46g07.r1 Strati gene	1.65e+01	491	16	1.1	395 22	CEIK027FXR	C.elegans CDNA clone Y	6.84e-01
C	419	16	1.1	370 9	T82209	Yd95g09.r1 Homo sapien	6.84e-01	492	16	1.1	395 20	HS769XG5	H.sapiens (D19S409) D	1.65e+01
C	420	16	1.1	370 14	W66652	me25e09.r1 Soares mus	6.84e-01	493	16	1.1	395 11	H16694	Ym26e10.s1 Homo sapien	1.65e+01
C	421	15	1.1	370 23	AA199576	zq75e07.s1 Strati gene	1.65e+01	494	15	1.1	395 11	H40890	Ym93d06.s1 Homo sapien	1.65e+01
C	422	15	1.1	370 26	AA474477	vd55d09.r1 Knowles Sol	6.84e-01	495	15	1.1	396 12	N68339	za67a12.s1 Homo sapien	6.84e-01
C	423	16	1.1	371 11	T33074	EST95584 Homo sapiens	6.84e-01	496	16	1.1	396 22	C06974	similar to insulin 1.	6.84e-01
C	424	16	1.1	371 17	AA235733	zt32b06.s1 Soares ovar	6.84e-01	497	16	1.1	396 16	AA018660	ze33f10.r1 Soares reti	6.84e-01
C	425	16	1.1	372 22	C18830	Human Placenta CDNA 5'	6.84e-01	498	16	1.1	396 10	RA15127	Yg72e12.r1 Homo sapien	6.84e-01
C	426	16	1.1	372 14	T25336	EST191R BL29 Burkitt's	6.84e-01	499	15	1.1	396 9	T08896	EST06788 Homo sapiens	1.65e+01
C	427	16	1.1	373 15	W55652	md07d04.r1 Soares mus	6.84e-01	500	15	1.1	396 9	W92103	ZH8c07.r1 Soares feta	1.65e+01
C	428	15	1.1	373 10	AA115597	Z105h09.s1 Soares preg	6.84e-01	501	15	1.1	397 16	C06806	similar to Insulinl.	6.84e-01
C	429	16	1.1	373 23	R1CS2781A	Rice cDNA, partial seq	1.65e+01	502	16	1.1	397 22	W08066	mb39d11.r1 Soares mus	6.84e-01
C	430	15	1.1	374 19	AA386975	vc81f05.r1 Ko mouse em	1.65e+01	503	16	1.1	398 14	T78615	Yd69d11.s1 Homo sapien	6.84e-01
C	431	15	1.1	374 23	AA445247	yf62c11.r1 Barstead MP	6.84e-01	504	16	1.1	398 9	W52257	zd46c12.s1 Soares sene	6.84e-01
C	432	16	1.1	374 11	H50445	Y029g12.s1 Homo sapien	6.84e-01	505	15	1.1	399 17	AA105818	EST58927 Infant brain	6.84e-01
C	433	16	1.1	375 19	HSPD04451	H.sapiens EST sequence	6.84e-01	506	16	1.1	399 19	AA351232	mp47d12.r1 Barstead MP	1.65e+01
C	434	15	1.1	375 14	W80291	me90c02.r1 Soares mus	1.65e+01	507	16	1.1	399 17	AA105818	mb57b06.r1 Soares mus	1.65e+01
C	435	15	1.1	375 9	T01872	WST02693 Caenorhadi	6.84e-01	508	15	1.1	399 19	HSPD06803	H.sapiens EST sequence	1.65e+01
C	436	16	1.1	376 22	C09096	C.elegans cDNA clone Y	6.84e-01	509	15	1.1	399 19	AA031841	ZK17d04.r1 Soares preg	1.65e+01
C	437	16	1.1	376 17	AA253984	va10a04.r1 Soares mus	6.84e-01	510	15	1.1	399 19	AA07230	EST02225 Mouse 7.5 dpc	1.65e+01
C	438	16	1.1	377 16	AA212155	mu80h08.r1 Strati gene	6.84e-01	511	15	1.1	399 19	AA07230	human STS SHGC-8334 cl	6.84e-01
C	439	16	1.1	377 10	AA188617	zp78c10.s1 Strati gene	1.65e+01	512	15	1.1	400 20	AA471241	human STS SHGC-8334 cl	6.84e-01
C	440	16	1.1	377 10	R80304	Y197d05.r1 Homo sapien	1.65e+01	513	15	1.1	400 20	AA471241	human STS SHGC-8334 cl	6.84e-01
C	441	15	1.1	378 11	H09467	Y197g05.s1 Homo sapien	1.65e+01	514	15	1.1	400 16	AA021500	z66a12.s1 Soares reti	1.65e+01
C	442	15	1.1	378 11	R26425	YH47d09.r1 Homo sapien	6.84e-01	515	15	1.1	400 16	AA021500	z66a12.s1 Soares reti	1.65e+01
C	443	15	1.1	379 9	M89353	CEI21f12 Caenorhadi	6.84e-01	516	15	1.1	400 16	AA181109	yp67c12.s1 Strati gene	1.65e+01
C	444	16	1.1	380 22	CEIK039D8R	C.elegans cDNA clone Y	1.65e+01	517	15	1.1	401 10	HUMSWX740	human chromosone X STS	1.65e+01
C	445	15	1.1	380 14	R58865	NTB2056 Normalized inf	1.65e+01	518	15	1.1	401 20	HUMSWX740	human chromosone X STS	1.65e+01
C	446	15	1.1	381 10	R78640	Y174f07.r1 Homo sapien	1.65e+01	519	15	1.1	401 9	R01195	Yf77e02.s1 Homo sapien	6.84e-01
C	447	15	1.1	381 10	R44401	Y936h08.s1 Homo sapien	1.65e+01	520	16	1.1	402 18	AA271231	Yb73e03.r1 Soares mus	1.65e+01
C	448	15	1.1	382 14	AA002809	mg55e05.s1 Soares mus	6.84e-01	521	15	1.1	403 13	AA002809	mg55e05.s1 Soares mus	6.84e-01
C	449	15	1.1	383 21	FR0018699	F.rubripes GSS sequenc	1.65e+01	522	16	1.1	403 23	AA483396	Yz68b11.s1 Soares test	6.84e-01
C	450	15	1.1	383 13	N75409	za82d02.s1 Homo sapien	1.65e+01	523	15	1.1	404 13	N80524	Y91e07.r1 Homo sapien	6.84e-01
C	451	15	1.1	383 12	H58757	EST00052 Homo sapiens	6.84e-01	524	16	1.1	404 12	N30465	Yx48c05.r1 Homo sapien	1.65e+01
C	452	16	1.1	382 16	W86590	zn62e10.s1 Soares feta	1.65e+01	525	15	1.1	405 10	R55659	Y988b09.r1 Homo sapien	6.84e-01
C	453	15	1.1					526	16	1.1				

527	15	405 19	AA54702	EST62999 Jurkat T-cell	1.65e+01
528	15	405 11	R86003	Yp12c03.r1 Homo sapien	1.65e+01
529	16	406 19	AA413038	Yp2b03.r1 Beadlignon	6.84e-01
530	16	406 11	T24171	Cris15.Ricinus commun	6.84e-01
531	16	406 23	AA446007	Zw82h05.r1 Soares test	6.84e-01
532	16	406 15	AA146711	Zc35e10.r1 Stratagene	6.84e-01
533	15	406 15	W72390	Zd66h05.r1 Soares feta	1.65e+01
534	15	407 16	AA160391	Zo64b03.r1 Stratagene	1.65e+01
535	15	407 13	MG9887	Za68c05.r1 Homo sapien	6.84e-01
536	15	408 9	T94350	Yp35b12.r1 Homo sapien	1.65e+01
537	15	408 10	R33804	Yh78c10.r1 Homo sapien	1.65e+01
538	16	409 18	AA127416	Zn90h12.r1 Stratagene	6.84e-01
539	16	409 18	AA274499	Vb02b08.r1 Soares para	6.84e-01
540	16	409 11	H50024	Yp26c03.r1 Homo sapien	6.84e-01
541	15	409 20	G22920	human STS WI-13765.	1.65e+01
542	16	410 16	AA097319	mm36b08.r1 Stratagene	6.84e-01
543	16	410 23	AA466189	Vg88c12.r1 Barstead mo	6.84e-01
544	15	410 23	AA112687	Zn70c09.r1 Stratagene	1.65e+01
545	16	411 23	AA499144	Vt84h02.r1 Stratagene	6.84e-01
546	16	411 12	NA9281	Yv73a12.r1 Homo sapien	6.84e-01
547	15	411 10	W98762	MG95b09.r1 Soares para	1.65e+01
548	16	411 10	R07241	Yt14e04.r1 Homo sapien	6.84e-01
549	16	412 23	AA472305	Vh01d03.r1 Soares para	6.84e-01
550	16	412 12	C06600	similar to insulin 1.	1.65e+01
551	15	412 12	MG3392	Yr53b04.r1 Homo sapien	1.65e+01
552	16	412 13	N77808	Zb16a05.r1 Homo sapien	6.84e-01
553	15	412 14	AA051775	Mj54h12.r1 Soares para	1.65e+01
554	15	413 11	R94945	Yq44b02.r1 Homo sapien	1.65e+01
555	16	414 22	AA405645	Zw39e10.r1 Soares tota	6.84e-01
556	15	414 21	B59880	CIT-HSP-2014723.TR CIT	1.65e+01
557	15	414 14	N91428	Za16f04.r1 Soares feta	1.65e+01
558	15	414 14	W24110	Zb48f02.r1 Soares feta	1.65e+01
559	15	414 20	G21242	human STS WI-16237.	1.65e+01
560	16	415 22	C06513	similar to insulin 1.	6.84e-01
561	15	415 14	AA000503	mg23e03.r1 Soares para	1.65e+01
562	15	415 14	W18514	mb88e08.r1 Soares para	1.65e+01
563	16	416 21	B40238	Za65h12.r1 Soares feta	6.84e-01
564	16	416 10	R79893	HS-1051-R1-F12-WF.abi	6.84e-01
565	15	416 13	W35967	Yt85d01.r1 Homo sapien	6.84e-01
566	15	416 15	AA082169	mc58a12.r1 Soares para	1.65e+01
567	15	416 17	AA108602	Zn42g03.r1 Stratagene	6.84e-01
568	15	417 17	AA109977	EST036722 Mouse 7.5 dpc	1.65e+01
569	15	417 10	P56445	Yp50h11.r1 Homo sapien	1.65e+01
570	15	417 13	W44127	mc74b01.r1 Soares para	1.65e+01
571	15	417 16	AA061149	ml39g10.r1 Stratagene	6.84e-01
572	16	418 22	C06840	similar to insulin 1.	6.84e-01
573	16	419 19	AA010275	Zi08e07.r1 Soares feta	6.84e-01
574	16	419 23	AA444179	ve34a12.r1 KO mouse em	6.84e-01
575	16	420 10	R31674	Zc30a09.r1 Soares para	6.84e-01
576	16	420 10	AA015788	Yp63b09.r1 Homo sapien	1.65e+01
577	15	420 23	AA443069	aa83c03.r1 Stratagene	1.65e+01
578	15	421 22	C07149	Yt82g03.r1 Homo sapien	6.84e-01
579	16	421 22	H89808	Yt82g03.r1 Homo sapien	6.84e-01
580	16	421 22	C07149	similar to insulin 1.	1.65e+01
581	16	421 22	H89348	human STS SHGC-35222.	1.65e+01
582	15	421 20	G29779	Yw28c02.r1 Homo sapien	1.65e+01
583	15	421 12	H90800	Yh98f02.r1 Homo sapien	1.65e+01
584	15	421 10	R18056	Yg15c09.r1 Homo sapien	1.65e+01
585	15	422 10	R69218	Yi39h02.r1 Homo sapien	1.65e+01
586	16	423 23	AA512051	Yi43b02.r1 Stratagene	6.84e-01
587	16	423 12	N45385	Yw97c07.r1 Homo sapien	6.84e-01
588	15	423 16	AA189120	Zc47f06.r1 Stratagene	6.84e-01
589	16	423 19	AA009768	Zi04c03.r1 Soares feta	6.84e-01
590	16	423 15	W15307	Zo40h12.r1 Stratagene	1.65e+01
591	16	424 15	W15307	Zc19e12.r1 Soares para	6.84e-01
592	16	425 14	W41315	mc47g02.r1 Soares para	6.84e-01
593	16	425 14	C06514	similar to insulin 1.	6.84e-01
594	16	425 16	AA024089	mh96b12.r1 Soares para	6.84e-01
595	15	426 14	AA407759	EST02433 Mouse 7.5 dpc	1.65e+01
596	15	426 19	AA050122	mjl10f09.r1 Soares para	1.65e+01
597	15	427 16	HSPD89187	H.sapiens EST sequence	1.65e+01
598	15	427 16	AA187949	ZP75d02.r1 Stratagene	1.65e+01
599	16	427 21	B33306	HS-1017-A1-D02-MF.abi	6.84e-01

C	673	15	1.1	448 17	AA237687	mx29604.r1	Soares	mous	1.65e+01	746	15	1.1	467 13	N75449	za83a07.s1	Homo sapien	1.65e+01		
C	674	15	1.1	448 12	N34960	yy50c12.s1	Homo sapien	1.65e+01	747	16	1.1	468 17	AA265813	mz71d08.r1	Soares	mous	6.84e-01		
C	675	16	1.1	448 17	T98279	ye59f02.s1	Homo sapien	6.84e-01	748	15	1.1	468 12	H80390	yus5904.r1	Homo sapien	1.65e+01			
C	676	16	1.1	448 17	AA170275	ms82e11.r1	Soares	mous	6.84e-01	749	15	1.1	468 15	W79682	zd79g04.r1	Soares	feta	1.65e+01	
C	677	16	1.1	448 18	AA312749	ESR183435	Jurkat T-cell	6.84e-01	750	16	1.1	468 16	AA026394	ze92d04.s1	Soares	feta	6.84e-01		
C	678	15	1.1	448 21	B23356	F28317R	IGF Arabidop	1.65e+01	751	15	1.1	468 13	ATRS1725	A. thaliana	transcript	6.84e-01			
C	679	15	1.1	448 11	R93056	YQ13808.s1	Homo sapien	1.65e+01	752	16	1.1	469 13	N74136	za76e01.s1	Homo sapien	6.84e-01			
C	680	15	1.1	448 14	AA034623	m153605.r1	Soares	mous	6.84e-01	753	16	1.1	469 20	G30645	human SMS	SHGC-37694	6.84e-01		
C	681	16	1.1	449 23	AA469742	v170b04.r1	Bartstead	mo	6.84e-01	754	16	1.1	470 17	AA261657	mz87f11.r1	Soares	mous	6.84e-01	
C	682	16	1.1	449 9	T81634	YQ34807.r1	Homo sapien	6.84e-01	755	15	1.1	470 14	AA123438	mp91e07.r1	Soares	2NDM	6.84e-01		
C	683	16	1.1	449 12	H85673	ys68a03.r1	Homo sapien	6.84e-01	756	16	1.1	470 17	N94350	zb75g08.s1	Soares	sene	1.65e+01		
C	684	15	1.1	449 10	R61344	YH15A02.s1	Homo sapien	1.65e+01	757	15	1.1	470 14	AA015158	m163b05.r1	Soares	mous	1.65e+01		
C	685	15	1.1	450 12	N40785	Yw62s07.r1	Homo sapien	1.65e+01	758	15	1.1	470 23	R1CS2533A	Rice	cdNA, partial	seq	1.65e+01		
C	686	15	1.1	450 22	AA436147	ZV22B01.r1	Soares	NHMK	1.65e+01	759	15	1.1	471 17	AA250039	YX12B04.r1	Soares	mous	1.65e+01	
C	687	16	1.1	450 16	W70094	Zd49g05.s1	Soares	feta	6.84e-01	760	16	1.1	472 11	H49315	YQ21s09.r1	Homo sapien	6.84e-01		
C	688	16	1.1	450 9	T51613	Yb27h01.s1	Homo sapien	6.84e-01	761	16	1.1	473 12	H96810	YX17h09.s1	Homo sapien	6.84e-01			
C	689	15	1.1	450 11	T28595	ESR48706	Homo sapiens	1.65e+01	762	16	1.1	473 10	R544715	YJ78e10.r1	Homo sapien	6.84e-01			
C	690	15	1.1	450 16	AA039477	ZF05609.s1	Soares	feta	1.65e+01	763	15	1.1	473 22	AA442062	ZW63s04.s1	Soares	tota	1.65e+01	
C	691	15	1.1	450 21	B47562	CTT-HSP-669G4	TPB	CTT-	1.65e+01	764	16	1.1	474 15	AA061554	mJ91g07.r1	Soares	mous	6.84e-01	
C	692	15	1.1	451 17	AA108823	mp39h02.r1	Bartstead	MP	6.84e-01	765	15	1.1	474 12	H98761	YX13h10.s1	Homo sapien	1.65e+01		
C	693	16	1.1	451 12	H80132	YH15B08.s1	Homo sapien	6.84e-01	766	15	1.1	475 11	R94422	YQ42s08.r1	Homo sapien	1.65e+01			
C	694	15	1.1	451 15	AA016257	ze33c01.s1	Soares	retl	1.65e+01	767	15	1.1	475 17	AA232419	ZQ23B08.r1	Stratagene	1.65e+01		
C	695	16	1.1	452 22	C06788	similar	to	Insulin 1.	6.84e-01	768	15	1.1	476 11	H48370	YQ63e05.r1	Homo sapien	1.65e+01		
C	696	15	1.1	452 23	AA500137	V197b07.r1	Bartstead	mo	6.84e-01	769	15	1.1	476 15	W84467	Zd89g09.r1	Soares	feta	1.65e+01	
C	697	16	1.1	452 11	R88121	Yp08d08.r1	Homo sapien	1.65e+01	770	16	1.1	477 13	W07558	Za98g07.r1	Soares	feta	6.84e-01		
C	698	15	1.1	453 15	AA132935	ZQ22g04.s1	Stratagene	1.65e+01	771	16	1.1	477 14	W61737	md63g11.r1	Soares	mous	6.84e-01		
C	699	15	1.1	453 14	W76773	me84e06.r1	Soares	mous	1.65e+01	772	16	1.1	477 21	B43196	HS-1057-A2	MR	abi	6.84e-01	
C	700	15	1.1	453 14	AA030436	m124c11.r1	Soares	mous	1.65e+01	773	16	1.1	477 10	R31488	YJ75e09.r1	Homo sapien	1.65e+01		
C	701	15	1.1	453 13	N78217	YJ75a05.r1	Homo sapien	1.65e+01	774	15	1.1	477 22	C05299	Human Heart	CDNA, clon	6.84e-01			
C	702	15	1.1	453 12	H73247	Ys10f02.r1	Homo sapien	1.65e+01	775	16	1.1	478 9	T87522	YH89d09.r1	Homo sapien	1.65e+01			
C	703	16	1.1	454 17	AA047332	ZK69e04.s1	Soares	preg	1.65e+01	776	15	1.1	479 21	B58726	CTT-HSP-2013N10	TP	CTT	1.65e+01	
C	704	15	1.1	454 17	AA261641	V499b08.r1	Soares	preg	1.65e+01	777	15	1.1	480 15	W89417	mt80s04.r1	Soares	mous	1.65e+01	
C	705	16	1.1	454 15	W31375	ZB95e04.s1	Soares	para	6.84e-01	778	15	1.1	481 12	N34475	YJ13e07.s1	Homo sapien	1.65e+01		
C	706	16	1.1	455 16	N43256	SW31CA695SK	Brugia	mal	6.84e-01	779	15	1.1	481 19	AA114850	ZI03e09.s1	Soares	preg	1.65e+01	
C	707	15	1.1	455 17	AA259932	VAS3c04.r1	Soares	mous	1.65e+01	780	15	1.1	482 18	AA288288	Vb12c02.r1	Soares	mous	1.65e+01	
C	708	15	1.1	455 18	AA315609	ESR187589	Colon	carcin	1.65e+01	781	15	1.1	482 16	AA022498	ze70e07.s1	Soares	feta	1.65e+01	
C	709	15	1.1	457 17	AA260573	VX11a08.r1	Soares	preg	6.84e-01	782	15	1.1	482 16	AA159821	ZQ83a11.s1	Stratagene	6.84e-01		
C	710	16	1.1	457 19	AA129931	YI14e12.s1	Soares	preg	1.65e+01	783	15	1.1	482 11	B62572	YJ22f19TR	TAMU	Arabidop	6.84e-01	
C	711	16	1.1	457 9	T67438	ZI12a02.s1	Homo sapien	1.65e+01	784	16	1.1	482 11	H14668	YJ19e04.r1	Homo sapien	1.65e+01			
C	712	15	1.1	457 17	AA139361	RPJ1401CG	Rat	Myometri	1.65e+01	785	15	1.1	482 21	B28498	HS-1024-F2	G10	MR	abi	1.65e+01
C	713	15	1.1	458 22	AA433857	ZW1f02.r1	Soares	ovar	6.84e-01	786	15	1.1	482 21	B34573	ze43f10.r1	Soares	feta	1.65e+01	
C	714	15	1.1	459 16	AA169305	YQ34h02.s1	Stratagene	6.84e-01	787	15	1.1	483 14	W04965	mt44e02.r1	Soares	mous	1.65e+01		
C	715	16	1.1	460 14	AA049505	ZJ34h02.r1	Soares	mous	6.84e-01	788	15	1.1	483 16	N76361	YJ39b06.r1	Soares	feta	1.65e+01	
C	716	16	1.1	460 14	AA002058	ZH85a02.s1	Soares	feta	6.84e-01	789	15	1.1	484 14	N93309	YJ3h08.r1	Soares	mous	6.84e-01	
C	717	16	1.1	460 19	AA131876	ZI37d04.s1	Soares	preg	1.65e+01	790	15	1.1	484 15	AA059664	nm55b07.r1	Soares	mous	6.84e-01	
C	718	15	1.1	460 15	AA015969	ze30f12.r1	Soares	retl	1.65e+01	791	16	1.1	485 23	AA067637	ZX07a07.r1	Soares	tota	1.65e+01	
C	719	15	1.1	460 17	AA139618	mq40a06.r1	Bartstead	MP	1.65e+01	792	16	1.1	485 21	AA448943	mt05a11.r1	Soares	2NDM	6.84e-01	
C	720	15	1.1	460 16	W86627	ZH62b03.s1	Soares	feta	1.65e+01	793	15	1.1	485 17	AA116221	CTT-HSP-2014A20	TR	CTT	1.65e+01	
C	721	15	1.1	461 18	AA274968	Vb07b05.r1	Soares	mous	1.65e+01	794	15	1.1	485 17	AA049900	mt88a04.r1	Soares	mous	6.84e-01	
C	722	15	1.1	462 14	AA033501	m144c02.r1	Homo sapien	6.84e-01	795	16	1.1	486 16	AA049900	mt11f07.r1	Soares	mous	6.84e-01		
C	723	16	1.1	462 14	H22426	YH68f10.r1	Homo sapien	6.84e-01	796	15	1.1	486 22	C18868	Human placenta	CDNA 5'	6.84e-01			
C	724	16	1.1	462 21	B71196	CIT-HSP-228M10	TRF	CIT	1.65e+01	797	16	1.1	487 14	AA051735	YH81c04.r1	Homo sapien	1.65e+01		
C	725	15	1.1	463 21	AA460966	ZX63c01.s1	Soares	tota	1.65e+01	798	15	1.1	487 13	N57311	mt30c11.r1	Soares	mous	6.84e-01	
C	726	15	1.1	463 15	W48828	me49d04.r1	Soares	sene	6.84e-01	799	16	1.1	488 16	AA015243	Human placenta	CDNA 5'	6.84e-01		
C	727	15	1.1	463 15	W78544	YQ36c02.r1	Soares	mous	1.65e+01	800	16	1.1	489 15	AA049900	mt11f07.r1	Soares	mous	6.84e-01	
C	728	16	1.1	463 23	AA510362	m164b12.r1	Soares	mous	6.84e-01	801	15	1.1	490 14	W96940	mt88a04.r1	Soares	mous	6.84e-01	
C	729	16	1.1	463 14	AA014539	ms96c07.r1	Soares	mous	6.84e-01	802	15	1.1	490 14	AA287222	ZF20e08.r1	Soares	ovar	1.65e+01	
C	730	16	1.1	463 17	AA175581	crs337	R1citus	communi	6.84e-01	803	16	1.1	491 12	W82458	mt05s04.r1	Soares	mous	6.84e-01	
C	731	16	1.1	464 12	T14899	YX48b05.r1	Homo sapien	1.65e+01	804	16	1.1	491 12	H72771	YU04g10.s1	Homo sapien	1.65e+01			
C	732	16	1.1	464 12	N30457	Yp42e08.r1	Homo sapien	1.65e+01	805	16	1.1	491 12	C07167	ze94c10.s1	Soares	feta	1.65e+01		
C	733	15	1.1	465 11	H30337	mb74c02.r1	Soares	mous	1.65e+01	806	15	1.1	492 15	AA2029631	YX48a12.r1	Homo sapien	1.65e+01		
C	734	15	1.1	465 14	W17365	Z196c06.r1	Stratagene	1.65e+01	807	16	1.1	492 12	N35193	ZK61c06.r1	Soares	preg	1.65e+01		
C	735	15	1.1	465 15	AA059402	YQ18e09.r1	Homo sapien	6.84e-01	808	15	1.1	493 16	AA040610	mJ65c05.r1	Soares	mous	1.65e+01		
C	736	15	1.1	465 23	AA509397	VQ78e09.r1	Homo sapien	1.65e+01	809	15	1.1	493 14	AA049168	ZP93d09.s1	Stratagene	1.65e+01			
C	737	15	1.1	465 11	H30840	YQ18e10.r1	Soares	mous	6.84e-01	810	16	1.1	493 15	AA181154	mk17c10.r1	Soares	mous	1.65e+01	
C	738	15	1.1	466 23	AA461985	VY65a03.r1	Soares	mous	6.84e-01	811	15	1.1	493 16	AA097917	zr39a09.r1	Soares	NHMK	1.65e+01	
C	739	16	1.1	466 12	N34316	YJ52d11.s1	Homo sapien	1.65e+01	812	15	1.1	493 22	AA193287	YQ39g05.r1	Homo sapien	1.65e+01			
C	740	16	1.1	466 12	W68813	ZD37e01.r1	Soares	feta	1.65e+01	813	15	1.1	493 9	AA306692	ESR177630	Jurkat T-cell	6.84e-01		
C	741	15	1.1	466 10	R60021	YH12b04.s1	Homo sapien	1.65e+01	814	15	1.1	493 18	AA306692	RP01114118	TP	RP0111	6.84e-01		
C	742	15	1.1	466 11	H05709	YH16f11.r1	Homo sapien	1.65e+01	815	16	1.1	494 21	B49104	Vd95b01.r1	Soares	mous	1.65e+01		
C	743	15	1.1	466 16	W50230	ZH													

819	16	1.1	496.11	T14940	crs426	Ridicous communi	6.84e-01	C	892	15	1.1	510.18	AA272928	v44ia05.r1	Soares mous	1.65e+01
820	16	1.1	497.14	W30797	zb77f04.r1	Soares sene	6.84e-01	C	893	15	1.1	511.16	AA191442	z584g03.s1	Stratagene	1.65e+01
821	15	1.1	497.14	W66857	me45h10.r1	Soares mous	1.65e-01	C	894	15	1.1	514.16	AA160477	z49b00.r1	Stratagene	1.65e+01
822	15	1.1	497.14	R35324	y955b03.r1	Homo sapien	1.65e+01	C	895	15	1.1	544.11	T45170	8433 Arabidopsis thali	1.65e+01	
823	16	1.1	498.14	N94451	zb77f04.s1	Soares sene	6.84e-01	C	896	15	1.1	545.23	AA459101	v332f02.r1	Barstead mo	1.65e+01
824	16	1.1	499.12	AA6890	yf58b05.r1	Homo sapien	6.84e-01	C	897	15	1.1	546.23	AA445571	v610f09.r1	Barstead mo	1.65e+01
825	15	1.1	500.14	NA015039	m163h06.r1	Soares mous	1.65e+01	C	898	16	1.1	546.12	N40419	yf89f03.r1	Homo sapien	6.84e-01
826	15	1.1	501.12	N32510	yy11c06.s1	Homo sapien	1.65e+01	C	899	16	1.1	547.18	AA2772272	CT-HSP-34422.TVD CIT	Barstead mo	1.65e+01
827	15	1.1	502.11	H12032	ym16906.r1	Homo sapien	6.84e-01	C	900	15	1.1	550.21	B61300	v685e02.r1	Barstead mo	1.65e+01
828	15	1.1	502.23	AA318507	y01e02.r1	Barstead mo	1.65e+01	C	901	15	1.1	551.16	AA067191	123PBR TAMU Arabidops	1.65e+01	
829	15	1.1	503.12	H91914	ys81h03.r1	Homo sapien	6.84e-01	C	902	15	1.1	551.17	AA220909	24 Pinus radiata somat	6.84e-01	
830	16	1.1	504.22	AA067062	mm31c10.r1	Stratagene	1.65e+01	C	903	15	1.1	552.17	AA026359	ze24e12.r1	Soares feta	1.65e+01
831	15	1.1	504.18	AA444819	zwe2f02.r1	Soares tota	1.65e+01	C	904	15	1.1	553.23	AA529285	y135c02.r1	Homo sapien	6.84e-01
832	16	1.1	504.12	AA267095	m255e09.r1	Soares mous	6.84e-01	C	905	15	1.1	553.16	AA181352	ze24b06.s1	Homo sapien	6.84e-01
833	15	1.1	504.19	AA399028	zt33g12.r1	Soares mous	6.84e-01	C	906	16	1.1	554.15	W82320	m045f12.r1	Stratagene	6.84e-01
834	15	1.1	505.12	NS1369	yz16c07.r1	Soares test	1.65e+01	C	907	16	1.1	554.22	AA46966	zt72905.r1	Soares mous	6.84e-01
835	15	1.1	505.9	T74480	yc60d09.r1	Homo sapien	1.65e+01	C	908	16	1.1	554.15	AA001385	ze45c12.r1	Soares tota	6.84e-01
836	16	1.1	507.23	AA538298	v198e10.r1	Homo sapien	6.84e-01	C	909	16	1.1	555.15	AA001385	ze45c12.r1	Soares tota	6.84e-01
837	16	1.1	507.22	AA35128	ve19d10.r1	Barstead mo	6.84e-01	C	910	15	1.1	555.22	C07148	ze37e07.r1	Soares reti	1.65e+01
838	16	1.1	508.20	G24367	human sts	WT-14184.	6.84e-01	C	911	15	1.1	558.18	AA276068	yc30c10.r1	Soares sene	6.84e-01
839	16	1.1	508.9	T90448	y42e212.r1	Homo sapien	6.84e-01	C	912	16	1.1	558.18	AA276068	yc30c10.r1	Barstead MP	1.65e+01
840	15	1.1	508.11	H09248	y198b10.r1	Homo sapien	1.65e+01	C	913	16	1.1	558.9	T69001	yc31d09.r1	Homo sapien	1.65e+01
841	15	1.1	508.10	R32324	yn68e06.s1	Homo sapien	1.65e+01	C	914	15	1.1	558.18	AA276068	yc31d09.r1	Barstead MP	1.65e+01
842	15	1.1	509.15	AA151935	zc02a08.s1	Stratagene	1.65e+01	C	915	15	1.1	558.9	T69001	yc31d09.r1	Barstead MP	1.65e+01
843	15	1.1	509.19	AA016624	znu0d08.r1	Soares test	1.65e+01	C	916	15	1.1	558.9	T69001	yc31d09.r1	Barstead MP	1.65e+01
844	15	1.1	509.14	AA014532	m984f11.r1	Soares mous	1.65e+01	C	917	16	1.1	559.17	AA198437	me33b06.r1	Homo sapien	6.84e-01
845	16	1.1	509.16	AA027547	m16b03.r1	Soares mous	6.84e-01	C	918	16	1.1	559.17	AA198437	me33b06.r1	Barstead MP	1.65e+01
846	15	1.1	509.11	H15003	y166c09.r1	Homo sapien	1.65e+01	C	919	15	1.1	559.17	AA198437	me33b06.r1	Barstead MP	1.65e+01
847	16	1.1	510.13	W46095	mc78c03.r1	Soares mous	6.84e-01	C	920	15	1.1	559.17	AA198437	me33b06.r1	Barstead MP	1.65e+01
848	16	1.1	511.16	AA165058	zc93f10.r1	Stratagene	6.84e-01	C	921	15	1.1	559.17	AA198437	me33b06.r1	Barstead MP	1.65e+01
849	15	1.1	512.15	W93978	zc97h09.r1	Soares feta	1.65e+01	C	922	15	1.1	559.21	B59209	CIT-HSP-2012C1T	Barstead MP	1.65e+01
850	16	1.1	513.14	W62070	m884e06.r1	Soares mous	6.84e-01	C	923	16	1.1	570.17	AA224681	CIT-HSP-2012C1T	Barstead MP	1.65e+01
851	15	1.1	513.14	W62070	zh72d11.r1	Soares mous	6.84e-01	C	924	16	1.1	570.23	AA537116	v455a11.r1	Soares mous	6.84e-01
852	15	1.1	514.17	AA213013	m86e06.r1	Soares mous	1.65e+01	C	925	16	1.1	574.15	W73275	v455a11.r1	Soares mous	6.84e-01
853	15	1.1	514.17	AA234013	z550c08.r1	Soares Nhm	1.65e+01	C	926	16	1.1	574.15	W73275	v455a11.r1	Soares mous	6.84e-01
854	15	1.1	515.14	AA028291	m120d07.r1	Soares mous	1.65e+01	C	927	16	1.1	575.23	AA530694	v750b08.r1	Stratagene	6.84e-01
855	15	1.1	516.15	W92769	zc93e03.s1	Soares feta	1.65e+01	C	928	16	1.1	575.23	AA530694	v750b08.r1	Stratagene	6.84e-01
856	15	1.1	517.13	N57266	yw93h10.r1	Homo sapien	1.65e+01	C	929	16	1.1	575.23	AA530694	v750b08.r1	Stratagene	6.84e-01
857	16	1.1	518.18	AA315135	ES1187139	Coclon garcin	6.84e-01	C	930	16	1.1	587.13	W28120	v787d05.r1	Knowles Sol	6.84e-01
858	16	1.1	519.15	N76183	yz20e05.r1	Soares mult	6.84e-01	C	931	15	1.1	587.13	W28120	v787d05.r1	Knowles Sol	6.84e-01
859	16	1.1	519.15	AA082832	z24f11.r1	Stratagene	1.65e+01	C	932	16	1.1	589.21	T67929	yc25d01.r1	Soares sene	1.65e+01
860	15	1.1	520.16	AA161339	z24f0509.r1	Homo sapien	1.65e+01	C	933	16	1.1	589.21	T67929	yc25d01.r1	Soares sene	1.65e+01
861	15	1.1	521.12	H90995	yub8g07.r1	Homo sapien	1.65e+01	C	934	16	1.1	590.21	FR0024761	F.rubripes	GSS sequenc	6.84e-01
862	15	1.1	521.22	AA42263	y651h05.s1	Soares test	1.65e+01	C	935	15	1.1	592.21	FR0024762	F.rubripes	GSS sequenc	6.84e-01
863	15	1.1	521.22	N29718	yw78f06.s1	Homo sapien	1.65e+01	C	936	15	1.1	593.10	R77187	y165e07.r1	Homo sapien	1.65e+01
864	16	1.1	522.17	AA116574	mp98h09.r1	Soares 2Nhm	6.84e-01	C	937	15	1.1	594.6	HS292336	z815009.s1	Soares para	1.65e+01
865	15	1.1	522.17	W05742	za88d02.r1	Soares feta	1.65e+01	C	938	16	1.1	595.15	W84344	z889e07.s1	Soares feta	1.65e+01
866	15	1.1	523.23	AA530058	v15e07.r1	Barstead mo	1.65e+01	C	939	16	1.1	595.15	W84344	z889e07.s1	Soares feta	1.65e+01
867	16	1.1	524.21	BA14852	3439D1	WT-7894	6.84e-01	C	940	15	1.1	596.16	AA055652	mm43f03.r1	Life Tech m	6.84e-01
868	15	1.1	524.17	AA253596	CPB8T.178	PKR11nHSCP	1.65e+01	C	941	15	1.1	597.16	FR0022365	F.rubripes	GSS sequenc	1.65e+01
869	15	1.1	524.15	W58601	zdl9e12.s1	Soares feta	1.65e+01	C	942	15	1.1	597.16	W79980	yy71a02.r1	Soares feta	1.65e+01
870	16	1.1	525.23	C24391	Dictyostelium discoide	6.84e-01	C	943	15	1.1	597.16	W79980	yy71a02.r1	Soares feta	1.65e+01	
871	15	1.1	525.18	AA318256	EST20319	Retina II Hom	1.65e+01	C	944	15	1.1	608.21	AA163412	mi18b12.r1	Soares mous	6.84e-01
872	16	1.1	527.14	AA050519	m15h04.r1	Soares mous	6.84e-01	C	945	16	1.1	608.21	AA163412	mi18b12.r1	Soares mous	6.84e-01
873	15	1.1	527.16	AA065516	m171a07.r1	Stratagene	1.65e+01	C	946	16	1.1	606.21	FR0023431	v001s09.r1	Soares mous	6.84e-01
874	16	1.1	527.16	AA058525	z582e02.s1	Soares preg	6.84e-01	C	947	16	1.1	606.21	FR0023431	v001s09.r1	Soares mous	6.84e-01
875	16	1.1	529.35	W89561	mx79h12.r1	Soares mous	6.84e-01	C	948	16	1.1	607.17	AA163412	mi18b12.r1	Soares mous	6.84e-01
876	16	1.1	530.23	AA456283	z599h06.r1	Soares Nhm	1.65e+01	C	949	16	1.1	608.21	AA163412	mi18b12.r1	Soares mous	6.84e-01
877	15	1.1	530.15	AA104640	mo55c06.r1	Life Tech m	6.84e-01	C	950	16	1.1	612.14	AA273431	mi70c12.r1	Soares mous	6.84e-01
878	16	1.1	531.18	AA285959	yb83g01.r1	Soares mous	6.84e-01	C	951	15	1.1	612.14	AA273431	mi70c12.r1	Soares mous	6.84e-01
879	16	1.1	531.14	W98519	mg09e03.r1	Soares mous	6.84e-01	C	952	15	1.1	612.14	AA273431	mi70c12.r1	Soares mous	6.84e-01
880	16	1.1	531.14	W98519	mg09e03.r1	Soares mous	6.84e-01	C	953	15	1.1	612.14	AA273431	mi70c12.r1	Soares mous	6.84e-01
881	16	1.1	531.14	W98519	mg09e03.r1	Soares mous	6.84e-01	C	954	15	1.1	612.14	AA273431	mi70c12.r1	Soares mous	6.84e-01
882	16	1.1	531.23	AA448150	z882h05.r1	Soares test	1.65e+01	C	955	16	1.1	612.14	AA273431	mi70c12.r1	Soares mous	6.84e-01
883	15	1.1	531.20	G06748	human sts	WT-7894	6.84e-01	C	956	16	1.1	612.14	AA273431	mi70c12.r1	Soares mous	6.84e-01
884	16	1.1	532.23	AA462086	v72c12.r1	Soares mous	6.84e-01	C	957	16	1.1	612.14	AA273431	mi70c12.r1	Soares mous	6.84e-01
885	16	1.1	534.14	AA050554	m120f06.r1	Soares mous	6.84e-01	C	958	16	1.1	612.14	AA273431	mi70c12.r1	Soares mous	6.84e-01
886	15	1.1	534.9	T62804	yb99h05.r1	Homo sapien	1.65e+01	C	959	16	1.1	612.14	AA273431	mi70c12.r1	Soares mous	6.84e-01
887	15	1.1	536.12	N24430	yz26a09.r1	Homo sapien	1.65e+01	C	960	16	1.1	612.14	AA273431	mi70c12.r1	Soares mous	6.84e-01
888	16	1.1	537.20	AA473279	vc44d09.r1	Barstead MP	6.84e-01	C	961	16	1.1	612.14	AA273431	mi70c12.r1	Soares mous	6.84e-01
889	16	1.1	538.14	G22422	human sts	WT-30011.	1.65e+01	C	962	16	1.1	612.14	AA273431	mi70c12.r1	Soares mous	6.84e-01
890	15	1.1	539.14	W97422	mf95h06.r1	Soares mous	6.84e-01	C	963	16	1.1	612.14	AA273431	mi70c12.r1	Soares mous	6.84e-01
891	16	1.1	540.9	T79223	yc22d02.s1	Homo sapien	1.65e+01	C	964	16	1.1	6				

Query Match 1.7%; Score 24; DB 10; Length 183;
 Best Local Similarity 92.3%; Pred. No. 2.83e-15;
 Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 38 GAGCTGCTACACCCCTATGATCCTGGC 63
 1 |||||
 QY 915 GTCTGCTACACCCCTATGATCCTGGC 940

RESULT 3
 LOCUS AA317847 206 bp mRNA EST
 DEFINITION EST19840 Retina II Homo sapiens cDNA 5' end.
 ACCESSION AA317847
 NID 91970173
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryotes; Mitochondrial eukaryotes; Metazoa; Chordata;
 Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae;
 Homo.

REFERENCE 1 (bases 1 to 206)
 AUTHORS Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
 Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
 White,O., Sutton,G., Blake,J.A., Brandon,R.C., Mar'Ni,C.,
 Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Ene,L.D.,
 Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
 Glodet,A., Gnehm,C.B., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr.,
 Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
 Moreno-Palancas,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
 Phillips,C.A., Ryder,S.E., Scott,J.L., Sauter,D.M., Shirley,R.,
 Smali,K.V., Spriggs,T.A., Utechtack,T.R., Weidman,J.F., Li,Y.,
 Debnarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
 Dinko,D., Feng,D.F., Ferris,A., Fischer,C., Hastings,G.A.,
 He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P.P., Kim,A.K.,
 Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Weissner,P.S., Olsen,H.,
 Raymond,L., Wei,Y.F., Wang,J., Xu,C., Yu,G.L., Ruden,S.M.,
 Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
 Fraser,C.M., and Venter,J.C.
 Initial assessment of human gene diversity and expression patterns
 based upon 83 million nucleotides of cDNA sequence
 Nature 377 (6547 Suppl), 3-174 (1995)
 96026280

TITLE
 JOURNAL
 MEDLINE
 COMMENT

FEATURES
 source
 Contact: Kerlavage, AR
 Bioinformatics
 The Institute for Genomic Research
 9712 Medical Center Drive, Rockville, MD 20850 USA
 Tel: 3018699056
 Fax: 3018699423
 Email: atkerlav@tigr.org
 For clone availability, additional sequence and expression
 information related to this EST, please check the TIGR Human Gene
 Index (<http://www.tigr.org/tdb/hgi/hgi.html>)
 Seq primer: M13 Reverse.

Location/Qualifiers
 1..206
 /organism="Homo sapiens"
 /note="Organ: retina; Vector: pBluescript SK-; Site_1:
 EcoRI; Site_2: XhoI"
 /db_xref="ATCC (inhost):118310"
 /db_xref="taxon:9606"
 /clone_lib="Retina II"
 /sex="mixed"
 /dev_stage="adult"
 <1..>206
 mRNA
 BASE COUNT 50 a 48 c 65 g 41 t 2 others
 ORIGIN
 Query Match 1.3%; Score 18; DB 18; Length 206;
 Best Local Similarity 100.0%; Pred. No. 5.42e-04;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 48 CCTGTGAGAGGCTCTGGC 65
 1 |||||
 QY 1067 CCTGTGAGAGGCTCTGGC 1084

RESULT 4
 LOCUS AA000300 349 bp mRNA EST
 DEFINITION mg32a09.t1 Soares mouse embryo NCM3.5 14.5 Mus musculus cDNA
 clone 425464 5'.
 ACCESSION AA000300
 NID 91436166
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryotes; Mitochondrial eukaryotes; Metazoa; Chordata;
 Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
 Murinae; Mus.

REFERENCE 1 (bases 1 to 349)
 AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
 Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
 Schellenberg,K., Stepien,M., Tan,F., Underwood,K., Moore,B.,
 Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
 Waterston,R.
 The WashU-HMI Mouse EST Project
 Unpublished (1996)

TITLE
 JOURNAL
 MEDLINE
 COMMENT

FEATURES
 source
 Contact: Marra M/Mouse EST Project
 WashU-HMI Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@wustl.edu
 This clone is available royalty-free through LIND; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:260016
 Seq primer: EYPrimer
 High quality sequence stop: 343.

Location/Qualifiers
 1..349
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /note="Vector: p773D-Pac (Pharmacia) with a modified
 polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
 was primed with a Not I - oligo(dT) primer [5'
 TGTACCAATCTCAAGTGGAGCGCGCGGGAATTTTCTTTTCTTTT
 T 3'], on equal amounts of mRNA from 2 13.5dpc and 2
 14.5dpc embryos [total RNA provided by Minoru Ko, Wayne
 State Univ., from 2]; double-stranded cDNA was ligated to
 Eco RI adaptors (Pharmacia), digested with Not I and
 cloned into the Not I and Eco RI sites of the modified
 p773 vector. Library went through one round of
 normalization, and was constructed by Bento Soares and
 M. Fatima Bonaldo."
 /db_xref="taxon:10090"
 /clone_lib="Soares mouse embryo NCM3.5 14.5"
 /clone="425464"
 /sex="unknown"
 /tissue_type="embryo"
 /dev_stage="13.5-14.5dpc total fetus"
 /lab_host="DH10B"
 <1..>349
 mRNA
 BASE COUNT 70 a 119 c 82 g 78 t
 ORIGIN
 Query Match 1.3%; Score 18; DB 14; Length 349;
 Best Local Similarity 100.0%; Pred. No. 5.42e-04;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 289 GAGGAGATCCAGGCCCA 306
 1 |||||
 QY 211 GAGGAGATCCAGGCCCA 228

RESULT 5
LOCUS R04688 352 bp mRNA EST 31-MAR-1995
DEFINITION PK27e08.r1 Caenorhabditis briggsae cDNA.
ACCESSION R04688
NID 6754424
KEYWORDS EST.
SOURCE
Caenorhabditis briggsae library=Kuwabara Mixed stage C. briggsae strain=616 Gujarat vector=Lambda gt10 primer=Commercially available M13 reverse dye primer Rsitel=EcocRI Rsitel2=EcocRI Stage:mixed, Sex:hermaphrodite. Library construction: First strand oligo(dT) primed. Second strand was as per Gubler/Hofman. Ligated to EcocRI adaptors. Library is non-directional. Library is not-normalized. Library constructed by P.F. Kuwabara. Additional details on construction of the library are described in P.F. Kuwabara and S. Shah, NAR 22: 4414 - 4418 (1994). Adaptor sequence: GAATTC GGTGGTGGC.

ORGANISM
Caenorhabditis briggsae
Eukaryote; mitochondrial eukaryotes; eukaryote crown group; Metazoa/Eumycozia group; Metazoa; Eumetazoa; Bilateria; Pseudocoelomata; Nematoda; Secernentea; Rhabdillia; Rhabdillida; Rhabdillina; Rhabdilloidea; Rhabdillidae; Caenorhabditis.

REFERENCE
AUTHORS
1 (bases 1 to 352)
Hallier,T., Chappell,B., Chisoe,S., Clark,N., Couch,J., Duque,T., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Kuwabara,P., Le,M., Maridis,E., Marra,M., Parsons,J., Rikkin,L., Rohlfing,T., Tan,F., Trevisakis,E., Waterston,R., Wohldmann,P. and Wilson,R.
Washington University Caenorhabditis briggsae EST project
Unpublished (1995)
Other_ESTs: PK27e08.s1

TITLE
JOURNAL
COMMENT
Contact: Marra MA
Washington University Genome Sequencing Center
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1455
Fax: 314 286 1810
Email: mmarr@wustl.edu
PCR_F: TGTAAACGAGCGCAGTGAAGTTCAGCCGCG
PCR_R: CAGGAACAGCTATGACCTATGATGATTCCTCCAGGCTA
SOURCE: Washington University Genome Sequencing Center
PCR amplified DNA is available from Washington University Genome Sequencing Center. Aliquots of the library may be requested from P. Kuwabara (peke@mc-lmb.cam.ac.uk).

FEATURES
source
1..352
/organism="Caenorhabditis briggsae"
/strain="G16 Gujarat"

BASE COUNT
126 a 58 c 86 g 82 t

ORIGIN
Query Match 1.3%; Score 18; DB 10; Length 352;
Best Local Similarity 100.0%; Pred. No. 5.42e-04;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 161 AGACAATGATGATGAGA 178
|||||
Cp 918 AGACAATGATGATGAGA 901

RESULT 6
LOCUS AA366615 364 bp mRNA EST 21-APR-1997
DEFINITION EST17582 Pancreas tumor III Homo sapiens cDNA 5' end.
ACCESSION AA366615
NID 92018933
KEYWORDS EST.
SOURCE
human.
Homo sapiens
Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE
1 (bases 1 to 364)
Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Feldner,R.A.,

Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-ai,C., Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,E., Fine,L.D., Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S., Glodet,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr., Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M., Moreno-Palacios,R.F., McDonald,L.A., Nguyen,D.T., Peligrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shiley,R., Small,K.V., Spriggs,T.A., Uterback,T.R., Weisman,J.F., Li,Y., Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J., Dimke,D., Feng,D.-F., Ferris,A., Fischer,C., Hastings,G.A., He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L., Kusch,C., Hungjun,J., Li,H., Malesner,P.S., Olsen,H., Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillon,P.J., Fennon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.
Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
Nature 377 (6547 Suppl), 3-174 (1995)

TITLE
JOURNAL
MEDLINE
COMMENT
Other_ESTs: THC148243
Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3016999056
Fax: 3016999423
Email: arkerl@vtgtr.org
For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (<http://www.tigr.org/tdb/hgi/ngi.html>)
Seq primer: M13 Reverse

FEATURES
source
1..364
/organism="Homo sapiens"
/note="Organ: pancreas; Vector: pbluescript SK-; Site_1: EcocRI; Site_2: XhoI"
/db_xref="ATCC (inhost):1171283"
/db_xref="taxon:9606"
/clone_id="Pancreas tumor III"
/dev_stage="adult"
<1..>364

BASE COUNT
90 a 92 c 65 g 111 t 6 others

ORIGIN
Query Match 1.3%; Score 18; DB 19; Length 364;
Best Local Similarity 100.0%; Pred. No. 5.42e-04;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 228 CAGCTGCCCTCTCCAGCT 245
|||||
Qy 1102 CAGCTGCCCTCTCCAGCT 1119

RESULT 7
LOCUS C15712 374 bp mRNA EST 03-SEP-1996
DEFINITION Human fetal brain cDNA 5'-end GEN-159G10.
ACCESSION C15712
NID 91570419
KEYWORDS EST; EST(expressed sequence tag); Human fetal brain.
SOURCE
Homo sapiens
Homo sapiens fetus brain cDNA to mRNA, clone:159G10.
Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE
1 (sites)
Fujiiwara,T., Hirano,H., Hishigaki,H., Horie,M., Kawai,A., Kuga,Y., Kyushiki,H., Nagata,M., Okuno,S., Ozaki,K., Shimizu,F., Shimada,Y., Shimomiyu,H., Suzuki,M., Takachi,A., Takeda,S., Watanabe,T., Maekawa,H., Nakamura,Y. and Takashi,E.
Otsuka cDNA Project
Unpublished (1996)
2 (bases 1 to 374)


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/organism="Homo sapiens"
/note="Organ: Liver and Spleen; Vector: p773D (Pharmacia)
1st strand cDNA was primed with a Pac I - oligo(dT) primer
15' AACGGCAAGATTAATTAAGAGCTTTTCTTTTCTTTTCTTTTCTTTT
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Pac I and cloned into the Pac I
and Eco RI sites of the modified p773 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M.Patima Bonaldo."
/db_xref="taxon:9606"
/clone="247254"
/clone.lib="soares fetal liver spleen 1NF5"
/sex="male"
/dev_stage="20 week-post conception fetus"

```

D_b 291 AGCTGGAGAGGGCAGCTG 308
 |||||
 C_p 1119 AGCTGGAGAGGGCAGCTG 1202

Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and
Wilson,R.
The WashU-Merck EST Project
Unpublished (1995)

TITLE
JOURNAL
COMMENT

FEATURES
source
Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 426
Source: IMAGE Consortium, LINT
This clone is available royalty-free through LINT; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Location/Qualifiers
1..448
/organism="Homo sapiens"
/clone="301148"

BASE COUNT 120 a 96 c 119 g 112 t 1 others
ORIGIN

Query Match 1.3%; Score 18; DB 13; Length 448;
Best Local Similarity 100.0%; Pred. No. 5,42e-04;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 428 CCCACAGCAAGCTGCC 445
|||||
QY 1093 CCCACAGCAAGCTGCC 1110

RESULT 13
LOCUS AA218901 466 bp mRNA EST 07-FEB-1997
DEFINITION zgle05.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone
629792 3'.
ACCESSION AA218901
NID 91832967
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Eukaryotes; Metazoa; Chordata;
Vertebrata; Euthera; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 466)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Tan,F., Trevaskis,E.,
Waterston,R., Williamson,A., Wohlmann,P. and Wilson,R.
WashU-Merck EST Project
Unpublished (1995)

TITLE
JOURNAL
COMMENT
Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LINT; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Seq primer: 41m3 fwd. ET from Amersham
High quality sequence stop: 383.
Location/Qualifiers
1..466

FEATURES
source
/organism="Homo sapiens"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI; Cloned unidirectionally. Primer: Oligo dt. Pooled
retinal tissue. Average insert size: 1.0 kb; Uni-ZAP XR
Vector; ~5' adaptor sequence: 5' GAATTCGACACAG 3' ~3'
adaptor sequence: 5' CTCGAGTTTCTTTTCTTTT 3'."
/db_xref="taxon:9606"

BASE COUNT 154 a 94 c 85 g 133 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 5,42e-04;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 63 ATCTCCGACCTTGGT 80
|||||
CP 797 ATCTCCGACCTTGGT 780

RESULT 14
LOCUS AA407460 477 bp mRNA EST 02-MAY-1997
DEFINITION EST00811 Mouse 7.5 dpc embryo ectoplacental cone cDNA library Mus
musculus cDNA clone C0002H09 5'.
ACCESSION AA407460
NID 92065726
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Euthera; Rodentia; Sciurognathi; Muridae;
Murinae; Mus.
1 (bases 1 to 477)
Ko,M.S.H., Theat,T.A., Horton,T.H., Wang,X., Cui,Y., Wang,X.,
Pryor,E., Paris,J., Wells-Smith,T., Fujiwara,H., Yotsumoto,S. and
Nakashima,H.
Systematic analyses of mouse genes expressed in embryo implantation
site
Unpublished (1997)
Other_ESTS: EST00810
Contact: Ko MSH
Center for Molecular Medicine and Genetics
Wayne State University
5047 Gullen Hall, Detroit, MI 48202
Tel: 3135776708
Fax: 3135776700
Email: msx@cmb.biosci.wayne.edu
Seq primer: M3 Reverse

TITLE
JOURNAL
COMMENT
Location/Qualifiers
1..477
/organism="Mus musculus"
/strain="C57BL/6J"
/note="Vector: pSPORL (Life Technologies); Site_1: SalI;
Site_2: NotI; Total RNAs were extracted from ectoplacental
cone of 7.5-dpc embryos. The double-stranded cDNA was
synthesized from total RNAs with an Oligo(dt) primer. The
library was constructed by Minoru S. H. Ko."
/db_xref="taxon:10090"
/clone="C0002H09"
/clone_lib="Mouse 7.5 dpc embryo ectoplacental cone cDNA
library"
/sex="unknown"
/dev-stage="embryonic day 7.5 postconception"
/lab_host="DH10B"
1..477
139 c 108 g 116 t 21 others

BASE COUNT 93 a 139 c 108 g 116 t 21 others
ORIGIN

Query Match 1.3%; Score 18; DB 19; Length 477;
Best Local Similarity 100.0%; Pred. No. 5,42e-04;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 275 GAGGAGGCCAGGCCCTA 292
|||||
QY 211 GAGGAGGCCAGGCCCTA 228


```

RESULT 15
LOCUS B35459 491 bp DNA GSS 16-OCT-1997
DEFINITION HS-1029-A1-E02-MK.abi CIT Human Genomic Sperm Library C Homo
sapiens genomic clone Plate=CT808 Col=3 Row=I.
ACCESSION B35459
NTID 92534828
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 491)
Mahairas,G.G., Zackrone,K.D., Smith,T., Tipton,S., Schmidt,S.,
Traicoff,R., Abajian,C., Blanchard,A., West,A. and Hood,L.E.
Construction of a Characterized Clone Resource for Genomic
Sequencing: Generation and Preliminary Analysis of 20,000 Sequence
Tagged Connectors
JOURNAL Unpublished (1997)
COMMENT
Contact: Mahairas GG, Zackrone KD, Hood L
University of Washington
Seattle, WA 98195, USA
Tel: (206) 616-8774
Fax: (206) 685-7301
Email: kzackrone@u.washington.edu
Sequence Tagged Connector
Plate: CT808 row: I column: 3
Class: BAC ends
High quality sequence stop: 491.
Location/Qualifiers
FEATURES
source
1..491
/organism="Homo sapiens"
/note="Organ: Sperm; Vector: pBelBAC11; BAC Clones in
E-Coli DH10B"
/db_xref="taxon:9606"
/clone="Plate=CT808 Col=3 Row=I"
/clone_lib="CIT Human Genomic Sperm Library C"
/sex="M"
BASE COUNT 129 a 107 c 106 g 149 t
ORIGIN
Query Match 1.3%; Score 18; DB 21; Length 491;
Best Local Similarity 100.0%; Pred. No. 5.42e-04;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 209 ACCAAGTCAGGAGAGAT 226
|||||
QY 780 ACCAAGTCAGGAGAGAT 797

```

Search completed: Tue Apr 21 00:47:07 1998
 Job time : 1182 secs.

C	88	18	1.8	1317	21	MTN87847	Monkeypox virus strain	2.54e+01	C	161	17	1.7	6041	18	SCSPAC2	S. cerevisiae SPA2 gen	1.11e+02
C	89	18	1.8	1320	21	MTN87845	Monkeypox virus strain	2.54e+01	C	162	17	1.7	6450	19	TINARZRW	T. thermophilus natg, n	1.11e+02
C	90	18	1.8	1416	18	VW651	V.vinifera mRNA for cy	2.54e+01	C	163	17	1.7	11391	19	MPAE000037	Mycoplasma pneumoniae	1.11e+02
C	91	18	1.8	1801	18	SCYGL223C	S.cerevisiae chromosom	2.54e+01	C	164	17	1.7	11725	25	I05447	Sequence 13 from Patent	1.11e+02
C	92	18	1.8	1805	14	MUSL2D	Mus musculus Id gene,	2.54e+01	C	165	17	1.7	11725	25	I07993	Sequence 1 from Patent	1.11e+02
C	93	18	1.8	2051	15	CFGPCR1	Canis familiaris RDC1	2.54e+01	C	166	17	1.7	14293	17	PFSC03052	Plasmodium falciparum	1.11e+02
C	94	18	1.8	2380	15	S73493	hepatin cofactor II-p1	2.54e+01	C	167	17	1.7	17267	18	SCU43834	Saccharomyces cerevisi	1.11e+02
C	95	18	1.8	2258	15	RA5NANOCOT	Oryctolagus cuniculus	2.54e+01	C	168	17	1.7	20108	17	CEC0443	Caenorhabditis elegans	1.11e+02
C	96	18	1.8	2258	25	I11726	Sequence 1 from Patent	2.54e+01	C	169	17	1.7	22700	17	CEP3663	Caenorhabditis elegans	1.11e+02
C	97	18	1.8	2267	14	MUSGRHRA	Mouse gonadotropin-rel	2.54e+01	C	170	17	1.7	24709	17	CEC26H9A	Caenorhabditis elegans	1.11e+02
C	98	18	1.8	2346	15	CFU91844	Canis familiaris gluco	2.54e+01	C	171	17	1.7	25402	17	CELT28H11	Caenorhabditis elegans	1.11e+02
C	99	18	1.8	2443	16	XINUTCEOL	X.laevius mRNA for nucl	2.54e+01	C	172	17	1.7	25934	17	CELT05811	Caenorhabditis elegans	1.11e+02
C	100	18	1.8	2497	14	RRARBP2	Rat mRNA for zinc fing	2.54e+01	C	173	17	1.7	28736	17	CEMT0666	Caenorhabditis elegans	1.11e+02
C	101	18	1.8	3002	15	RABCTP7A	Rabbit cholesterol-7-a	2.54e+01	C	174	17	1.7	30190	17	CEK524	Caenorhabditis elegans	1.11e+02
C	102	18	1.8	3154	17	LMGCR2	L.migratoria gcr1 mRNA	2.54e+01	C	175	17	1.7	30563	17	CEJ2765	Caenorhabditis elegans	1.11e+02
C	103	18	1.8	3154	17	LMGCR2	L.migratoria gcr1 mRNA	2.54e+01	C	176	17	1.7	31628	17	CEJ22105	Caenorhabditis elegans	1.11e+02
C	104	18	1.8	3706	14	MUSGRHRA01	Mus musculus gonadotro	2.54e+01	C	177	17	1.7	32088	18	SC32KBP	S.cerevisiae 32kb DNA	1.11e+02
C	105	18	1.8	8809	17	DRODISABE	Drosophila melanogaste	2.54e+01	C	178	17	1.7	33490	17	CEZK20	Caenorhabditis elegans	1.11e+02
C	106	18	1.8	9470	19	PDU34346	Paracoccus denitrifica	2.54e+01	C	179	17	1.7	34576	26	CEMT01A9	Caenorhabditis elegans	1.11e+02
C	107	18	1.8	22847	16	SPAC13B11	S.pombe chromosome I c	2.54e+01	C	180	17	1.7	35959	17	CEMT02D3	Caenorhabditis elegans	1.11e+02
C	108	18	1.8	27016	17	CEP40E10	Caenorhabditis elegans	2.54e+01	C	181	17	1.7	36640	26	CEM02B4	Caenorhabditis elegans	1.11e+02
C	109	18	1.8	34197	17	CELR28F2	Caenorhabditis elegans	2.54e+01	C	182	17	1.7	37049	19	LMACEA	M.lepreae acea gene for	1.11e+02
C	110	18	1.8	39187	17	CELC01F1	Caenorhabditis elegans	2.54e+01	C	183	17	1.7	38734	19	SC10A5	Streptomyces coelicolo	1.11e+02
C	111	18	1.8	41452	17	CEB06F6	Caenorhabditis elegans	2.54e+01	C	184	17	1.7	41000	26	AC002085	S.cerevisiae chromosom	1.11e+02
C	112	18	1.8	44082	18	SPAC29A4	S.pombe chromosome I c	2.54e+01	C	185	17	1.7	43661	18	SCXCO5M83	Caenorhabditis elegans	1.11e+02
C	113	18	1.8	91979	18	ATAC002510	Arabidopsis thaliana c	2.54e+01	C	186	17	1.7	43849	17	CEP25B12	Caenorhabditis elegans	1.11e+02
C	114	18	1.8	187647	26	CEY16B4	Caenorhabditis elegans	2.54e+01	C	187	17	1.7	44512	26	HS36768	Human DNA sequence ***	1.11e+02
C	115	18	1.8	202028	26	CEY19D2	Caenorhabditis elegans	2.54e+01	C	188	17	1.7	448297	17	AC003701	Drosophila melanogaste	1.11e+02
C	116	17	1.7	27	25	I33193	Sequence 5 from patent	1.11e+02	C	189	17	1.7	49790	26	HS415C1	Human DNA sequence ***	1.11e+02
C	117	17	1.7	321	19	MYCRGS	Mycoplasma pneumoniae	1.11e+02	C	190	17	1.7	78844	18	AB006708	Arabidopsis thaliana g	1.11e+02
C	118	17	1.7	354	24	CP067928	Gavia porcellus mu-op1	1.11e+02	C	191	17	1.7	89779	18	AB005234	Arabidopsis thaliana g	1.11e+02
C	119	17	1.7	489	25	E04057	CDNA encoding human c	1.11e+02	C	192	17	1.7	100145	26	AC003104	*** SEQUENCING IN PROG	1.11e+02
C	120	17	1.7	678	18	SC026257	Saccharomyces cerevisi	1.11e+02	C	193	17	1.7	100145	26	AC003104	Caenorhabditis elegans	1.11e+02
C	121	17	1.7	708	18	OSU17900	Orf10myes sp. cyclop	1.11e+02	C	194	17	1.7	100177	26	CEY55D9	Human DNA sequence ***	1.11e+02
C	122	17	1.7	851	17	LCU03760	Ustilidia cuprina chymot	1.11e+02	C	195	17	1.7	114747	26	HS422H11	Human DNA sequence ***	1.11e+02
C	123	17	1.7	954	16	IC0RDE	Ictalurus punctatus DN	1.11e+02	C	196	17	1.7	128000	26	AC004046	*** SEQUENCING IN PROG	1.11e+02
C	124	17	1.7	1084	19	TPPSAZURN	T.pantotropa mRNA for	1.11e+02	C	197	17	1.7	137357	26	AC003003	*** SEQUENCING IN PROG	1.11e+02
C	125	17	1.7	1154	19	ACCA61C	Acinetobacter haemolyt	1.11e+02	C	198	17	1.7	137404	26	AC002375	Homo sapiens: HTGS pha	1.11e+02
C	126	17	1.7	1215	15	OCPP1A	Rabbit mRNA for type-1	1.11e+02	C	199	17	1.7	140000	26	AC004047	*** SEQUENCING IN PROG	1.11e+02
C	127	17	1.7	1252	15	BTIN1LK6P	B.taurus DNA for Inter	1.11e+02	C	200	17	1.7	159877	26	HS217C2	Human DNA sequence ***	1.11e+02
C	128	17	1.7	1291	16	X1CALR	X.laevius mRNA for calr	1.11e+02	C	201	17	1.7	169646	26	AC004019	*** SEQUENCING IN PROG	1.11e+02
C	129	17	1.7	1293	14	ATHECK2B	Arabidopsis thaliana m	1.11e+02	C	202	17	1.7	171097	26	HS471M3	Human DNA sequence ***	1.11e+02
C	130	17	1.7	1346	18	AGGLN1	A.glutinosa mRNA for g	1.11e+02	C	203	17	1.7	176781	26	AC002989	*** SEQUENCING IN PROG	1.11e+02
C	131	17	1.7	1349	15	OCPP1A	Rabbit mRNA for type-1	1.11e+02	C	204	17	1.7	188833	26	AC004125	*** SEQUENCING IN PROG	1.11e+02
C	132	17	1.7	1353	18	PVGSR2	Phaseolus vulgaris mRN	1.11e+02	C	205	17	1.7	216371	26	AC002549	Homo sapiens: HTGS pha	1.11e+02
C	133	17	1.7	1369	18	ATU12858	Arabidopsis thaliana c	1.11e+02	C	206	17	1.7	220709	26	AC002268	*** SEQUENCING IN PROG	1.11e+02
C	134	17	1.7	1458	16	DRAJ1596	Danio rerio mRNA for c	1.11e+02	C	207	17	1.7	250611	14	MMAE000663	Mus musculus TOR beta	1.11e+02
C	135	17	1.7	1492	15	OCPP1	Rabbit mRNA for ptecl	1.11e+02	C	208	17	1.7	252128	26	CEY18D10	Caenorhabditis elegans	1.11e+02
C	136	17	1.7	1532	14	MSM2G09	Mus musculus single-mi	1.11e+02	C	209	17	1.7	261012	26	HS343C1	Human DNA sequence ***	1.11e+02
C	137	17	1.7	1538	14	RNU36898	Rattus norvegicus puta	1.11e+02	C	210	17	1.7	320751	26	AC003978	Homo sapiens: HTGS pha	1.11e+02
C	138	17	1.7	1651	14	AF000236	Mus musculus RDC1 orph	1.11e+02	C	211	16	1.6	31	25	I62294	Sequence 1 from patent	4.48e+02
C	139	17	1.7	2012	14	MAA02271	Mus musculus mRNA for	1.11e+02	C	212	16	1.6	54	25	AI2890	Nucleotide sequence 6	4.48e+02
C	140	17	1.7	2020	18	SCYUR011C	S.cerevisiae chromosom	1.11e+02	C	213	16	1.6	75	25	AY07526	Nucleotide sequence 6	4.48e+02
C	141	17	1.7	2399	18	CCU25129	Cochliobolus carbosom	1.11e+02	C	214	16	1.6	84	25	SYN1NSP1	Rat insulin-I gene sig	4.48e+02
C	142	17	1.7	2564	15	SSU22108	Sus scrofa g probe-2	1.11e+02	C	215	16	1.6	90	25	I49638	Sequence 5 from patent	4.48e+02
C	143	17	1.7	2654	16	AF026039	Xenopus laevis pphb2-t	1.11e+02	C	216	16	1.6	112	21	E00026	DNA coding of insulin	4.48e+02
C	144	17	1.7	2837	26	AC003913	*** SEQUENCING IN PROG	1.11e+02	C	217	16	1.6	112	21	ACBPB82	avian erythroblastosis	4.48e+02
C	145	17	1.7	2914	14	RATMS1M6T	Mouse mRNA for m51m,	1.11e+02	C	218	16	1.6	128	25	A07535	Nucleotide sequence 16	4.48e+02
C	146	17	1.7	2987	14	RATLSYSHX	Rattus norvegicus l5y	1.11e+02	C	219	16	1.6	171	23	SYNDUM1NA	Synthetic human insul	4.48e+02
C	147	17	1.7	3071	14	MSA2554	Mus musculus sim trans	1.11e+02	C	220	16	1.6	181	16	E09184	Synthetic DNA sequence	4.48e+02
C	148	17	1.7	3113	19	MESARG	M.barkeri argininosucc	1.11e+02	C	221	16	1.6	187	16	SAVFOK3	S.leucomenis leucomae	4.48e+02
C	149	17	1.7	3120	14	MMJ000262	Mus musculus mRNA for	1.11e+02	C	222	16	1.6	187	16	SAVFOK10	S.leucomenis leucomae	4.48e+02
C	150	17	1.7	3213	18	ATHHSP81	A.thaliana HSP81-1 gen	1.11e+02	C	223	16	1.6	191	16	SAVFOK6	S.leucomenis leucomae	4.48e+02
C	151	17	1.7	3314	21	U23770	Murine adenovirus type	1.11e+02	C	224	16	1.6	206	16	SAVFOK1	S.leucomenis leucomae	4.48e+02
C	152	17	1.7	3336	17	LCU75355	Drosophila cuprina ecyst	1.11e+02	C	225	16	1.6	221	18	SCU21484	Schizophyllum commune	4.48e+02
C	153	17	1.7	3565	17	DMAC544	Drosophila melanogaste	1.11e+02	C	226	16	1.6	221	18	SCU21485	Schizophyllum commune	4.48e+02
C	154	17	1.7	3614	14	D64135	Mus musculus Slm2 mRNA	1.11e+02	C	227	16	1.6	222	18	SCU21485	Schizophyllum commune	4.48e+02
C	155	17	1.7	3957	18	SPURF4	S.pombe (972 h-) DNA f	1.11e+02	C	228	16	1.6	246	18	EAR80L	Arabidopsis thaliana p	4.48e+02
C	156	17	1.7	3957	18	YSPHPR	Schizosaccharomyces po	1.11e+02	C	229	16	1.6	252	18	S78910	Equisetum arvense pol	4.48e+02
C	157	17	1.7	3969	18	SCYUR010W	S.cerevisiae chromosom	1.11e+02	C	230	16	1.6	270	25	I71933	[M1 element insertion	4.48e+02
C	158	17	1.7	3959	18	MMU40576	Mus musculus single-mi	1.11e+02	C	231	16	1.6	273	25	I00910	Sequence 2 from Patent	4.48e+02
C	159	17	1.7	5354	18	SCYLL021M	S.cerevisiae chromosom	1.11e+02	C	232	16	1.6	273	25	I00910	Sequence 2 from Patent	4.48e+02
C	160	17	1.7	6031	17	DMPOSTSX	D.melanogaster mRNA fo	1.11e+02	C	233	16	1.6	273	25	E00074	DNA sequence of human-	4.48e+02

234	16	1.6	277 23	ARHSINS	Artificial gene for hu	4.48e+02	307	16	1.6	1797 14	MUSSTR3A	Mouse somatostatin rec	4.48e+02
235	16	1.6	286 23	SYNINSGSA	Synthetic human protins	4.48e+02	308	16	1.6	1813 14	AF022743	Rattus norvegicus thro	4.48e+02
236	16	1.6	295 18	YSC-187	Yeast (S.cerevisiae) 1	4.48e+02	309	16	1.6	1832 18	SCRIS3G	Yeast h3s3 gene for im	4.48e+02
237	16	1.6	300 16	YSC-187	S.cerevisiae imidazole	4.48e+02	310	16	1.6	1836 18	CACCEI2	Cannum mRNA for endo	4.48e+02
238	16	1.6	351 23	SYNINSGS	Human (synthetic) insu	4.48e+02	311	16	1.6	1842 18	ATGSKPFI	A.thaliana mRNA for 65	4.48e+02
239	16	1.6	353 25	E00001	DNA coding of rat pro-	4.48e+02	312	16	1.6	1914 17	SEI8SRKN	S.elegans gene encodin	4.48e+02
240	16	1.6	354 25	I03587	Sequence 3 from patent	4.48e+02	313	16	1.6	1920 18	SYCOER440	Synechocystis sp. ORF4	4.48e+02
241	16	1.6	354 25	I02834	Sequence 1 from patent	4.48e+02	314	16	1.6	1945 17	CEU61236	Caenorhabditis elegans	4.48e+02
242	16	1.6	378 16	PIHNT1A	Pituitary melanoleucus	4.48e+02	315	16	1.6	1946 14	MMU79774	Mus musculus NMP-1 var	4.48e+02
243	16	1.6	405 16	S79054	Pl anti-gen-1-truncated	4.48e+02	316	16	1.6	1995 15	SALACCD	Staphylococcus aureus	4.48e+02
244	16	1.6	409 21	ALVERBBA	Avian leukosis virus (4.48e+02	317	16	1.6	2028 25	I08037	Sequence 3 from patent	4.48e+02
245	16	1.6	480 25	A40255	Sequence 5 from patent	4.48e+02	318	16	1.6	2067 21	MEHNF3G	M.musculus HNF-3gamma	4.48e+02
246	16	1.6	481 16	FR095622	Fugu rubripes hydroxyb	4.48e+02	319	16	1.6	2091 21	ACBNERB8H	Avian erythroblastosis	4.48e+02
247	16	1.6	483 14	MMU58202	Mus musculus ISG15 gen	4.48e+02	320	16	1.6	2141 15	S48813	Beta-adrenergic recept	4.48e+02
248	16	1.6	495 16	CHKEBB	Chicken erbB gene (hom	4.48e+02	321	16	1.6	2178 19	BACPHOAI	B.licheniformis Aprase	4.48e+02
249	16	1.6	498 15	OC092804	Oryctolagus cuniculus	4.48e+02	322	16	1.6	2187 15	OMAG3159	Oncorhynchus mykiss mR	4.48e+02
250	16	1.6	503 16	CCALPHAB	C.coccitlax mRNA for al	4.48e+02	323	16	1.6	2198 16	KMAJ76	Kluiveromyces marxianu	4.48e+02
251	16	1.6	526 16	GGAGL1	Messenger RNA for a ne	4.48e+02	324	16	1.6	2208 21	S69372	...eny (Rous Associa	4.48e+02
252	16	1.6	526 16	CHKEBAM	Chicken alpha-globin m	4.48e+02	325	16	1.6	2242 14	MMMDLPA3	M.musculus mRNA for M-	4.48e+02
253	16	1.6	530 16	AF019707	Melagris gallopavo m	4.48e+02	326	16	1.6	2280 16	XLU12588	Xenopus laevis protein	4.48e+02
254	16	1.6	542 16	GGAGLS	Chicken messenger RNA	4.48e+02	327	16	1.6	2337 18	AF030290	Arabidopsis thaliana p	4.48e+02
255	16	1.6	542 16	CHKEBAA	Chicken hemoglobin alp	4.48e+02	328	16	1.6	2340 14	CPH84488	Cavia porcellus transm	4.48e+02
256	16	1.6	545 16	AF019708	Melagris gallopavo m	4.48e+02	329	16	1.6	2356 14	MUSK12F	Mus musculus zinc finy	4.48e+02
257	16	1.6	567 25	E08479	gDNA encoding phosphol	4.48e+02	330	16	1.6	2360 16	ISCDAP7A	Saccharomyces cerevisi	4.48e+02
258	16	1.6	607 14	RATINS1A	Rat insulin 1 gene, ex	4.48e+02	331	16	1.6	2431 19	S57688	slr Operon: rpsG-rbos	4.48e+02
259	16	1.6	721 14	RATINS1	Rat gene for insulin (4.48e+02	332	16	1.6	2491 14	AF044676	Cricetulus griseus gin	4.48e+02
260	16	1.6	728 14	MMIRP	Mus musculus mRNA inte	4.48e+02	333	16	1.6	2520 14	MM84012	Mus musculus hippocamp	4.48e+02
261	16	1.6	822 25	E07985	DNA encoding floral bu	4.48e+02	334	16	1.6	2545 16	AF044676	Trichoderma harzianum	4.48e+02
262	16	1.6	892 21	REAEV3TR	Avian erythroblastosis	4.48e+02	335	16	1.6	2632 25	E01922	DNA encoding catalase	4.48e+02
263	16	1.6	900 17	DMNINAP	Drosophila melanogaste	4.48e+02	336	16	1.6	2632 25	E01922	C.vividdissima CREB gen	4.48e+02
264	16	1.6	924 17	DD06370	Dictyostelium discoid	4.48e+02	337	16	1.6	2632 25	E01922	C.vividdissima CREB gen	4.48e+02
265	16	1.6	976 25	I32609	Sequence 8 from patent	4.48e+02	338	16	1.6	2632 25	E01922	Mus musculus gene for	4.48e+02
266	16	1.6	976 25	I32609	Sequence 7 from patent	4.48e+02	339	16	1.6	2632 25	E01922	S.cerevisiae tRNA-Val,	4.48e+02
267	16	1.6	1049 19	ACCAC61H	Acinetobacter baumann	4.48e+02	340	16	1.6	2632 25	E01922	Mouse mRNA for mutine	4.48e+02
268	16	1.6	1107 15	BOVSOMREC	Bos taurus somatostat	4.48e+02	341	16	1.6	2632 25	E01922	P.subcordiformis mtoc	4.48e+02
269	16	1.6	1107 15	BOVSOMREC	Bos taurus somatostat	4.48e+02	342	16	1.6	2632 25	E01922	Drosophila hyaeli 28S r	4.48e+02
270	16	1.6	1112 19	BCU89504	Burkholderia cepacia, p	4.48e+02	343	16	1.6	2632 25	E01922	Rat fatty acid synthet	4.48e+02
271	16	1.6	1149 15	OMU14109	Ovis aries Mel-1a mela	4.48e+02	344	16	1.6	2632 25	E01922	*** SEQUENCING IN PROG	4.48e+02
272	16	1.6	1173 14	RNKTR62	R.norvegicus mRNA for	4.48e+02	345	16	1.6	2632 25	E01922	*** SEQUENCING IN PROG	4.48e+02
273	16	1.6	1179 15	AF006262	Oryctolagus cuniculus	4.48e+02	346	16	1.6	2632 25	E01922	Rattus norvegicus gona	4.48e+02
274	16	1.6	1216 16	CHKEBADA2	Chicken alpha-globin g	4.48e+02	347	16	1.6	2632 25	E01922	S.cerevisiae chromoso	4.48e+02
275	16	1.6	1216 16	GGG103	Gallus gallus gene enc	4.48e+02	348	16	1.6	2632 25	E01922	Candida tropicalis cat	4.48e+02
276	16	1.6	1218 17	TC092486	Trypanosoma cruzi Ap-e	4.48e+02	349	16	1.6	2632 25	E01922	Sequence 5 from patent	4.48e+02
277	16	1.6	1226 18	RICRIT1A1	Oryza sativa transcrip	4.48e+02	350	16	1.6	2632 25	E01922	Sequence 7 from patent	4.48e+02
278	16	1.6	1230 14	SCYU1035C	S.cerevisiae chromoso	4.48e+02	351	16	1.6	2632 25	E01922	Mouse mRNA for amyloid	4.48e+02
279	16	1.6	1234 14	MMMACR	M.musculus mRNA for ma	4.48e+02	352	16	1.6	2632 25	E01922	Plasmodium falciparum	4.48e+02
280	16	1.6	1251 18	YSCDPA13	Human gila-derived neu	4.48e+02	353	16	1.6	2632 25	E01922	Mouse mRNA for amyloid	4.48e+02
281	16	1.6	1260 25	E01330	H.sapiens mRNA for gila	4.48e+02	354	16	1.6	2632 25	E01922	Avian erythroblastosis	4.48e+02
282	16	1.6	1260 25	E01330	H.sapiens mRNA for gila	4.48e+02	355	16	1.6	2632 25	E01922	S.tuberosum mRNA for s	4.48e+02
283	16	1.6	1280 19	CLOCCE1A	C.thermocellum celc ge	4.48e+02	356	16	1.6	2632 25	E01922	Sequence 1 from patent	4.48e+02
284	16	1.6	1290 14	RN044897	Rattus norvegicus ATP-	4.48e+02	357	16	1.6	2632 25	E01922	C.elegans mRNA for DNA	4.48e+02
285	16	1.6	1296 15	OCADH1A	O.cuniculus Adhl mRNA	4.48e+02	358	16	1.6	2632 25	E01922	G.domestis mRNA for	4.48e+02
286	16	1.6	1349 18	APPROPHOB	A.thaliana protein pho	4.48e+02	359	16	1.6	2632 25	E01922	Rat mRNA for ATP-sensi	4.48e+02
287	16	1.6	1351 25	I13404	Sequence 5 from patent	4.48e+02	360	16	1.6	2632 25	E01922	S.cerevisiae SMI1 gene	4.48e+02
288	16	1.6	1351 25	AF038995	Mus musculus putative	4.48e+02	361	16	1.6	2632 25	E01922	S.cerevisiae chromoso	4.48e+02
289	16	1.6	1415 15	DOGCB	Dog brain creatine kin	4.48e+02	362	16	1.6	2632 25	E01922	Drosophila melanogaste	4.48e+02
290	16	1.6	1457 16	GGSP1RFA	G.gallus mRNA for Spl-	4.48e+02	363	16	1.6	2632 25	E01922	Mouse mRNA for amyloid	4.48e+02
291	16	1.6	1482 14	D61687	Rattus norvegicus mRNA	4.48e+02	364	16	1.6	2632 25	E01922	Avian erythroblastosis	4.48e+02
292	16	1.6	1486 14	MUSIRKCA	Mouse mRNA for inward	4.48e+02	365	16	1.6	2632 25	E01922	S.tuberosum mRNA for s	4.48e+02
293	16	1.6	1499 19	CLOC307	C.thermocellum celc307	4.48e+02	366	16	1.6	2632 25	E01922	Sequence 1 from patent	4.48e+02
294	16	1.6	1518 25	I33192	Sequence 3 from patent	4.48e+02	367	16	1.6	2632 25	E01922	C.elegans mRNA for DNA	4.48e+02
295	16	1.6	1526 14	MMU73626	Mus musculus ATP-sensi	4.48e+02	368	16	1.6	2632 25	E01922	Rat mRNA for ATP-sensi	4.48e+02
296	16	1.6	1602 14	AF020773	Mus musculus impotin	4.48e+02	369	16	1.6	2632 25	E01922	S.cerevisiae SMI1 gene	4.48e+02
297	16	1.6	1643 18	YSACATPO	C.tropicalis peroxisom	4.48e+02	370	16	1.6	2632 25	E01922	S.cerevisiae chromoso	4.48e+02
298	16	1.6	1665 14	RN090121	Rattus norvegicus thro	4.48e+02	371	16	1.6	2632 25	E01922	Sequence 3 from patent	4.48e+02
299	16	1.6	1680 21	REAEV34E	Caenorhabditis elegans	4.48e+02	372	16	1.6	2632 25	E01922	M.musculus HNF-3gamma	4.48e+02
300	16	1.6	1727 17	CEUF2582	D.suboscurea scute gen	4.48e+02	373	16	1.6	2632 25	E01922	Avian erythroblastosis	4.48e+02
301	16	1.6	1742 17	DSCCUTB	Horse alcohol dehydrog	4.48e+02	374	16	1.6	2632 25	E01922	Beta-adrenergic recept	4.48e+02
302	16	1.6	1761 15	HRASD8H	Hsae scrofa mRNA for C-	4.48e+02	375	16	1.6	2632 25	E01922	Oncorhynchus mykiss mR	4.48e+02
303	16	1.6	1762 15	AB005545	Sus scrofa mRNA for C-	4.48e+02	376	16	1.6	2632 25	E01922	Kluiveromyces marxianu	4.48e+02
304	16	1.6	1770 16	ORZALAR	Oryzias latipes alphas	4.48e+02	377	16	1.6	2632 25	E01922	...eny (Rous Associa	4.48e+02
305	16	1.6	1788 21	ACVERBBA	Avian erythroblastosis	4.48e+02	378	16	1.6	2632 25	E01922	M.musculus mRNA for M-	4.48e+02
306	16	1.6	1796 25	I13407	Sequence 11 from paten	4.48e+02	379	16	1.6	2632 25	E01922	Xenopus laevis protein	4.48e+02

380	15	3947 19	MBU77466	Mycobacterium bovis BC	4.48e+02	453	15	13045 21	GHU17705	Callit d herpesvirus 1 i	4.48e+02
381	16	3985 14	RNCPROCR	R.norvegicus mRNA for	4.48e+02	454	16	13143 19	U67563	Methanococcus jannasch	4.48e+02
382	16	4076 21	BVDP126	Bovine viral diarrhoea	4.48e+02	455	16	13305 15	U67588	Methanococcus jannasch	4.48e+02
383	16	4082 18	ADCPH2E	A. capillus-venereis L.	4.48e+02	456	16	13332 17	DDID16466	Cellular slime mold M1	4.48e+02
384	16	4117 14	RNAJ696	Rattus norvegicus mRNA	4.48e+02	457	16	13548 19	D90858	E.coli genomic DNA, Ko	4.48e+02
385	16	4224 17	DM5HT26	D.melanogaster mRNA fo	4.48e+02	458	16	14011 17	CER26G10	Caenorhabditis elegans	4.48e+02
386	16	4235 19	ECU58768	Escherichia coli ela 1	4.48e+02	459	16	15212 19	D90795	E.coli genomic DNA, Ko	4.48e+02
387	16	4260 17	D38159	Bombyx mori mRNA for x	4.48e+02	460	16	15495 19	U93694	Mycoplasma genitalium	4.48e+02
388	16	4304 14	MAK1N1	M.musculus mRNA for ki	4.48e+02	461	16	15598 16	GAIRPA2MR	G.gallus mRNA for LRP/	4.48e+02
389	16	4305 19	STKPTF	S.mutans fructosyltran	4.48e+02	462	16	15676 19	D90857	E.coli genomic DNA, Ko	4.48e+02
390	16	4314 17	AF017084	Hirudo medicinalis rec	4.48e+02	463	16	15827 23	CV013189	Cloning vector pVACneo	4.48e+02
391	16	4443 23	PRS303	Yeast integrative vect	4.48e+02	464	16	16383 19	D90794	E.coli genomic DNA, Ko	4.48e+02
392	16	4456 23	PRS403	Yeast integrative vect	4.48e+02	465	16	16383 19	D90794	E.coli genomic DNA, Ko	4.48e+02
393	16	4461 17	GGAAD	Chicken alpha-A and al	4.48e+02	466	16	19024 14	CER39H11	Caenorhabditis elegans	4.48e+02
394	16	4481 16	PSC03060	Plasmidum falciparum	4.48e+02	467	16	19515 17	CER05F1A	Caenorhabditis elegans	4.48e+02
395	16	4484 19	ECU23775	Escherichia coli GalP	4.48e+02	468	16	20159 26	AC003666	Homo sapiens, HT6s p1a	4.48e+02
396	16	4495 17	DM037018	Drosophila melanogaste	4.48e+02	469	16	21115 17	AB005911	Bombyx mori DNA for xa	4.48e+02
397	16	4667 23	PRS313	Yeast centromere vecto	4.48e+02	470	16	22245 17	CER27E9	Caenorhabditis elegans	4.48e+02
398	16	4670 23	PRS413	Yeast centromere vecto	4.48e+02	471	16	23713 14	RNFASNA	R.norvegicus FAS gene	4.48e+02
399	16	5038 18	SCYJ106W	S.cerevisiae chromosom	4.48e+02	472	16	23738 17	CER08H9	Caenorhabditis elegans	4.48e+02
400	16	5365 17	CEYJ3C74L	Caenorhabditis elegans	4.48e+02	473	16	24711 17	CERF03D2	Caenorhabditis elegans	4.48e+02
401	16	5380 19	BKSDHCAB	R.macerans SDHC, sdha,	4.48e+02	474	16	24903 17	CERAC7	Caenorhabditis elegans	4.48e+02
402	16	5425 14	PATINS1	Rat insulin-I (ins-I),	4.48e+02	475	16	25951 16	AB004829	Fugu rubripes gene for	4.48e+02
403	16	5429 23	CVU89928	Cloning vector pHTS1-1	4.48e+02	476	16	26180 17	CER01B7	Caenorhabditis elegans	4.48e+02
404	16	5586 23	AF041808	Cloning vector yGalste	4.48e+02	477	16	27323 19	AB000789	Borrelia burgdorferi p	4.48e+02
405	16	5597 18	NCU50264	Neurospora crassa two-	4.48e+02	478	16	27848 17	CER01E5	Caenorhabditis elegans	4.48e+02
406	16	5703 14	MSMGA51	Mus musculus smooch mu	4.48e+02	479	16	29807 14	MMT73107	Mus musculus adenosine	4.48e+02
407	16	5767 14	D83002	Mouse mRNA for tyrosin	4.48e+02	480	16	29950 19	AF015775	Bacillus subtilis Y00A	4.48e+02
408	16	5797 23	PRS423	Yeast episomal vector	4.48e+02	481	16	30100 19	AF006665	Bacillus subtilis 168	4.48e+02
409	16	5798 21	HSMCP4A	Marek's disease virus	4.48e+02	482	16	30969 17	CERU13B5	Caenorhabditis elegans	4.48e+02
410	16	6143 18	FNU62930	Alphadelta219a neofom	4.48e+02	483	16	32793 17	CERU18F3	Caenorhabditis elegans	4.48e+02
411	16	6373 14	AEVPDNA	Avian erythroblastosis	4.48e+02	484	16	32965 17	CER001G7	Caenorhabditis elegans	4.48e+02
412	16	6373 14	MSMNS	M.musculus mRNA for SN	4.48e+02	485	16	33010 17	CERU3196	Caenorhabditis elegans	4.48e+02
413	16	6388 19	MTU66108	Mycobacterium tubercul	4.48e+02	486	16	33539 17	CERF54F7	Caenorhabditis elegans	4.48e+02
414	16	6400 15	SSCYMC	S.scrota c-myc gene.	4.48e+02	487	16	34073 17	CERF11D11	Caenorhabditis elegans	4.48e+02
415	16	6446 17	AF023484	Drosophila melanogaste	4.48e+02	488	16	35126 17	CERK678	Caenorhabditis elegans	4.48e+02
416	16	6509 18	ATPHPTOCHB	Arabidopsis thaliana p	4.48e+02	489	16	35976 17	CERF25B5	Caenorhabditis elegans	4.48e+02
417	16	6543 18	NCU53189	Neurospora crassa osmo	4.48e+02	490	16	36532 17	CERF57B1	Caenorhabditis elegans	4.48e+02
418	16	6563 16	CHKRB3F	Chicken c-erbB oncogen	4.48e+02	491	16	36759 17	CER05F1	Caenorhabditis elegans	4.48e+02
419	16	6597 21	MEAL1	Measles virus mRNA for	4.48e+02	492	16	36819 19	MTI20H10	Mycobacterium tubercul	4.48e+02
420	16	6675 17	DMAC001881	Drosophila melanogaste	4.48e+02	493	16	37154 17	CERU148	Caenorhabditis elegans	4.48e+02
421	16	6778 17	DNADHG	Drosophila mulleri adh	4.48e+02	494	16	37549 26	HSCB33B7	Human DNA sequence ***	4.48e+02
422	16	6786 23	CVU89927	S.pneumoniae parC, par	4.48e+02	495	16	37549 26	HSCB33B7	S.cerevisiae DNA from	4.48e+02
423	16	6812 19	SPARCETP	S.pneumoniae parC, par	4.48e+02	496	16	38383 17	CER35H8	Caenorhabditis elegans	4.48e+02
424	16	6824 25	A25909	Yeast integraton vect	4.48e+02	497	16	39215 17	CERU1054	Caenorhabditis elegans	4.48e+02
425	16	7097 14	MM082624	Mus musculus amyloid p	4.48e+02	498	16	39520 17	CERF45E7	Caenorhabditis elegans	4.48e+02
426	16	7173 18	NTU59683	Nicotiana tabacum squa	4.48e+02	499	16	40124 17	CERF09E8	Caenorhabditis elegans	4.48e+02
427	16	7241 21	HS1ATIR1	HSV1 (Strain F) alpha-	4.48e+02	500	16	40830 18	SPAC2C6	S.pombe chromosome I C	4.48e+02
428	16	7254 19	KPU93843	Klebsiella pneumoniae	4.48e+02	501	16	40897 17	CERU32B4	Caenorhabditis elegans	4.48e+02
429	16	7305 18	PTGWIN62B	P.trichocarpa chitinas	4.48e+02	502	16	41212 17	CERF32B4	Caenorhabditis elegans	4.48e+02
430	16	7689 17	DMTME1	Drosophila melanogaste	4.48e+02	503	16	41351 17	CERF42C5	Caenorhabditis elegans	4.48e+02
431	16	8673 19	AF003541	Mycoplasma pulmonis re	4.48e+02	504	16	42042 17	CER34B4	Caenorhabditis elegans	4.48e+02
432	16	8936 14	RNFAS	Rat mRNA for fatty aci	4.48e+02	505	16	42793 18	SC9168	S.cerevisiae chromosom	4.48e+02
433	16	9039 21	HYWEL5	Human T-cell leukemia	4.48e+02	506	16	42844 17	CERU35D6	Caenorhabditis elegans	4.48e+02
434	16	9133 14	RATFASA	Rattus norvegicus fatt	4.48e+02	507	16	43090 14	CER008B6	Caenorhabditis elegans	4.48e+02
435	16	9143 14	RNFASNA	R.norvegicus FAS mRNA	4.48e+02	508	16	43576 14	AC003994	Mouse cosmid m538271	4.48e+02
436	16	9265 19	U39723	Mycoplasma genitalium	4.48e+02	509	16	43584 17	CERB0207	Caenorhabditis elegans	4.48e+02
437	16	9675 19	BTP612XX	Bacillus thuringiensis	4.48e+02	510	16	43895 18	SPAC4A8	S.pombe chromosome I C	4.48e+02
438	16	10010 19	H1U52709	Haemophilus influenzae	4.48e+02	511	16	44000 26	HSAC000047	Homo sapiens clone c11	4.48e+02
439	16	10080 19	MYCGIRX	Mycoplasma pulmonis g1	4.48e+02	512	16	45022 19	CERU34D1	Caenorhabditis elegans	4.48e+02
440	16	10080 19	MYCGIRX	Mycoplasma pulmonis g1	4.48e+02	513	16	45022 19	SS56KBR	S.solfataricus 56 kbp	4.48e+02
441	16	10161 19	AE000797	Methanobacterium therm	4.48e+02	514	16	56170 26	CERF01D5	Caenorhabditis elegans	4.48e+02
442	16	10166 23	UCU89960	Cloning vector pEG302	4.48e+02	515	16	58382 26	CERF28A8	Caenorhabditis elegans	4.48e+02
443	16	10181 19	ECAB000492	Escherichia coli K-12	4.48e+02	516	16	65143 19	D83026	Bacillus subtilis geno	4.48e+02
444	16	10380 19	AE000932	Methanobacterium therm	4.48e+02	517	16	70307 18	ATT10114	Arabidopsis thaliana D	4.48e+02
445	16	10409 19	ECAB000316	Escherichia coli K-12	4.48e+02	518	16	76329 18	AB007648	Arabidopsis thaliana G	4.48e+02
446	16	10633 14	ECAB000249	Escherichia coli K-12	4.48e+02	519	16	78064 26	HSAC000376	*** SEQUENCING IN PROG	4.48e+02
447	16	10833 14	MMZB3G	Mus musculus mRNA for	4.48e+02	520	16	78344 18	TM017A05	Arabidopsis thaliana B	4.48e+02
448	26	11370 18	PMCSG910	Pneumocystis carinii g	4.48e+02	521	16	78615 14	AC000398	Genomic sequence from	4.48e+02
449	16	11454 23	XXU01086	Cloning vector pVAC4 f	4.48e+02	522	16	79046 18	AB008267	Arabidopsis thaliana g	4.48e+02
450	16	11463 19	RHNMOLBTU	Rhizobium fredii nodu1	4.48e+02	523	16	80689 17	AC003053	Drosophila melanogaste	4.48e+02
451	16	11844 19	AE000107	Rhizobium sp. NGR234 p	4.48e+02	524	16	80770 18	AB005240	Arabidopsis thaliana g	4.48e+02
452	16	12571 19	AE000986	Archaeoglobus fulgidus	4.48e+02	525	16	82692 17	AC003924	Drosophila melanogaste	4.48e+02

526	1.6	82697	18	AT9A21	Arabidopsis thaliana D	4.48e-02	599	1.6	207730	19	BSDB0011	Bacillus subtilis comp	4.48e+02
527	1.6	82918	18	AB010071	Arabidopsis thaliana g	4.48e-02	600	1.6	212150	19	BSDB0020	Bacillus subtilis comp	4.48e+02
528	1.6	83450	17	AB003054	Arabidopsis thaliana 9	4.48e-02	601	1.6	218062	26	BS388M5	Human DNA sequence ***	4.48e-02
529	1.6	85065	18	AC001660	Drosophila melanogaster	4.48e-02	602	1.6	222295	25	CEV7A9	Cenorchaditis elegans	4.48e-02
530	1.6	86566	8	HSU90583	Human 86K contig from	4.48e-02	603	1.6	222295	25	CEV7A9	Cenorchaditis elegans	4.48e-02
531	1.6	94382	26	AC003680	*** SEQUENCING IN PROG	4.48e-02	604	1.6	226018	26	HS90D6	Human DNA sequence ***	4.48e+02
532	1.6	95134	26	HS265J14	Human DNA sequence ***	4.48e-02	605	1.6	229546	26	HS268H5	Human DNA sequence ***	4.48e+02
533	1.6	97226	26	HS299D23	Human DNA sequence ***	4.48e-02	606	1.6	238582	26	AC003059	Human DNA sequence ***	4.48e+02
534	1.6	102815	26	HS366N23	Human DNA sequence ***	4.48e-02	607	1.6	242470	26	CEV51H1	Cenorchaditis elegans	4.48e-02
535	1.6	104861	18	ATU93215	Arabidopsis thaliana c	4.48e+02	608	1.6	249452	26	AC004085	Cenorchaditis elegans	4.48e-02
536	1.6	106929	26	HS821D11	Human DNA sequence ***	4.48e-02	609	1.6	256664	26	CEV39G8	Human DNA sequence ***	4.48e+02
537	1.6	107379	19	SRGCP1R	S. hygroscopicus gene c	4.48e+02	610	1.6	257948	26	HS212G6	Cenorchaditis elegans	4.48e-02
538	1.6	108360	21	HS11UR	Herpes simplex virus t	4.48e+02	611	1.6	263842	26	HS333P23	Human DNA sequence ***	4.48e+02
539	1.6	109560	21	FS114	Sequence of BAC FS114	4.48e+02	612	1.6	268735	26	AC003684	Human DNA sequence ***	4.48e+02
540	1.6	110362	26	HSAC001237	*** SEQUENCING IN PROG	4.48e-02	613	1.6	276261	26	HSAC000406	*** SEQUENCING IN PROG	4.48e+02
541	1.6	112444	26	AC003022	*** SEQUENCING IN PROG	4.48e-02	614	1.6	280217	26	CEV14E3	Cenorchaditis elegans	4.48e-02
542	1.6	112726	26	CEV21F11	Cenorchaditis elegans	4.48e-02	615	1.6	281821	26	CEV34G9	Cenorchaditis elegans	4.48e+02
543	1.6	114505	18	F20P5	Sequence of BAC F20P5	4.48e-02	616	1.6	286873	26	CEV48E1	Cenorchaditis elegans	4.48e+02
544	1.6	116156	18	ATAC002343	Arabidopsis thaliana B	4.48e-02	617	1.6	307751	26	CEV48B6	Cenorchaditis elegans	4.48e+02
545	1.6	118743	26	HS516C23	Human DNA sequence ***	4.48e-02	618	1.6	318534	19	ECOWW93	Escherichia coli K-12	4.48e+02
546	1.6	120000	26	HSAC000005	*** SEQUENCING IN PROG	4.48e-02	619	1.5	44	16	CHK01H02	Chicken ovalbumin	1.66e+03
547	1.6	122928	18	ATAC002387	Arabidopsis thaliana c	4.48e-02	620	1.5	161	16	AB001864	Kokanee salmon DNA for	1.66e+03
548	1.6	124225	18	IG002N01	Arabidopsis thaliana B	4.48e+02	621	1.5	171	16	OVR3FRK7	Quail DNA for fibrobla	1.66e+03
549	1.6	124235	18	IG002N01	Arabidopsis thaliana B	4.48e+02	622	1.5	188	15	OVR3GH2	Ovis aries growth horm	1.66e+03
550	1.6	124689	26	AC003060	*** SEQUENCING IN PROG	4.48e+02	623	1.5	217	15	OVR3GH4	Ovis aries growth horm	1.66e+03
551	1.6	126581	26	AC003957	*** SEQUENCING IN PROG	4.48e+02	624	1.5	270	18	TOBRANA	Nicotiana tabacum smal	1.66e+03
552	1.6	128116	26	HS191L6	Human DNA sequence ***	4.48e+02	625	1.5	273	17	FHD10316	Fasciola hepatica clon	1.66e+03
553	1.6	128340	26	AC002419	*** SEQUENCING IN PROG	4.48e+02	626	1.5	293	14	RNVN01	Rat gene fragment for	1.66e+03
554	1.6	128538	19	HS313L4	Synechocystis sp. PCC6	4.48e+02	627	1.5	328	14	AF014497	Mus musculus sorbitol	1.66e+03
555	1.6	128607	26	HS313L4	Synechocystis sp. PCC6	4.48e+02	628	1.5	331	14	MMALCDS	M. musculus MAL gene, e	1.66e+03
556	1.6	131597	26	AC004005	*** SEQUENCING IN PROG	4.48e+02	629	1.5	384	21	HPCGTS1P	Ovis aries growth horm	1.66e+03
557	1.6	134708	19	HS230G1	Human DNA sequence ***	4.48e+02	630	1.5	393	15	OVR3GH2	Hepatitis C virus (iso	1.66e+03
558	1.6	134708	19	D90913	Human DNA sequence ***	4.48e+02	631	1.5	408	18	AFU19999	mRNA sequence coding f	1.66e+03
559	1.6	146360	26	HS104C13	Synechocystis sp. PCC6	4.48e+02	632	1.5	428	15	MTBRCPTN10	Retus horvagicus glyc	1.66e+03
560	1.6	147339	26	AC003667	Human DNA sequence ***	4.48e+02	633	1.5	481	14	RATMUSG17	B. taurus cpm 10 mRNA.	1.66e+03
561	1.6	148103	26	HS1216H12	Human DNA sequence ***	4.48e+02	634	1.5	523	25	VFLBKM	Sequence 2 from parent	1.66e+03
562	1.6	148103	26	HS1216H12	Human DNA sequence ***	4.48e+02	635	1.5	549	18	XIBGLR	V. faba mRNA for leghem	1.66e+03
563	1.6	148142	26	D90915	Synechocystis sp. PCC6	4.48e+02	636	1.5	598	16	HS21CPI0	Xenopus laevis mRNA fo	1.66e+03
564	1.6	148583	26	CEV17D7	Cenorchaditis sp. PCC6	4.48e+02	637	1.5	649	21	CHKATH	Herpes simplex virus t	1.66e+03
565	1.6	148640	26	AC004103	Human DNA sequence ***	4.48e+02	638	1.5	694	16	MUSCSP1A	Gallus gallus avian th	1.66e+03
566	1.6	149436	26	HS222E13	Human DNA sequence ***	4.48e+02	639	1.5	706	16	MUSCSP1A	Mus musculus for gamma-c	1.66e+03
567	1.6	150894	19	D90904	Herpes simplex virus (4.48e-02	640	1.5	722	18	SCCYCL	Yeast mRNA for cycloph	1.66e+03
568	1.6	152261	21	HS64D12	Human DNA sequence ***	4.48e-02	641	1.5	740	19	AF001201	Mus musculus mRNA for pr	1.66e+03
569	1.6	152708	26	AC003106	Homo sapiens: HTGS pha	4.48e+02	642	1.5	755	15	OVR3GH2	Ovis aries growth horm	1.66e+03
570	1.6	153638	26	AC003020	*** SEQUENCING IN PROG	4.48e+02	643	1.5	772	14	MMPCSP2	Onchocerca volvulus cy	1.66e+03
571	1.6	155398	26	HS18601	Human DNA sequence ***	4.48e+02	644	1.5	826	17	OV047812	Artificial sequence (c	1.66e+03
572	1.6	155900	26	HS217C2	*** SEQUENCING IN PROG	4.48e+02	645	1.5	847	25	E02766	S. cerevisiae (clone pF	1.66e+03
573	1.6	160214	26	AC002327	*** SEQUENCING IN PROG	4.48e+02	646	1.5	853	25	A04353	D. rerio mRNA for HHR-3	1.66e+03
574	1.6	164723	26	AC000097	Cenorchaditis elegans	4.48e+02	647	1.5	920	14	MUSGCA	Mouse mRNA for gamma-c	1.66e+03
575	1.6	166819	26	CEV22E5	Cenorchaditis elegans	4.48e+02	648	1.5	940	14	MUSGRC	Mouse mRNA for gamma-c	1.66e+03
576	1.6	169646	26	AC004019	*** SEQUENCING IN PROG	4.48e+02	649	1.5	966	17	PAP1E	Pseudomonas aeruginosa	1.66e+03
577	1.6	170215	26	AC004127	*** SEQUENCING IN PROG	4.48e+02	650	1.5	975	17	DDCABP1	D. discoideum CAP1 gen	1.66e+03
578	1.6	170309	26	AC003061	Cenorchaditis elegans	4.48e+02	651	1.5	1029	25	HGSPIT	Heterodera glycines mR	1.66e-03
579	1.6	170789	26	CEV76A2	Cenorchaditis elegans	4.48e+02	652	1.5	1036	14	RNASH	CDNA sequence coding f	1.66e-03
580	1.6	170789	26	AC002118	*** SEQUENCING IN PROG	4.48e+02	653	1.5	1060	15	MP078340	R. norvegicus ash mRNA.	1.66e+03
581	1.6	170891	26	HSAC407	*** SEQUENCING IN PROG	4.48e+02	654	1.5	1062	15	ELD78330	Mus musculus 12S r	1.66e+03
582	1.6	173187	26	HSAC407	*** SEQUENCING IN PROG	4.48e+02	655	1.5	1064	14	MRTMP35	Mustela putorius 12S r	1.66e+03
583	1.6	179000	26	HSAC002059	Human DNA sequence ***	4.48e+02	656	1.5	1083	18	AF016283	Human DNA sequence ***	1.66e+03
584	1.6	183555	26	HS269M15	Human DNA sequence ***	4.48e+02	657	1.5	1096	16	DUSF8AT	Saccharomyces cerevisi	1.66e+03
585	1.6	185402	26	AC003066	Homo sapiens: HTGS pha	4.48e-02	658	1.5	1142	25	MW040720	Mallard duck (A. platyr	1.66e+03
586	1.6	185907	26	CEV32E6	Cenorchaditis elegans	4.48e-02	659	1.5	1187	17	GIAPSP2	Mus musculus anterior-	1.66e+03
587	1.6	186306	26	CEV32E6	Cenorchaditis elegans	4.48e-02	660	1.5	1189	17	DMW51071	Giardia lamblia Vsp ge	1.66e+03
588	1.6	187816	26	CEV32E6	Cenorchaditis elegans	4.48e-02	661	1.5	1195	15	DMW51086	Drosophila willistoni	1.66e+03
589	1.6	190289	21	MCU60315	Molluscum contagiosum	4.48e+02	662	1.5	1198	17	DMW51061	B. taurus (Fresian) Bol	1.66e+03
590	1.6	190577	26	HS170A21	Human DNA sequence ***	4.48e+02	663	1.5	1201	17	DMW51061	Drosophila willistoni	1.66e+03
591	1.6	193091	26	AC000052	*** SEQUENCING IN PROG	4.48e+02	664	1.5	1207	17	DMW51056	Drosophila willistoni	1.66e+03
592	1.6	194435	26	CEV51P9	Cenorchaditis elegans	4.48e+02	665	1.5					
593	1.6	196633	26	CEV51P9	Cenorchaditis elegans	4.48e+02	666	1.5					
594	1.6	199125	26	CEV51P9	Cenorchaditis elegans	4.48e+02	667	1.5					
595	1.6	200635	26	HS34P24	Human DNA sequence ***	4.48e+02	668	1.5					
596	1.6	200853	26	HS101A4	Human DNA sequence ***	4.48e+02	669	1.5					
597	1.6	202083	26	HS119E23	Human DNA sequence ***	4.48e+02	670	1.5					
598	1.6	207674	18	ATFC8	Arabidopsis thaliana D	4.48e+02	671	1.5					

672	15	1.5	1207	17	DMW51058	Drosophila willistonii	1.66e+03	745	15	1.5	2831	19	SSOACPREP	Staphylococcus sp. gen	1.66e+03
673	15	1.5	1213	17	DP051080	Drosophila paulistorum	1.66e+03	746	15	1.5	2843	18	SCYR125W	S.cerevisiae chromosom	1.66e+03
674	15	1.5	1220	17	DM030470	Drosophila melanogaste	1.66e+03	747	15	1.5	2871	18	YSCRNAPOOL	Saccharomyces cerevisi	1.66e+03
675	15	1.5	1222	15	BOVAR1B	Bovine BOLA-DRA mRNA f	1.66e+03	748	15	1.5	2885	16	DRPOU	D.erio zp-50 POU gene	1.66e+03
676	15	1.5	1224	15	BTENKE	Bovine messenger RNA f	1.66e+03	749	15	1.5	2931	17	DML81570	Drosophila melanogaste	1.66e+03
677	15	1.5	1232	14	AF015311	Rattus norvegicus c-fos	1.66e+03	750	15	1.5	3002	17	557174	arrestin homolog [locu	1.66e+03
678	15	1.5	1238	18	BTU10847	Rattus norvegicus conn	1.66e+03	751	15	1.5	3004	18	YSCGFC1	S.cerevisiae transcrip	1.66e+03
679	15	1.5	1239	25	T55000	Brassica juncea mRNA f	1.66e+03	752	15	1.5	3012	25	I40808	Sequence 1 from patent	1.66e+03
680	15	1.5	1253	17	CELIIN39A	Caenorhabditis elegans	1.66e+03	753	15	1.5	3012	25	I68246	Sequence 1 from patent	1.66e+03
681	15	1.5	1278	16	GGRAB501P	G.gallus mRNA for rab5	1.66e+03	754	15	1.5	3015	19	CCU30321	Clostridium cellulolyt	1.66e+03
682	15	1.5	1285	16	SCUT5453	Serinus canaria growth	1.66e+03	755	15	1.5	3027	18	SCYDL128W	S.cerevisiae chromosom	1.66e+03
683	15	1.5	1292	18	ATPBPAC	Arabidopsis thaliana p	1.66e+03	756	15	1.5	3037	14	RNSCEAL	R.norvegicus mRNA I fo	1.66e+03
684	15	1.5	1309	16	CCOPD1B	Cyprinus carpio mRNA f	1.66e+03	757	15	1.5	3061	16	DRRAHBLI	Danio rerio p10a mRNA	1.66e+03
685	15	1.5	1331	14	MMU01915	Mus musculus DNA topol	1.66e+03	758	15	1.5	3071	14	RNSCSA3	R.norvegicus mRNA for	1.66e+03
686	15	1.5	1350	21	RVU22633	Rabies virus 8721AFS n	1.66e+03	759	15	1.5	3111	17	DROZ2DC96Z	Drosophila melanogaste	1.66e+03
687	15	1.5	1380	19	BACAR1	B.steatothymophilus a	1.66e+03	760	15	1.5	3126	14	RNSCEA2	R.norvegicus mRNA II f	1.66e+03
688	15	1.5	1388	17	D50584	Hemigrapsus sanguineus	1.66e+03	761	15	1.5	3134	25	I14728	Sequence 7 from patent	1.66e+03
689	15	1.5	1429	16	CHKRG	Chicken B-g mRNA, 3' e	1.66e+03	762	15	1.5	3138	19	ECCODAB	E.coli codA operon en	1.66e+03
690	15	1.5	1478	25	I36807	Sequence 27 from paten	1.66e+03	763	15	1.5	3199	15	DOGSNCE	Dog cardiac sarcolemma	1.66e+03
691	15	1.5	1484	18	SCYR152W	S.cerevisiae chromosom	1.66e+03	764	15	1.5	3209	19	ECU23148	Escherichia coli gluta	1.66e+03
692	15	1.5	1512	14	MMU0656	Mus musculus sex deter	1.66e+03	765	15	1.5	3344	14	AFU04666	Mus musculus sodium-ca	1.66e+03
693	15	1.5	1517	14	MLM76F112	M.musculus Ly-6F.1 gen	1.66e+03	766	15	1.5	3390	25	I68269	Sequence 26 from paten	1.66e+03
694	15	1.5	1528	14	RATCGA	Rattus norvegicus (clo	1.66e+03	767	15	1.5	3405	17	DMA0001719	Drosophila melanogaste	1.66e+03
695	15	1.5	1549	14	MMU0657	Mus musculus castaneus	1.66e+03	768	15	1.5	3426	25	I40830	Sequence 24 from paten	1.66e+03
696	15	1.5	1610	19	NGAURIN	Neisseria gonorrhoeae	1.66e+03	769	15	1.5	3423	17	SGCYC88PV	S.granularis mRNA for	1.66e+03
697	15	1.5	1622	19	MSESCAC0AD	Megaspheera elsendeni s	1.66e+03	770	15	1.5	3432	17	DMPTX1ROM	Drosophila melanogaste	1.66e+03
698	15	1.5	1638	18	ATHAHBPIB	A.thaliana mRNA for AH	1.66e+03	771	15	1.5	3443	17	DRO37DC12Z	Drosophila melanogaste	1.66e+03
699	15	1.5	1677	14	MUSJGR1AX	Mus musculus guanin n	1.66e+03	772	15	1.5	3456	17	DMODE	D.melanogaster lodesta	1.66e+03
700	15	1.5	1682	19	ANAPETFL	Anabaena pectli gene fo	1.66e+03	773	15	1.5	3463	17	OATSHR	Ovis aries mRNA for th	1.66e+03
701	15	1.5	1711	14	RNCYP2B6	Rattus norvegicus cyto	1.66e+03	774	15	1.5	3494	18	PMCMGSE	Pneumocystis carinii (1.66e+03
702	15	1.5	1711	14	MUSJGR1A	Mus musculus guanine n	1.66e+03	775	15	1.5	3500	14	RNU93052	Rattus norvegicus calc	1.66e+03
703	15	1.5	1736	14	RAISR13	Rat SRI3 myelin protei	1.66e+03	776	15	1.5	3504	17	DMKMR1	Drosophila Krt1 gene f	1.66e+03
704	15	1.5	1739	25	E07739	CDNA encoding beta 1/3	1.66e+03	777	15	1.5	3537	17	EHVSA	E.histolytica mRNA for	1.66e+03
705	15	1.5	1762	17	DROSIAB	Drosophila virilis SEV	1.66e+03	778	15	1.5	3574	14	MUSPREMPB	Mouse PRP gene encodin	1.66e+03
706	15	1.5	1790	16	CHKBGA	Chicken B-G mRNA, comp	1.66e+03	779	15	1.5	3660	17	SEPP3A2	S.pupparatus mRNA for	1.66e+03
707	15	1.5	1800	14	MUSGAS3A	Mouse growth arrest sp	1.66e+03	780	15	1.5	3758	17	CELCIL1	C.elegans cse-1 kinas	1.66e+03
708	15	1.5	1807	17	CEICOL19A	C.elegans collagen (c	1.66e+03	781	15	1.5	3830	19	CLOCELB	Clostridium josui celb	1.66e+03
709	15	1.5	1816	25	I14726	Sequence 5 from paten	1.66e+03	782	15	1.5	3840	19	PDBCI	P.denitrificans bol g	1.66e+03
710	15	1.5	1822	25	I14727	Sequence 6 from patent	1.66e+03	783	15	1.5	3840	19	PDBCI	P.denitrificans bol op	1.66e+03
711	15	1.5	1888	18	SCNMRIW30	Saccharomyces cerevisi	1.66e+03	784	15	1.5	3897	16	CHBK33A1	Chicken histone gene e	1.66e+03
712	15	1.5	1912	15	BOVATPSYN	Bovine mtchochondrial a	1.66e+03	785	15	1.5	3899	15	SHPEHGV	Ovine growth hormone g	1.66e+03
713	15	1.5	1915	15	MMU01P2	M.musculus mRNA for ul	1.66e+03	786	15	1.5	4075	19	SOORFS	S.pneumoniae yorfla,B,	1.66e+03
714	15	1.5	1937	14	RATASPARB	Rat aspartate aminotra	1.66e+03	787	15	1.5	4075	14	MMU66473	Mus musculus preprogra	1.66e+03
715	15	1.5	1993	21	ADRORF1G	Mastadenovirus susi pv	1.66e+03	788	15	1.5	4082	18	YSCHATP	S.cerevisiae vacuolar	1.66e+03
716	15	1.5	1996	14	RROU15660	Rattus norvegicus orph	1.66e+03	789	15	1.5	4118	17	SCU52347	Stomoxys calcitrans pu	1.66e+03
717	15	1.5	2056	16	CCDOPD1A4	Cyprinus carpio mRNA f	1.66e+03	790	15	1.5	4166	21	D86577	Human hepesvirus type	1.66e+03
718	15	1.5	2057	16	XELCRXB	Xenopus laevis gamma-c	1.66e+03	791	15	1.5	4289	19	DMRUBCI	D.melanogaster genes R	1.66e+03
719	15	1.5	2099	14	RATASHM	Rat mRNA for Ash-m. co	1.66e+03	792	15	1.5	4320	18	LETPRFL	L. esculentum TPRP-FL	1.66e+03
720	15	1.5	2124	18	SCYDL129W	S.cerevisiae chromosom	1.66e+03	793	15	1.5	4339	18	YSCPDR1	Yeast (S.cerevisiae) p	1.66e+03
721	15	1.5	2169	18	SCYOR323C	S.cerevisiae chromosom	1.66e+03	794	15	1.5	4378	19	STYCARABA	Salmonella typhimurium	1.66e+03
722	15	1.5	2235	14	AFU28009	Mus musculus proteinh k	1.66e+03	795	15	1.5	4531	14	MMT1MP3XI	M.musculus (Bab/C) TI	1.66e+03
723	15	1.5	2243	14	YSCIF395C	Yeast transcripion fa	1.66e+03	796	15	1.5	4676	21	CHU25806	Cercopithecine herpesv	1.66e+03
724	15	1.5	2248	14	RATRCBSC	Rat cystathionine beta	1.66e+03	797	15	1.5	4937	18	ATCCYP450D	A.thaliana gene cyclo-h	1.66e+03
725	15	1.5	2253	14	MUSGIR	Mouse G-protein couple	1.66e+03	798	15	1.5	4968	15	AFU034077	Bqrus caballus alpha-1	1.66e+03
726	15	1.5	2255	17	SEU15038	Spodoptera frugiperda	1.66e+03	799	15	1.5	4980	15	BTROSOC1	Bos taurus rod outier s	1.66e+03
727	15	1.5	2273	18	PAAS1GNA	P.anserina ASI gene, c	1.66e+03	800	15	1.5	5124	19	AFU04822	Neisseria meningitidis	1.66e+03
728	15	1.5	2298	14	MUSHEP70	Mouse heat shock-relat	1.66e+03	801	15	1.5	5264	14	RNU61261	Rattus norvegicus lam1	1.66e+03
729	15	1.5	2340	15	AMCHRB	Mouse mRNA for chromog	1.66e+03	802	15	1.5	5322	17	DMAHAPBS1	D.melanogaster Hg-Atpa	1.66e+03
730	15	1.5	2365	25	A38773	Sequence 11 from Paten	1.66e+03	803	15	1.5	5352	14	ECNTSA2	E.coli nsa operon inc	1.66e+03
731	15	1.5	2370	14	MUSDNAB1ND	Mouse myocyte nuclear	1.66e+03	804	15	1.5	5423	19	ECNTSA2	E.coli nsa operon inc	1.66e+03
732	15	1.5	2374	15	BTU15570	Bos taurus thyrotropin	1.66e+03	805	15	1.5	5467	25	I12880	Sequence 12 from paten	1.66e+03
733	15	1.5	2393	14	MUSRSPK	Mouse mRNA for tyrosin	1.66e+03	806	15	1.5	5686	15	CLOCE1GE	Clostridium cellulolyt	1.66e+03
734	15	1.5	2408	14	MININS1G	Mouse preproinsulin ge	1.66e+03	807	15	1.5	5721	17	DMO80223	Drosophila melanogaste	1.66e+03
735	15	1.5	2412	18	BNGRP10G	B.napus BNGRP10 gene e	1.66e+03	808	15	1.5	5783	17	ABU07850	Atthalia rosea mRNA for	1.66e+03
736	15	1.5	2445	25	A34990	H.sapiens TSH receptor	1.66e+03	809	15	1.5	5794	14	WZU14952	Weeksella zoohelcum Ac	1.66e+03
737	15	1.5	2477	18	BRU76555	Brassica rapa zinc-fin	1.66e+03	810	15	1.5	5798	14	RNU92079	Rattus norvegicus GUGF	1.66e+03
738	15	1.5	2504	17	OCTODEA	C.dofleini hemocyanin	1.66e+03	811	15	1.5	5900	19	AFU034614	Zymomonas mobilis carb	1.66e+03
739	15	1.5	2573	16	CCFRFX	C.cortulnix PREK mRNA f	1.66e+03	812	15	1.5	6108	18	AMG10B	A.majus globosa gene.	1.66e+03
740	15	1.5	2580	15	ERU97339	Elephantulus rufescens	1.66e+03	813	15	1.5	6730	14	D86949	Mouse mRNA for plexin	1.66e+03
741	15	1.5	2641	18	SCYR123C	S.cerevisiae chromosom	1.66e+03	814	15	1.5	7020	18	ATSHB21	Arabidopsis thaliana S	1.66e+03
742	15	1.5	2674	18	ENU37803	Emeriocella nidulans ca	1.66e+03	815	15	1.5	7065	19	STU81859	Salmonella typhimurium	1.

C	818	15	1.5	7560 17	TCBH	T. castaneum hunchback	1.66e+03	891	15	1.5	40340 18	YSL8004	Saccharomyces cerevisi	1.66e+03
C	819	15	1.5	7578 19	PTU53507	Pseudomonas JRI isopro	1.66e+03	892	15	1.5	42759 18	AB004535	Schizosaccharomyces po	1.66e+03
C	820	15	1.5	7713 14	MUSSLIMA	Mouse Lmd-a2 repeatl1	1.66e+03	893	15	1.5	43046 17	CEIC0988	Caenorhabditis elegans	1.66e+03
C	821	15	1.5	7829 19	RPLPLAS	Bufoera aphidicola of	1.66e+03	894	15	1.5	43441 17	CEID2005	Caenorhabditis elegans	1.66e+03
C	822	15	1.5	8143 19	EAT97504	Erwinia amylovora Hrpw	1.66e+03	895	15	1.5	43468 18	SC8358	Caenorhabditis elegans	1.66e+03
C	823	15	1.5	8421 17	DVU39746	Drosophila virilis gra	1.66e+03	896	15	1.5	43492 17	CEIC1459	Caenorhabditis elegans	1.66e+03
C	824	15	1.5	8473 17	DROFATFA	Fruitfly fat facets mla	1.66e+03	897	15	1.5	43947 17	CEIC0149	Caenorhabditis elegans	1.66e+03
C	825	15	1.5	8608 15	OCBOCHIT	O. cuniculus mRNA for b	1.66e+03	898	15	1.5	44264 17	CEIC07D12	Caenorhabditis elegans	1.66e+03
C	826	15	1.5	9138 16	DUXFASA	Duck (A. platyrhynchos)	1.66e+03	899	15	1.5	44773 17	CEIC04D12	Caenorhabditis elegans	1.66e+03
C	827	15	1.5	9155 16	ABE00084	Rhizobium sp. NGR234 p	1.66e+03	900	15	1.5	45189 17	CEIC34P11	C. elegans cosmid C50C	1.66e+03
C	828	15	1.5	9603 21	AF014811	Zucchini yellow mosaic	1.66e+03	901	15	1.5	45510 17	CEIC32A3	Caenorhabditis elegans	1.66e+03
C	829	15	1.5	9603 14	CG009104	Cricetulus griseus SIN	1.66e+03	902	15	1.5	46822 18	AB008266	Caenorhabditis elegans	1.66e+03
C	830	15	1.5	9915 15	BTATPAA	B. laurus atp1 gene fo	1.66e+03	903	15	1.5	50425 26	CEH7N21	Arabidopsis thaliana g	1.66e+03
C	831	15	1.5	10042 19	HPAE00574	Helicobacter pylori se	1.66e+03	904	15	1.5	53899 26	CEH7N21	Caenorhabditis elegans	1.66e+03
C	832	15	1.5	10213 19	U39716	Mycoplasma genitalium	1.66e+03	905	15	1.5	5403 26	CEH08C2	Caenorhabditis elegans	1.66e+03
C	833	15	1.5	10372 19	HTU32734	Haemophilus influenzae	1.66e+03	906	15	1.5	62031 14	AF021335	Mus musculus T cell re	1.66e+03
C	834	15	1.5	10312 19	ECAB000381	Escherichia coli K-12	1.66e+03	907	15	1.5	62031 14	AF021335	Saccharomyces cerevisi	1.66e+03
C	835	15	1.5	10536 19	U67488	Methanococcus jannasch	1.66e+03	908	15	1.5	69023 18	SCB0035	Caenorhabditis elegans	1.66e+03
C	836	15	1.5	10580 19	U67488	Methanococcus jannasch	1.66e+03	909	15	1.5	70640 26	CEH32K21	Caenorhabditis elegans	1.66e+03
C	837	15	1.5	11817 14	MMU70015	Mus musculus lysosomal	1.66e+03	910	15	1.5	73471 26	AC002509	*** SEQUENCING IN PROG	1.66e+03
C	838	15	1.5	12260 21	AF041040	Pestivirus type 1 poly	1.66e+03	911	15	1.5	78064 26	HSAC000376	*** SEQUENCING IN PROG	1.66e+03
C	839	15	1.5	12720 25	TE0980	Sequence 11 from paten	1.66e+03	912	15	1.5	81493 18	ATB1KBEN	*** SEQUENCING IN PROG	1.66e+03
C	840	15	1.5	12934 18	SCYKR054C	S. cerevisiae chromosom	1.66e+03	913	15	1.5	82810 6	HS067941	A. thaliana 81Ks genom	1.66e+03
C	841	15	1.5	13435 19	BSORIGS	Escherichia coli K-12	1.66e+03	914	15	1.5	83646 18	AB005248	Human DNA sequence ***	1.66e+03
C	842	15	1.5	13605 19	ESCP0157	E. coli plasmid p0157 D	1.66e+03	915	15	1.5	84510 18	AB006658	Arabidopsis thaliana g	1.66e+03
C	843	15	1.5	14162 19	BCP0157	Human respiratory sync	1.66e+03	916	15	1.5	87831 26	HS892F13	Human DNA sequence ***	1.66e+03
C	844	15	1.5	14275 17	CEH57C2	Caenorhabditis elegans	1.66e+03	917	15	1.5	88960 26	HS892F13	Human DNA sequence ***	1.66e+03
C	845	15	1.5	15222 21	HRU50363	Human respiratory sync	1.66e+03	918	15	1.5	93037 18	ATB0F16	Mouse BAC24H12 Chromo	1.66e+03
C	846	15	1.5	15222 21	HRU50362	Human respiratory sync	1.66e+03	919	15	1.5	93037 18	ATB0F16	Arabidopsis thaliana D	1.66e+03
C	847	15	1.5	15222 21	HRU50362	Human respiratory sync	1.66e+03	920	15	1.5	93158 26	AC002334	*** SEQUENCING IN PROG	1.66e+03
C	848	15	1.5	15935 18	SCYKR106C	S. cerevisiae chromosom	1.66e+03	921	15	1.5	95568 26	CEH05L14	Caenorhabditis elegans	1.66e+03
C	849	15	1.5	16036 17	CEH26F2	Caenorhabditis elegans	1.66e+03	922	15	1.5	95645 26	AC003688	*** SEQUENCING IN PROG	1.66e+03
C	850	15	1.5	16356 18	S58126	LEU1-ATP1 loci: LEU1.	1.66e+03	923	15	1.5	98234 26	AC003102	*** SEQUENCING IN PROG	1.66e+03
C	851	15	1.5	17293 16	TFU5TFBPA	Snake (habu) griftp ge	1.66e+03	924	15	1.5	98324 26	AC003102	*** SEQUENCING IN PROG	1.66e+03
C	852	15	1.5	17516 17	CEH48E1A	Caenorhabditis elegans	1.66e+03	925	15	1.5	100145 26	AC004044	Arabidopsis thaliana B	1.66e+03
C	853	15	1.5	19371 17	CEH10E7	Caenorhabditis elegans	1.66e+03	926	15	1.5	102972 26	AC003104	*** SEQUENCING IN PROG	1.66e+03
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C	857	15	1.5	22071 17	CEH07G5	Caenorhabditis elegans	1.66e+03	930	15	1.5	106973 26	U89959	Human DNA sequence ***	1.66e+03
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C	864	15	1.5	27777 17	AC002447	Drosophila melanogaste	1.66e+03	937	15	1.5	113566 18	AC002330	Caenorhabditis elegans	1.66e+03
C	865	15	1.5	28396 17	CEH10E7	Caenorhabditis elegans	1.66e+03	938	15	1.5	115067 26	CEH37A05	Caenorhabditis elegans	1.66e+03
C	866	15	1.5	28322 17	CEIC43G2	Caenorhabditis elegans	1.66e+03	939	15	1.5	118155 26	HS884K20	Human DNA sequence ***	1.66e+03
C	867	15	1.5	29366 18	SC9571X	S. cerevisiae chromosom	1.66e+03	940	15	1.5	119184 19	D90909	Synschoecyrtis sp. PC06	1.66e+03
C	868	15	1.5	29820 17	CEH48F7	Caenorhabditis elegans	1.66e+03	941	15	1.5	119704 18	OSCHLPLX	O. sinensis complete ch	1.66e+03
C	869	15	1.5	30940 17	CEH41D9	Caenorhabditis elegans	1.66e+03	942	15	1.5	120201 26	HS506	Human DNA sequence ***	1.66e+03
C	870	15	1.5	31418 17	CEC03C10	Caenorhabditis elegans	1.66e+03	943	15	1.5	121174 26	CEH69E1	Caenorhabditis elegans	1.66e+03
C	871	15	1.5	32458 17	CEH10E11	Caenorhabditis elegans	1.66e+03	944	15	1.5	121811 26	AC000096	*** SEQUENCING IN PROG	1.66e+03
C	872	15	1.5	32880 17	CEH40F12	Caenorhabditis elegans	1.66e+03	945	15	1.5	122459 26	HSAC000384	*** SEQUENCING IN PROG	1.66e+03
C	873	15	1.5	33010 19	LMCV9F9	Mycobacterium tubercol	1.66e+03	946	15	1.5	123080 26	HS10H16	Human DNA sequence ***	1.66e+03
C	874	15	1.5	34396 17	CEH1R1G1	Caenorhabditis elegans	1.66e+03	947	15	1.5	123388 18	AC002131	Sequence of BAC F12P1	1.66e+03
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C	876	15	1.5	36535 17	CEH08H2	Caenorhabditis elegans	1.66e+03	949	15	1.5	128614 26	HS63G5	Human DNA sequence ***	1.66e+03
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C	879	15	1.5	37404 18	SC8119	S. cerevisiae chromosom	1.66e+03	952	15	1.5	131318 26	CEY42N10	Caenorhabditis elegans	1.66e+03
C	880	15	1.5	37404 18	SC8119	S. cerevisiae chromosom	1.66e+03	953	15	1.5	131977 26	AC003977	*** SEQUENCING IN PROG	1.66e+03
C	881	15	1.5	37730 18	YSL8543	Saccharomyces cerevisi	1.66e+03	954	15	1.5	132613 26	HS37J18	Human DNA sequence ***	1.66e+03
C	882	15	1.5	37787 18	CEH12B7	S. pombe chromosome I C	1.66e+03	955	15	1.5	133626 21	HS15005	Human DNA sequence ***	1.66e+03
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C	884	15	1.5	38889 26	HS033B10	Human DNA sequence ***	1.66e+03	957	15	1.5	137404 26	AC0002375	Human DNA sequence ***	1.66e+03
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C	886	15	1.5	39292 18	SPAC11D3	S. pombe chromosome I C	1.66e+03	959	15	1.5	144861 21	HS043400	Human herpesvirus-7 (H	1.66e+03
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C	888	15	1.5	39375 17	CEH11D12	Caenorhabditis elegans	1.66e+03	961	15	1.5	146640 26	AC004103	Homo sapiens: HTGS pha	1.66e+03
C	889	15	1.5	39581 17	CEH1K1248	Caenorhabditis elegans	1.66e+03	962	15	1.5	150000 26	AC004064	*** SEQUENCING IN PROG	1.66e+03
C	890	15	1.5	40012 17	CEH57C3	Caenorhabditis elegans	1.66e+03	963	15	1.5	151901 26	HS431P23	Human DNA sequence ***	1.66e+03

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980	1.5	184427	21	EHYU20824	Equine herpesvirus 2,	1.66e+03
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991	1.5	224681	26	HS44N10	Human DNA sequence ***	1.66e+03
992	1.5	226018	26	HS90L6	Human DNA sequence ***	1.66e+03
993	1.5	232597	26	AC002353	Homo sapiens; HTGS pha	1.66e+03
994	1.5	241361	26	HS94M16	Human DNA sequence ***	1.66e+03
995	1.5	256000	26	HSAC000353	Homo sapiens chromosome	1.66e+03
996	1.5	268735	26	AC003684	Homo sapiens; HTGS pha	1.66e+03
997	1.5	288886	26	AC002406	Mus musculus; HTGS pha	1.66e+03
998	1.5	330740	21	PBU42580	Paramecium bursaria Ch	1.66e+03
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ALIGNMENTS

RESULT 1 A48343 1142 bp DNA PAT 07-MAR-1997
LOCUS
DEFINITION Sequence 1 from Patent WO9601898.
ACCESSION A48343
NID 92302133

KEYWORDS
SOURCE
ORGANISM

unidentified.
unclassified.
1 (bases 1 to 1142)
Kieffer, B. and Simolin, F.
HUMAN KAPPA OPIOID RECEPTOR, NUCLEIC ACIDS AND USES THEREOF
Patent: WO 9601898-A 1 25-JAN-1996;
JOURNAL UNIV PASTEUR (FR)
COMMENT Other publication FR 2722209 960112.
FEATURES
source location/Qualifiers

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BASE COUNT

236 a 337 c 283 g 286 t

ORIGIN

Query Match 73.3%; Score 729; DB 25; Length 1142;

Best Local Similarity 98.8%; Pred. No. 0.00e+00; Mismatches 10; Indels 0; Gaps 0;

Matches 849; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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Qy	820	ATCCCATCTCTACAGCTTCTTGTGATGAAGAACTCAAGCGGTGTTCCGSGACTTCTGCT	879
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Qy	940	ATCCTGCTTACCTGAGGA 958	

RESULT 2 CP004092 1733 bp mRNA ROD 24-MAY-1995
LOCUS
DEFINITION Cavia porcellus Hartley kappa opioid receptor mRNA, complete cds.
ACCESSION U04092
NID 9476106
KEYWORDS

SOURCE
ORGANISM guinea pig.
Cavia porcellus

REFERENCE
AUTHORS Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Hystriognathi; Cavidae; Cavia.
1 (bases 1 to 1733)
Xie,G.X., Meng,F., Mansour,A., Thompson,R.C., Hoversten,M.T., Goldstein,A., Watson,S.J. and Akil,H.
Primary structure and functional expression of a guinea pig kappa opioid (dynorphin) receptor
Proc. Natl. Acad. Sci. U.S.A. 91 (9), 3779-3783 (1994)

TITLE
JOURNAL
MEDLINE
REFERENCE
AUTHORS
TITLE
JOURNAL
AUTHORS

FEATURES
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YSMDLEKICVFVFAVYIPVLIITVCTLMLRLKSVRLSGSEKDRNLRTIRIV
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BASE COUNT 409 a 416 c 505 g 403 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 4,79e-25;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 489 GATGATGACTCTCTGCTGGGACCTCTTCATGAGATCTGGCTTT 535
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RESULT 3
LOCUS NM16998 432 bp DNA
DEFINITION Mus musculus kappa opioid receptor (oprk1) gene, partial cds.
ACCESSION U16998
NID 9595936
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus.
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae; Murinae; Mus.
1 (bases 1 to 432)
Grandy,D.K.
REFERENCE
AUTHORS Mapping of the human kappa opioid receptor gene to chromosome 8q11.2-q12: no evidence for multiple kappa opioid receptor genes
JOURNAL unpublished
REFERENCE 2 (bases 1 to 432)
AUTHORS Grandy,D.K.

TITLE
JOURNAL
AUTHORS

FEATURES
source
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BASE COUNT 114 a 92 c 85 g 141 t
ORIGIN

Query Match 3.3%; Score 33; DB 14; Length 432;
Best Local Similarity 100.0%; Pred. No. 1.76e-11;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 336 ATAGTCCTTGAGGACCAACACTCAGGGAAGT 368
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QY 423 ATAGTCCTTGAGGACCAACACTCAGGGAAGT 455
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RESULT 4
LOCUS MUSMORGDP2 488 bp DNA
DEFINITION Mouse MORGD gene for kappa-opioid receptor, exon 2.
ACCESSION D31664
NID 9643594
KEYWORDS
SEGMENT
SOURCE
ORGANISM
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 488)
Nishi,M., Takeshima,H., Mori,M., Nakagawa,K. and Takeuchi,T.
Structure and chromosomal mapping of genes for the mouse +kappa-opioid receptor and an opioid receptor homolog (MOR-C)
Biochemical and Biophysical Research Communication 205, 1353-1357 (1994)
2 (bases 1 to 488)
Takeshima,H.
REFERENCE
AUTHORS Direct Submission
TITLE Submitted (28-MAY-1994) to the DDBJ/EMBL/GenBank databases. Hiroshi
JOURNAL Takeshima, Tokyo Institute of Psychiatry, Department of
Neurochemistry, 2-1-8 Kamikitazawa, Setagaya-ku, Tokyo 156, Japan
(tel:03-3304-5701(ex:312), Fax:03-3329-8035)
Submitted (28-May-1994) to DDBJ by:
Hiroshi Takeshima
Department of Neurochemistry
Tokyo Institute of Psychiatry
2-1-8 Kamikitazawa, Setagaya-ku
Tokyo 156
Japan
Phone: 03-3304-5701 x312

FEATURES Fax: 03-3329-8035.
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BASE COUNT 129 a 103 c 97 g 159 t
 ORIGIN Chromosome 1 A2-3.

Query Match 3.3%; Score 33; DB 14; Length 488;
 Best Local Similarity 100.0%; Pred. No. 1,76e-11;
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 411 ATAGTCCTTGAGGACCAAGTCAGGGAAGT 443
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 Qy 423 ATAGTCCTTGAGGACCAAGTCAGGGAAGT 455

RESULT 5
 LOCUS RNROR2 658 bp DNA ROD 25-MAR-1995
 DEFINITION Rattus norvegicus kappa oploid receptor gene, exon 3.
 ACCESSION U17994
 NID 9727257

KEYWORDS
 SEGMENT 2 of 3
 SOURCE Norway rat.
 ORGANISM Rattus norvegicus
 Eukaryotes; Mitochondrial eukaryotes; Metazoa; Chordata;
 Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
 Murinae; Rattus.
 1 (bases 1 to 658)
 Yakovlev,A.G., Krueger,K.E. and Faden,A.I.
 TITLE Structure and expression of a rat kappa oploid receptor gene
 JOURNAL J Biol. Chem. 270 (12), 6421-6424 (1995)
 MEDLINE 95204422
 REFERENCE 2 (bases 1 to 658)
 Yakovlev,A.G.
 AUTHORS Direct Submission
 TITLE Submitted (02-DEC-1994) Alexander G. Yakovlev, Georgetown
 JOURNAL University School of Medicine, Neurology, 3900 Reservoir Rd.,
 Washington, DC 20007, USA

FEATURES
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 201 a 128 c 122 g 207 t

BASE COUNT 201 a 128 c 122 g 207 t
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Db 548 ATAGTCCTTGAGGACCAAGTCAGGGAAGT 580
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 Qy 423 ATAGTCCTTGAGGACCAAGTCAGGGAAGT 455

RESULT 6

LOCUS S77868S2 1109 bp DNA ROD 26-SEP-1995
 DEFINITION kappa oploid receptor [mice, genomic, 1109 nt, segment 2 of 3].
 ACCESSION S77869
 NID 9998530
 KEYWORDS
 SEGMENT 2 of 3
 SOURCE Mus sp.
 ORGANISM Mus sp.
 Eukaryotes; Mitochondrial eukaryotes; Metazoa; Chordata;
 Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Mus.
 1 (bases 1 to 1109)
 Liu,H.C.; Lu,S., Augustin,L.B., Felsheim,R.F., Chen,H.C., Ioh,H.H.
 and Wei,L.N
 TITLE Cloning and promoter mapping of mouse kappa oploid receptor gene
 JOURNAL Biochem. Biophys. Res. Commun. 209 (2), 635-647 (1995)
 MEDLINE 95251663
 REMARK GenBank staff at the National Library of Medicine created this
 entry [NCBI gibsseq 165534] from the original journal article.
 This sequence comes from Fig. 2.
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 1..1109
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 /db_xref="taxon:10095"

BASE COUNT 331 a 213 c 204 g 361 t
 ORIGIN

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 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Qy 423 ATAGTCCTTGAGGACCAAGTCAGGGAAGT 455

RESULT 7
 LOCUS RNROR2 1273 bp mRNA ROD 21-DEC-1993
 DEFINITION Rat mRNA for oploid receptor, complete cds.
 ACCESSION D16534
 NID 9409390
 KEYWORDS
 SOURCE Rattus norvegicus (strain Wistar) adult brain cDNA to mRNA, clone
 pROR2.
 ORGANISM Rattus norvegicus
 Eukaryotes; Mitochondrial eukaryotes; Metazoa; Chordata;
 Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
 Murinae; Rattus.
 1 (bases 1 to 1273)
 Nishi,M., Takeshima,H., Fukuda,K., Kato,S. and Mori,K.
 TITLE cDNA cloning and pharmacological characterization of an oploid
 JOURNAL receptor with high affinities for kappa-subtype-selective ligands
 MEDLINE 93380575
 REFERENCE 2 (bases 1 to 1273)
 Takeshima,H.
 TITLE Direct Submission
 JOURNAL Submitted (19-JUN-1993) to the DDBJ/EMBL/GenBank databases. Hiroshi
 Takeshima, International Institute for Advanced Studies; c/o
 Shimadzu Corporation N-80, 1 Nishinokyo-Kuawahara-cho, Kyoto 604,
 Japan (Tel:075-823-1208, Fax:075-811-8186)
 COMMENT Submitted (19-JUN-1993) to DDBJ by:
 Hiroshi Takeshima
 International Institute
 for Advanced Studies
 c/o Shimadzu Corporation
 N-80
 1 Nishinokyo-Kuawahara-cho
 Kyoto 604
 Japan
 Phone: 075-823-1208
 Fax: 075-811-8186.
 Location/Qualifiers


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BASE COUNT      278 a      340 c      294 g      361 t
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Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 337 TACATATTACCTGGCTTGGCAGATGCTT 368
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QY 132 TACATATTACCTGGCTTGGCAGATGCTT 163

RESULT 8
LOCUS      S81111      1288 bp      mRNA      ROD      02-AUG-1996
DEFINITION kappa-opioid receptor [alternatively spliced] [mice, C58/J, R1.1
ACCESSION      S81111
NID      91478285
KEYWORDS      Mus sp. C58/J R1.1 thymoma cells.
SOURCE      Mus sp.
ORGANISM      Mus sp.
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Mus.
1 (bases 1 to 1288)
Belkowsky, S.M., Zhu, J., Liu, Chen, L.Y., Eisenstein, T.X., Adler, M.W.
and Rogers, T.J.
Sequence of kappa-opioid receptor cDNA in the R1.1 thymoma cell
line
J. Neuroimmunol. 62 (1), 113-117 (1995)
96084989
GenBank staff at the National Library of Medicine created this
entry [NCBI gibbs3 175931] from the original journal article.
This sequence comes from Fig. 3.
longer of two transcripts.
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JOURNAL
MEDLINE
REMARK
COMMENT
FEATURES
SOURCE
gene
CDS
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 1.44e-10;
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QY 132 TACATATTACCTGGCTTGGCAGATGCTT 163

RESULT 9
LOCUS      RANKORIA      1358 bp      mRNA      ROD      21-OCT-1993
DEFINITION Rat kappa opioid receptor mRNA, complete cds.
ACCESSION      L22001
NID      9409236
KEYWORDS      kappa opioid receptor; opioid receptor.
SOURCE      Rattus norvegicus whole brain cDNA to mRNA.
ORGANISM      Rattus norvegicus
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
Murinae; Rattus.
1 (bases 1 to 1358)
Chen, Y., Westek, A., Liu, J. and Yu, L.
Molecular cloning of a rat kappa opioid receptor reveals sequence
similarities to the mu and delta opioid receptors
Biochem. J. 295, 625-628 (1993)
94059008
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QY 132 TACATATTACCTGGCTTGGCAGATGCTT 163

RESULT 10
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DEFINITION Mouse kappa opioid receptor mRNA, complete cds.
ACCESSION      L11065
NID      9348248
KEYWORDS      kappa opioid receptor.
SOURCE      Mus musculus (library: Clontech #MT1030a) brain cDNA to mRNA.
ORGANISM      Mus musculus
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
Murinae; Mus.
1 (bases 1 to 1410)
Yasuda, K., Raynor, K., Kong, H., Breder, C.D., Takeda, T., Reisine, T.
and Bell, G.I.
Cloning and functional comparison of kappa and delta opioid
receptors from mouse brain

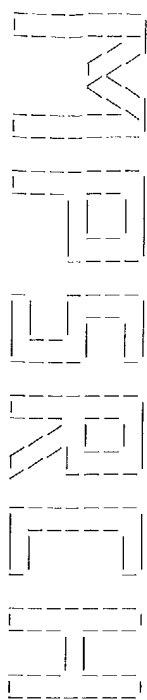
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LOCUS	E08874	2481 bp	RNA	PAT	26-NOV-1996
DEFINITION	cDNA coding rat kappa-opioid receptor.				
ACCESSION	E08874				
NID	G21766978				
KEYWORDS	UP 1995070191-A/1.				
SOURCE	Rattus sp.				
ORGANISM	Rattus sp. Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. 1 (bases 1 to 2481)				
REFERENCE	Kimimichi, S.				
AUTHORS	RECEPTOR PROTEIN, ITS PRODUCTION AND USE THEREOF				
TITLE	Patent: JP 1995070191-A 1 14-MAR-1995;				
JOURNAL	TAKEDA CHEM IND LTD				
COMMENT	OS Rattus sp. (rat) PN JP 1995070191-A/1 PD 14-MAR-1995 PF 30-JUL-1993 JP 1893190261 PR 09-JUL-1993 JP 53P 170591 PI SATO KIMIMICHI PC C07K14/47, C12N1/21, C12N15/09, C12P21/02, A61K38/00, A61K38/00; PC C12N1/21, C12R1/19, C12P21/02, C12R1/19, C07K99:00; CC strandedness: Double; CC topology: Linear; FH Key Location/Qualifiers FI source 1..2481 FI /organism="Rattus sp." FI CDS 111..1253 FI /product="rat kappa-opioid receptor". FEATURES source location/Qualifiers 1..2481 /organism="Rattus sp." /db_xref="taxon:10118" BASE COUNT 629 a 588 c 544 g 720 t ORIGIN				
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LOCUS	RATKOR	2481 bp	RNA	ROD	02-DEC-1993
DEFINITION	Rattus norvegicus mRNA for kappa opioid receptor, complete cds.				
ACCESSION	D18829				
NID	G404115				
KEYWORDS	kappa opioid receptor. Rattus norvegicus cDNA to mRNA.				
SOURCE	Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.				

REFERENCE 1 (bases 1 to 2481)
 AUTHORS Minami,M., Toyota,T., Kato,Y., Maekawa,K., Nakamura,S., Onogi,T.,
 Kaneko,S. and Satoh M.
 TITLE Cloning and expression of a cDNA for the rat kappa-opioid receptor
 JOURNAL PNAS Lett. 329 (3), 291-295 (1993)
 MEDLINE 93374033
 REFERENCE 2 (bases 1 to 2481)
 AUTHORS Minami,M.
 TITLE Direct Submission
 JOURNAL Submitted (21-JUL-1993) to the DDBJ/EMBL/GenBank databases.
 Masabumi Minami, Faculty of Pharmaceutical Sciences, Kyoto
 University, Department of Pharmacology; Kyoto 606-01, Japan
 (E-mail:fs1250@sakura.kudpc.kyoto-u.ac.jp, Tel:075-753-4546,
 Fax:075-753-4586)
 COMMENT Submitted (21-JUL-1993) to DDBJ by:
 Masabumi Minami
 Department of Pharmacology
 Faculty of Pharmaceutical Sciences
 Kyoto University
 Kyoto, Kyoto 606-01
 Japan
 Phone: 075-753-4546
 Fax: 075-753-4586.
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 DEFINITION Rattus norvegicus kappa opioid receptor gene, exon 4 and complete
 cds.
 ACCESSION U17995
 NID 9727258
 KEYWORDS
 SEGMENT
 SOURCE 3 of 3
 ORGANISM Norway rat.
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 Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
 Vertebrata; Euthera; Rodentia; Sciurognathi; Myomorpha; Muridae;
 Murinae; Rattus.
 1 (bases 1 to 4048)
 REFERENCE Yakovlev,A.G., Krueger,K.E. and Faden,A.I.
 AUTHORS Structure and expression of a rat kappa opioid receptor gene
 JOURNAL J. Biol. Chem. 270 (12), 6421-6424 (1995)
 MEDLINE 95204422
 REFERENCE 2 (bases 1 to 4048)
 AUTHORS Yakovlev,A.G.
 TITLE Direct Submission
 JOURNAL Submitted (02-DEC-1994) Alexander G. Yakovlev, Georgetown

University School of Medicine, Neurology, 3900 Reservoir Rd.,
 Washington, DC 20007, USA
 FEATURES
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 DEFINITION Rattus norvegicus kappa opioid receptor mRNA, complete cds.
 ACCESSION U00442
 NID 9403486
 KEYWORDS
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 ORGANISM Norway rat.
 Rattus norvegicus
 Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
 Vertebrata; Euthera; Rodentia; Sciurognathi; Myomorpha; Muridae;
 Murinae; Rattus.
 1 (bases 1 to 4742)
 REFERENCE Meng,F., Xie,G.-X., Thompson,R.C., Mansour,A., Goldstein,A.,
 AUTHORS Watson,S.J. and Akil,H.
 TITLE Cloning and pharmacological characterization of a rat kappa opioid
 receptor
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 90, 9954-9958 (1993)
 MEDLINE 94052210
 REFERENCE 2 (bases 1 to 4742)
 AUTHORS Meng,F.
 TITLE Direct Submission
 JOURNAL Submitted (05-AUG-1993) Fan Meng, Mental Health Research Institute,
 University of Michigan, 205 Zina Pitcher Place, Ann Arbor, Michigan
 48109, USA
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(TM)

Release 3.0.4A John F. Collins, Biocomputing Research Unit.
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Distribution rights by Oxford Molecular Ltd

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Run on: Tue Apr 21 01:24:58 1998; MasPar time 142.36 Seconds
Tabular output not generated. 810.633 Million cell updates/sec

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Scoring table: TABLE jmetric
Gap 60

Mmatch STD : Dbase 0; Query 0

Searched: 159651 segs; 57698962 bases x 2

Post-processing: Minimum Match 0%
Listing first 1000 summaries

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8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33

Statistics: Mean 7.723; Variance 3.020; scale 2.557

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	729	73.3	1142	20	T12550 Human kappa oploid re	1.31e-231
3	245	24.6	2447	10	Q56702 Partial sequence of t	1.31e-231
4	32	3.2	1410	13	Q75926 Mouse kappa oploid re	1.52e-11
5	32	3.2	2481	15	Q86725 Murine kappa oploid re	1.52e-11
6	29	2.9	1821	10	Q56700 Sequence of murine de	5.30e-09
7	29	2.9	2216	11	Q66655 Murine delta oploid r	5.30e-09
8	29	2.9	2272	13	Q75927 Mouse delta oploid re	5.30e-09
9	26	2.6	1618	14	Q88223 Transcription regulat	1.52e-06
10	26	2.6	1618	14	Q88222 Rat mu oploid recep	1.52e-06
11	26	2.6	2070	12	Q79199 Rat mu-subtype oploid	1.52e-06
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13	25	2.5	1610	14	Q89226 Human mu oploid recep	9.56e-06
14	25	2.5	2160	15	Q93102 Human mu oploid recep	9.56e-06
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16	20	2.0	20	20	T12552 Human kappa oploid re	5.76e-02
17	20	2.0	39	20	T12554 Human kappa oploid re	5.76e-02
18	20	2.0	1265	7	Q45654 Murine somatostatin r	5.76e-02
19	20	2.0	1330	13	Q75928 Mouse oploid receptor	5.76e-02
20	20	2.0	1567	14	Q89233 Rat oploid receptor c	5.76e-02
21	20	2.0	1634	7	Q45653 Human somatostatin re	5.76e-02
22	20	2.0	1981	10	Q56705 Partial sequence of t	5.76e-02
23	20	2.0	2600	14	Q90906 Mouse kappa-3 oploid	5.76e-02
24	20	2.0	2706	15	Q92972 Rat oporph receptor	5.76e-02
25	18	1.8	1227	9	Q54832 Sequence of clone W22	1.41e+00
26	18	1.8	1227	23	T37306 Murine gonadotropin-r	1.41e+00
27	18	1.8	1296	7	Q45657 Human somatostatin re	1.41e+00
28	18	1.8	2237	15	Q89779 Cotransporter protein	1.41e+00
29	17	1.7	489	5	Q34771 Eps-1lon oploid recep	6.47e+00
30	17	1.7	1538	31	T69549 PCENP-3-1 cDNA.	6.47e+00
31	17	1.7	2643	6	Q39212 Rat pheromone recepto	6.47e+00
32	17	1.7	1715	1	N81564 CEN-B cDNA.	6.47e+00
33	17	1.7	11724	2	N70102 Complete genomic sequ	6.47e+00
34	17	1.7	11725	33	T79723 Human protein C gene.	6.47e+00
35	17	1.7	11725	22	T32796 Human protein C gene.	6.47e+00
36	17	1.7	20	30	T13871 Human K-Arp channel s	2.80e+01
37	16	1.6	88	4	N10118 Gene encoding human i	2.80e+01
38	16	1.6	90	4	N10117 Insulin B-chain duple	2.80e+01
39	16	1.6	134	2	N61204 Sequence of avian ery	2.80e+01
40	16	1.6	176	15	Q94407 Sargine derived osteo	2.80e+01
41	16	1.6	270	2	N81773 Sequence encoding hum	2.80e+01
42	16	1.6	354	3	N40255 Sequence encoding pro	2.80e+01
43	16	1.6	480	12	Q78151 potato starch branchi	2.80e+01
44	16	1.6	726	31	T77788 G-protein coupled rec	2.80e+01
45	16	1.6	822	12	Q74408 New flower bud induci	2.80e+01
46	16	1.6	959	8	Q49499 Nucleotide sequence (2.80e+01
47	16	1.6	976	29	T63288 Partial human tryptop	2.80e+01
48	16	1.6	976	29	T63288 Partial human tryptop	2.80e+01
49	16	1.6	1130	20	T69250 Human somatostatin re	2.80e+01
50	16	1.6	1149	20	T09948 High-affinity melatin	2.80e+01
51	16	1.6	1173	29	T61866 Human ATP sensitive p	2.80e+01
52	16	1.6	1257	2	N70394 Mouse ATP sensitive p	2.80e+01
53	16	1.6	1278	30	T67088 Sequence encoding hum	2.80e+01
54	16	1.6	1332	30	T67087 Human K-Arp channel s	2.80e+01
55	16	1.6	1511	7	Q45653 Human somatostatin re	2.80e+01
56	16	1.6	1796	7	Q45658 Epsilon oploid recept	2.80e+01
57	16	1.6	2028	15	Q89924 Murine somatostatin r	2.80e+01
58	16	1.6	2029	3	Q20494 PN-1 alpha analogue,	2.80e+01
59	16	1.6	2029	3	Q20496 PN-1 alpha analogue,	2.80e+01
60	16	1.6	2029	3	Q20496 PN-1 alpha analogue,	2.80e+01
61	16	1.6	2031	1	N81281 Sequence of coding re	2.80e+01
62	16	1.6	2031	15	Q89925 Protease Nexin-1 type	2.80e+01
63	16	1.6	2032	3	Q22587 PN-1 beta analogue, p	2.80e+01
64	16	1.6	2032	3	Q22585 PN-1 beta analogue, p	2.80e+01
65	16	1.6	2032	3	Q22586 PN-1 beta analogue, p	2.80e+01
66	16	1.6	2032	3	Q22586 PN-1 beta analogue, p	2.80e+01
67	16	1.6	2032	3	Q22586 PN-1 beta analogue, p	2.80e+01
68	16	1.6	2032	3	Q22586 PN-1 beta analogue, p	2.80e+01
69	16	1.6	2032	3	Q22586 PN-1 beta analogue, p	2.80e+01
70	16	1.6	2032	3	Q22586 PN-1 beta analogue, p	2.80e+01
71	16	1.6	2032	3	Q22586 PN-1 beta analogue, p	2.80e+01
72	16	1.6	2032	3	Q22586 PN-1 beta analogue, p	2.80e+01
73	16	1.6	2032	3	Q22586 PN-1 beta analogue, p	2.80e+01
74	16	1.6	2032	3	Q22586 PN-1 beta analogue, p	2.80e+01
75	16	1.6	2032	3	Q22586 PN-1 beta analogue, p	2.80e+01
76	16	1.6	2032	3	Q22586 PN-1 beta analogue, p	2.80e+01
77	16	1.6	2032	3	Q22586 PN-1 beta analogue, p	2.80e+01
78	16	1.6	2032	3	Q22586 PN-1 beta analogue, p	2.80e+01
79	16	1.6	2032	3	Q22586 PN-1 beta analogue, p	2.80e+01
80	16	1.6	2032	3	Q22586 PN-1 beta analogue, p	2.80e+01
81	16	1.6	2032	3	Q22586 PN-1 beta analogue, p	2.80e+01
82	16	1.6	2032	3	Q22586 PN-1 beta analogue, p	2.80e+01
83	16	1.6	2032	3	Q22586 PN-1 beta analogue, p	2.80e+01
84	16	1.6	2032	3	Q22586 PN-1 beta analogue, p	2.80e+01
85	16	1.6	2032	3	Q22586 PN-1 beta analogue, p	2.80e+01
86	16	1.6	2032	3	Q22586 PN-1 beta analogue, p	2.80e+01
87	16	1.6	2032	3	Q22586 PN-1 beta analogue, p	2.80e+01
88	16	1.6	2032	3	Q22586 PN-1 beta analogue, p	2.80e+01
89	16	1.6	2032	3	Q22586 PN-1 beta analogue, p	2.80e+01
90	16	1.6	2032	3	Q22586 PN-1 beta analogue, p	2.80e+01
91	16	1.6	2032	3	Q22586 PN-1 beta analogue, p	2.80e+01
92	16	1.6	2032	3	Q22586 PN-1 beta analogue, p	2.80e+01
93	16	1.6	2032	3	Q22586 PN-1 beta analogue, p	2.80e+01
94	16	1.6	2032	3	Q22586 PN-1 beta analogue, p	2.80e+01
95	16	1.6	2032	3	Q22586 PN-1 beta analogue, p	2.80e+01
96	16	1.6	2032	3	Q22586 PN-1 beta analogue, p	2.80e+01
97	16	1.6	2032	3	Q22586 PN-1 beta analogue, p	2.80e+01
98	16	1.6	2032	3	Q22586 PN-1 beta analogue, p	2.80e+01
99	16	1.6	2032	3	Q22586 PN-1 beta analogue, p	2.80e+01
100	16	1.6	2032	3	Q22586 PN-1 beta analogue, p	2.80e+01

C	89	16	1.6	11478	32	T79805	Full length potato st	2.80e+01	162	15	1.5	984	28	T58676	Human luteinising hor	1.13e+02
C	90	16	1.6	11478	32	T79784	Full length potato st	2.80e+01	163	15	1.5	1029	4	Q26957	Guinea pig platelet a	1.13e+02
C	91	16	1.6	580073	24	T58840	Myoplasma genitalium	1.80e+01	164	15	1.5	1155	4	Q26553	RIN10 CDNA clone.	1.13e+02
C	92	15	1.5	20	14	Q89232	Rat opioid receptor P	1.3e+02	165	15	1.5	1221	5	Q33105	pig coding sequence f	1.13e+02
C	93	15	1.5	26	23	T38625	Chimaeric human/murin	1.13e+02	166	15	1.5	1228	1	N80606	Lambda SMW4 encodin	1.13e+02
C	94	15	1.5	26	15	Q94511	Human/murine chimeric	1.13e+02	167	15	1.5	1228	1	Q10016	Clone lambda SMW4 vi	1.13e+02
C	95	15	1.5	26	23	T38626	Chimaeric human/murin	1.13e+02	168	15	1.5	1228	7	Q42663	Clone lambda SMW4 en	1.13e+02
C	96	15	1.5	26	15	Q94512	Human/murine chimeric	1.13e+02	169	15	1.5	1239	21	T29530	Human ventricule A2a r	1.13e+02
C	97	15	1.5	36	20	T13181	Human insulin coding	1.13e+02	170	15	1.5	1239	17	T00645	Human A2a adenosine r	1.13e+02
C	98	15	1.5	66	9	Q55099	DNA encoding signal p	1.13e+02	171	15	1.5	1239	18	T07649	Human adenosine recep	1.13e+02
C	99	15	1.5	66	5	Q29921	Hexa-histidine encodi	1.13e+02	172	15	1.5	1240	16	Q48415	Human A2a adenosine r	1.13e+02
C	100	15	1.5	66	17	T16100	Locust adipokinetic h	1.13e+02	173	15	1.5	1240	16	T02359	TIMP-3 DNA clone Tim	1.13e+02
C	101	15	1.5	96	31	T43258	HYR1 region of E2 gen	1.13e+02	174	15	1.5	1270	15	Q44340	Sequence encoding a p	1.13e+02
C	102	15	1.5	112	4	Q25961	Human PAR receptor 5	1.13e+02	175	15	1.5	1276	14	Q82747	Human tissue inhibito	1.13e+02
C	103	15	1.5	117	10	Q76929	Human genome fragmen	1.13e+02	176	15	1.5	1285	15	Q86744	TIMP-3 metalloprotein	1.13e+02
C	104	15	1.5	228	8	Q59897	Human brain Expressed	1.13e+02	177	15	1.5	1449	17	Q98951	bgl7 insert encoding	1.13e+02
C	105	15	1.5	242	32	T79802	Potato starch branchi	1.13e+02	178	15	1.5	1461	1	Q06633	Unique sequence fragm	1.13e+02
C	106	15	1.5	242	32	T79781	Potato starch branchi	1.13e+02	179	15	1.5	1478	22	T37066	Tomato green fruit-8p	1.13e+02
C	107	15	1.5	250	20	T22215	Human gene signature	1.13e+02	180	15	1.5	1506	22	T36070	Mullerian inhibiting	1.13e+02
C	108	15	1.5	256	12	Q71165	Merlin gene fragment	1.13e+02	181	15	1.5	1518	8	Q49764	Mist2A/mist2B.	1.13e+02
C	109	15	1.5	261	20	T17831	Optimised insulin cod	1.13e+02	182	15	1.5	1553	17	T03109	Human luteinising hor	1.13e+02
C	110	15	1.5	290	18	T19174	Human gene signature	1.13e+02	183	15	1.5	1602	12	Q72217	Human adrenergic rece	1.13e+02
C	111	15	1.5	315	21	T22951	Human gene signature	1.13e+02	184	15	1.5	1633	9	Q51227	Human MSH-R gene.	1.13e+02
C	112	15	1.5	331	8	Q61093	Human brain Expressed	1.13e+02	185	15	1.5	1653	27	T59022	Guinea pig platelet a	1.13e+02
C	113	15	1.5	372	10	Q57441	Glycogenin like prote	1.13e+02	186	15	1.5	1660	5	Q32869	Human PMP-22 CDNA.	1.13e+02
C	114	15	1.5	374	18	T19518	Human gene signature	1.13e+02	187	15	1.5	1673	15	Q97268	Dopamine receptor D5	1.13e+02
C	115	15	1.5	379	23	T38628	Chimaeric human/murin	1.13e+02	188	15	1.5	1701	11	Q65617	Human zona pellucida	1.13e+02
C	116	15	1.5	379	23	T38627	Chimaeric human/murin	1.13e+02	189	15	1.5	1736	5	Q32870	Rat PMP CDNA.	1.13e+02
C	117	15	1.5	379	23	T38635	Chimaeric human/murin	1.13e+02	190	15	1.5	1739	11	Q67067	Beta-1,3-galactosylt	1.13e+02
C	118	15	1.5	379	15	Q94521	Human/murine chimeric	1.13e+02	191	15	1.5	1771	3	Q21014	Dopamine D1 receptor	1.13e+02
C	119	15	1.5	379	15	Q94514	Human/murine chimeric	1.13e+02	192	15	1.5	1809	10	Q58776	Human glucagon recept	1.13e+02
C	120	15	1.5	379	23	T38634	Chimaeric human/murin	1.13e+02	193	15	1.5	1816	17	Q98948	bgl4 insert encoding	1.13e+02
C	121	15	1.5	379	15	Q94520	Human/murine chimeric	1.13e+02	194	15	1.5	1822	17	Q98949	bgl3 insert encoding a	1.13e+02
C	122	15	1.5	379	15	Q94517	Human/murine chimeric	1.13e+02	195	15	1.5	1834	1	Q04690	Encores Mammalian anl	1.13e+02
C	123	15	1.5	379	23	T38631	Chimaeric human/murin	1.13e+02	196	15	1.5	1848	14	Q86998	Aminopeptidase O12 cl	1.13e+02
C	124	15	1.5	379	15	Q94513	Human/murine chimeric	1.13e+02	197	15	1.5	1872	11	Q66176	Seven transmembrane r	1.13e+02
C	125	15	1.5	381	8	Q61274	Human brain Expressed	1.13e+02	198	15	1.5	1978	12	Q72212	Truncated human alpha	1.13e+02
C	126	15	1.5	397	8	Q60786	Human brain Expressed	1.13e+02	199	15	1.5	1987	21	T11624	Human truncated alpha	1.13e+02
C	127	15	1.5	413	13	Q73709	Retrolactospon probe	1.13e+02	200	15	1.5	1997	21	T11600	Human alpha-1C adrene	1.13e+02
C	128	15	1.5	421	8	Q60935	Human brain Expressed	1.13e+02	201	15	1.5	1998	12	Q72213	Human alpha-1C adrene	1.13e+02
C	129	15	1.5	523	17	Q98945	bgl28 insert encoding	1.13e+02	202	15	1.5	2004	21	T11599	Human alpha-1C adrene	1.13e+02
C	130	15	1.5	525	17	Q98944	Partial bgl28 insert e	1.13e+02	203	15	1.5	2005	12	Q72211	Human alpha-1C adrene	1.13e+02
C	131	15	1.5	538	33	T73917	E6-binding protein b6	1.13e+02	204	15	1.5	2104	13	Q83844	Human interleukin-12	1.13e+02
C	132	15	1.5	538	17	T08639	HPV E6-binding protei	1.13e+02	205	15	1.5	2104	28	T59732	Human interleukin-12	1.13e+02
C	133	15	1.5	623	33	T70417	Mouse rhodopsin CDNA	1.13e+02	206	15	1.5	2160	9	Q54833	Sequence encoding hum	1.13e+02
C	134	15	1.5	629	33	T70430	Human peripheral CDNA	1.13e+02	207	15	1.5	2160	23	T37307	Human gondotropin-re	1.13e+02
C	135	15	1.5	641	4	N30130	Sequence of VP3 gene	1.13e+02	208	15	1.5	2178	3	N30016	Sequence of the promo	1.13e+02
C	136	15	1.5	641	16	Q91408	Human olfactory recep	1.13e+02	209	15	1.5	2217	17	Q51427	g16 insert encoding a	1.13e+02
C	137	15	1.5	644	16	Q91407	Human olfactory recep	1.13e+02	210	15	1.5	2344	9	Q51427	Human FACC CDNA clone	1.13e+02
C	138	15	1.5	645	16	Q91409	Human olfactory recep	1.13e+02	211	15	1.5	2363	10	Q58126	Phytase gene.	1.13e+02
C	139	15	1.5	645	16	Q91410	Human olfactory recep	1.13e+02	212	15	1.5	2365	11	Q62815	Riboflavin 7 gene (ri	1.13e+02
C	140	15	1.5	702	4	N30148	Sequence encoding a p	1.13e+02	213	15	1.5	2379	15	Q56944	A. niger phytase gene	1.13e+02
C	141	15	1.5	705	7	Q42589	Human Fc polypeptide	1.13e+02	214	15	1.5	2410	29	T63176	Human TSH-receptor CD	1.13e+02
C	142	15	1.5	705	7	T40788	Human Fc polypeptide	1.13e+02	215	15	1.5	2413	2	Q11124	Human TSH-receptor co	1.13e+02
C	143	15	1.5	734	18	T20481	Human gene signature	1.13e+02	216	15	1.5	2415	2	Q12868	Human Thyroid Stimula	1.13e+02
C	144	15	1.5	780	11	Q67207	Gly184, Ala186-Canine	1.13e+02	217	15	1.5	2416	12	Q71200	scd61, a subclone of	1.13e+02
C	145	15	1.5	780	11	Q67206	Canine growth hormone	1.13e+02	218	15	1.5	2452	11	Q68670	pmgM1.3 Mycoplasma ga	1.13e+02
C	146	15	1.5	781	2	N60349	Sequence encoding gam	1.13e+02	219	15	1.5	2453	28	T51536	Mycobacterium gallise	1.13e+02
C	147	15	1.5	792	2	N80193	Sequence of probe "cl	1.13e+02	220	15	1.5	2465	32	T58086	Human heat shock prot	1.13e+02
C	148	15	1.5	806	4	N50697	Rat pre-proANP DNA.	1.13e+02	221	15	1.5	2469	2	Q12359	Human Thyroid Stimula	1.13e+02
C	149	15	1.5	806	4	Q41456	Rat pre-proANP DNA.	1.13e+02	222	15	1.5	2520	33	T73337	Rat CRIT CDNA.	1.13e+02
C	150	15	1.5	820	16	T03361	TIMP-3 clone Timp3CM	1.13e+02	223	15	1.5	2547	29	T67908	H. pylori cytoplasmic	1.13e+02
C	151	15	1.5	829	1	N90234	Gastrin recombinant D	1.13e+02	224	15	1.5	2575	9	Q54641	Human A2a adenosine r	1.13e+02
C	152	15	1.5	843	29	T67423	H. pylori cytoplasmic	1.13e+02	225	15	1.5	2686	24	T45081	Beta-1,4-galactosylt	1.13e+02
C	153	15	1.5	847	15	Q86965	Clone conty. yeast pp	1.13e+02	226	15	1.5	2707	10	Q57014	PKC epsilon.	1.13e+02
C	154	15	1.5	847	15	Q86972	Clone conty. yeast pp	1.13e+02	227	15	1.5	2809	28	T51531	Mycobacterium gallise	1.13e+02
C	155	15	1.5	847	15	Q10546	Yeast peptidyl-prolyl	1.13e+02	228	15	1.5	2881	31	Q68668	pmgA 1.2 and partial	1.13e+02
C	156	15	1.5	853	3	N30073	DNA sequence capable	1.13e+02	229	15	1.5	2942	31	T68334	Human host cell prote	1.13e+02
C	157	15	1.5	853	3	N46212	DNA sequence capable	1.13e+02	230	15	1.5	3012	10	Q36997	CDNA encoding human cal	1.13e+02
C	158	15	1.5	866	11	Q79681	Cynomolgus Monkey zon	1.13e+02	231	15	1.5	3130	17	Q98950	bgl8 insert encoding a	1.13e+02
C	159	15	1.5	951	30	T68792	Melanocortin-1 recep	1.13e+02	232	15	1.5	3154	9	Q51428	Human FACC CDNA clone	1.13e+02
C	160	15	1.5	963	16	T03360	TIMP-3 DNA clone Tim	1.13e+02	233	15	1.5	3231	23	T34615	NTT1-1 nerve protein	1.13e+02
C	161	15	1.5	984	17	T03108	Human luteinising hor	1.13e+02	234	15	1.5	3390	10	Q62283	CDNA coding human pla	1.13e+02

C	235	1.5	3416	10	063282	cDNA coding human ova	1.13e+02	308	14	1.4	435	23	T37121	GM-CSF (N-linked site	4.24e+02
C	236	1.5	3504	1	065304	Clone Rmd2 encoding 1	1.13e+02	309	14	1.4	476	28	T47769	Xenopus laevis luminesce	4.24e+02
C	237	1.5	3510	19	T18696	RAP-1 radiation prote	1.13e+02	310	14	1.4	476	29	T60501	5' lux fragment of PB	4.24e+02
C	238	1.5	3521	7	041226	Clone Gg3 encoding ma	1.13e+02	311	14	1.4	495	15	068357	Human granulocyte mac	4.24e+02
C	239	1.5	3558	3	022596	Coding region of plas	1.13e+02	312	14	1.4	495	15	068357	Vaccinia E8L promoter	4.24e+02
C	240	1.5	3560	14	087444	Drosophila semaphorin	1.13e+02	313	14	1.4	499	12	067878	Sequence of new sigma	4.24e+02
C	241	1.5	3566	10	056643	Human tyrosinase gene	1.13e+02	314	14	1.4	501	5	029154	Partial sequence of p	4.24e+02
C	242	1.5	3592	7	042411	Human CTR cDNA clone.	1.13e+02	315	14	1.4	514	2	012781	hGM-CSF/IL23Asp27Gln	4.24e+02
C	243	1.5	3710	2	012164	Sequence encoding Hum	1.13e+02	316	14	1.4	514	15	068358	Human granulocyte mac	4.24e+02
C	244	1.5	3856	1	003097	Bnrd2b genomic clone.	1.13e+02	317	14	1.4	563	2	011773	Sequence encoding can	4.24e+02
C	245	1.5	4417	2	012163	Sequence encoding can	1.13e+02	318	14	1.4	563	9	055055	Sequence of orphan re	4.24e+02
C	246	1.5	4488	8	051426	Human RMC cDNA clone	1.13e+02	319	14	1.4	573	11	063729	pig somatotropin gene	4.24e+02
C	247	1.5	4670	4	025107	DHRP-Ap fusion prote	1.13e+02	320	14	1.4	574	1	N91699	Part of the sequence	4.24e+02
C	248	1.5	6232	5	028269	Human calcium channel	1.13e+02	321	14	1.4	579	4	026671	Recombinant porcine s	4.24e+02
C	249	1.5	6578	19	T18767	RSV RNA-dependent RNA	1.13e+02	322	14	1.4	633	31	T60688	cDNA encoding soluble	4.24e+02
C	250	1.5	7175	6	037818	Sequence encoding the	1.13e+02	323	14	1.4	641	18	T19851	Human gene signature	4.24e+02
C	251	1.5	7175	6	084658	Human neuronal calcit	1.13e+02	324	14	1.4	654	31	T60686	cDNA encoding soluble	4.24e+02
C	252	1.5	7362	15	084657	Human neuronal calcit	1.13e+02	325	14	1.4	654	2	Q10269	Human BMP.	4.24e+02
C	253	1.5	7362	6	037817	Sequence encoding the	1.13e+02	326	14	1.4	661	2	N60246	Human granulocyte mac	4.24e+02
C	254	1.5	8201	20	T21170	pJG4-5-CDK-BP cDNA cl	1.13e+02	327	14	1.4	665	2	N70571	Sequence encoding hum	4.24e+02
C	255	1.5	9515	14	035145	pseudomonas aeruginos	1.13e+02	328	14	1.4	672	11	070140	Cadherin cDNA.	4.24e+02
C	256	1.5	10266	22	T33007	Mouse SKV-related gen	1.13e+02	329	14	1.4	684	29	T67447	H. pylori transpore	4.24e+02
C	257	1.5	10684	23	T33758	Control region isolat	1.13e+02	330	14	1.4	702	31	T67704	cDNA encoding soluble	4.24e+02
C	258	1.5	11298	33	T86756	Human high affinity 1	1.13e+02	331	14	1.4	716	3	N40283	H. pylori transpore	4.24e+02
C	259	1.5	11357	9	051024	Human FeCR1 beta chai	1.13e+02	332	14	1.4	723	29	T67921	DNA fragment function	4.24e+02
C	260	1.5	12720	10	064211	L.lactis branched am1	1.13e+02	333	14	1.4	737	13	N40082	Sequence encoding por	4.24e+02
C	261	1.5	13104	7	046852	Clone of recombinant	1.13e+02	334	14	1.4	744	2	N92401	Sequence encoding 11p	4.24e+02
C	262	1.5	14704	3	020685	PKS 741 insert contg.	1.13e+02	335	14	1.4	744	2	N70674	Sequence encoding 11p	4.24e+02
C	263	1.5	15223	29	T63430	Respiratory syncytial	1.13e+02	336	14	1.4	755	1	N81117	Porcine somatotropin	4.24e+02
C	264	1.5	28804	23	T37329	Sphingian biosynthetic	1.13e+02	337	14	1.4	773	2	004018	Granulocyte macrophag	4.24e+02
C	265	1.5	580073	27	T59840	Mycoplasma genitalium	1.13e+02	338	14	1.4	773	2	N60457	Colony stimulating fa	4.24e+02
C	266	1.4	21	6	Q40363	Sequence of PCR prime	4.24e+02	339	14	1.4	787	14	N93066	Sequence encoding hum	4.24e+02
C	267	1.4	21	14	083684	Epsilon oploid recepi	4.24e+02	340	14	1.4	787	2	N80223	Close encoding bovine	4.24e+02
C	268	1.4	28	21	T33202	yeast CAMP-dependent	4.24e+02	341	14	1.4	787	14	Q84865	Close pcd-human-GM-CS	4.24e+02
C	269	1.4	29	9	053869	Plasmodium yoelii spo	4.24e+02	342	14	1.4	793	4	N60364	Human granulocyte mac	4.24e+02
C	270	1.4	30	2	013759	D2 receptor probe.	4.24e+02	343	14	1.4	793	4	N20008	Hybrid human leukocyt	4.24e+02
C	271	1.4	30	23	T18890	Calcium channel domai	4.24e+02	344	14	1.4	795	1	004263	Encodes Colon Cancer	4.24e+02
C	272	1.4	37	5	028822	Ribozyme.	4.24e+02	345	14	1.4	799	3	015228	arod gene.	4.24e+02
C	273	1.4	38	9	055262	Stable hairpin ribozy	4.24e+02	346	14	1.4	813	4	Q24524	GM-CSF/IL-3 fusion pr	4.24e+02
C	274	1.4	40	29	T69522	Plasmid p182Sfil comp	4.24e+02	347	14	1.4	813	4	Q27810	GM-CSF/IL-3 fusion pr	4.24e+02
C	275	1.4	42	5	033464	PACR Primer #6.	4.24e+02	348	14	1.4	813	4	Q27810	PIXX 321.	4.24e+02
C	276	1.4	42	5	028821	Anti-tumour ribozyme	4.24e+02	349	14	1.4	825	2	010950	IL-3/GM-CSF fusion pr	4.24e+02
C	277	1.4	56	5	Q28822	Anti-tumour ribozyme	4.24e+02	350	14	1.4	825	2	010950	Human IL-3/GM-CSF fus	4.24e+02
C	278	1.4	57	18	T05755	Polymerase Bst restri	4.24e+02	351	14	1.4	825	2	Q27811	Partial sequence of t	4.24e+02
C	279	1.4	79	5	033795	Microsatellite sequen	4.24e+02	352	14	1.4	825	2	010950	H. pylori secreted or	4.24e+02
C	280	1.4	83	23	T33403	Oligonucleotide 220 f	4.24e+02	353	14	1.4	825	2	010950	Ecoti fragment common	4.24e+02
C	281	1.4	90	7	Q47048	GM-CSF oligomer, saps	4.24e+02	354	14	1.4	825	2	010950	Sequence encoding exo	4.24e+02
C	282	1.4	91	23	T34404	Oligonucleotide 221 f	4.24e+02	355	14	1.4	825	2	Q20271	Human IL-3/GM-CSF fus	4.24e+02
C	283	1.4	101	18	T19410	Human gene signature	4.24e+02	356	14	1.4	825	2	Q20271	Human IL-3/GM-CSF fus	4.24e+02
C	284	1.4	107	31	T60683	Beta chain of Class I	4.24e+02	357	14	1.4	825	2	Q20271	Human IL-3/GM-CSF fus	4.24e+02
C	285	1.4	111	31	T47135	Human gene signature	4.24e+02	358	14	1.4	825	2	Q20271	Human IL-3/GM-CSF fus	4.24e+02
C	286	1.4	125	21	T22554	Human gene signature	4.24e+02	359	14	1.4	825	2	Q20271	Human IL-3/GM-CSF fus	4.24e+02
C	287	1.4	125	21	T22554	Human gene signature	4.24e+02	360	14	1.4	825	2	Q20271	Human IL-3/GM-CSF fus	4.24e+02
C	288	1.4	125	21	T22554	Human gene signature	4.24e+02	361	14	1.4	825	2	Q20271	Human IL-3/GM-CSF fus	4.24e+02
C	289	1.4	125	21	T22554	Human gene signature	4.24e+02	362	14	1.4	825	2	Q20271	Human IL-3/GM-CSF fus	4.24e+02
C	290	1.4	125	21	T22554	Human gene signature	4.24e+02	363	14	1.4	825	2	Q20271	Human IL-3/GM-CSF fus	4.24e+02
C	291	1.4	125	21	T22554	Human gene signature	4.24e+02	364	14	1.4	825	2	Q20271	Human IL-3/GM-CSF fus	4.24e+02
C	292	1.4	125	21	T22554	Human gene signature	4.24e+02	365	14	1.4	825	2	Q20271	Human IL-3/GM-CSF fus	4.24e+02
C	293	1.4	125	21	T22554	Human gene signature	4.24e+02	366	14	1.4	825	2	Q20271	Human IL-3/GM-CSF fus	4.24e+02
C	294	1.4	125	21	T22554	Human gene signature	4.24e+02	367	14	1.4	825	2	Q20271	Human IL-3/GM-CSF fus	4.24e+02
C	295	1.4	125	21	T22554	Human gene signature	4.24e+02	368	14	1.4	825	2	Q20271	Human IL-3/GM-CSF fus	4.24e+02
C	296	1.4	125	21	T22554	Human gene signature	4.24e+02	369	14	1.4	825	2	Q20271	Human IL-3/GM-CSF fus	4.24e+02
C	297	1.4	125	21	T22554	Human gene signature	4.24e+02	370	14	1.4	825	2	Q20271	Human IL-3/GM-CSF fus	4.24e+02
C	298	1.4	125	21	T22554	Human gene signature	4.24e+02	371	14	1.4	825	2	Q20271	Human IL-3/GM-CSF fus	4.24e+02
C	299	1.4	125	21	T22554	Human gene signature	4.24e+02	372	14	1.4	825	2	Q20271	Human IL-3/GM-CSF fus	4.24e+02
C	300	1.4	125	21	T22554	Human gene signature	4.24e+02	373	14	1.4	825	2	Q20271	Human IL-3/GM-CSF fus	4.24e+02
C	301	1.4	125	21	T22554	Human gene signature	4.24e+02	374	14	1.4	825	2	Q20271	Human IL-3/GM-CSF fus	4.24e+02
C	302	1.4	125	21	T22554	Human gene signature	4.24e+02	375	14	1.4	825	2	Q20271	Human IL-3/GM-CSF fus	4.24e+02
C	303	1.4	125	21	T22554	Human gene signature	4.24e+02	376	14	1.4	825	2	Q20271	Human IL-3/GM-CSF fus	4.24e+02
C	304	1.4	125	21	T22554	Human gene signature	4.24e+02	377	14	1.4	825	2	Q20271	Human IL-3/GM-CSF fus	4.24e+02
C	305	1.4	125	21	T22554	Human gene signature	4.24e+02	378	14	1.4	825	2	Q20271	Human IL-3/GM-CSF fus	4.24e+02
C	306	1.4	125	21	T22554	Human gene signature	4.24e+02	379	14	1.4	825	2	Q20271	Human IL-3/GM-CSF fus	4.24e+02
C	307	1.4	125	21	T22554	Human gene signature	4.24e+02	380	14	1.4	825	2	Q20271	Human IL-3/GM-CSF fus	4.24e+02

C	381	14	1.4	1183	24	T42222	Human TATA-binding pr	4.24e+02	C	454	14	1.4	1849	15	Q91284	F. longibrachiatum en	4.24e+02
C	382	14	1.4	1238	23	T35596	Triticum tauschii CRE	4.24e+02	C	455	14	1.4	1849	22	T32223	Tritoderma endogluc	4.24e+02
C	383	14	1.4	1241	4	Q27368	UGT1F Exon 1 from th	4.24e+02	C	456	14	1.4	1855	30	T65381	Human adrenal gland c	4.24e+02
C	384	14	1.4	1244	7	Q45566	Murine somatostatin r	4.24e+02	C	457	14	1.4	1864	40	Q46240	Herpes simplex virus	4.24e+02
C	385	14	1.4	1245	2	O10268	Xenopus neurogenic di	4.24e+02	C	458	14	1.4	1909	2	O11919	Toxoplasma gondii clo	4.24e+02
C	386	14	1.4	1275	32	T74888	RAC protein kinase C-	4.24e+02	C	459	14	1.4	1919	8	O51094	JM haemagglutinin	4.24e+02
C	387	14	1.4	1302	33	T67134	E. coli thymidine pho	4.24e+02	C	460	14	1.4	1928	22	T36140	Gutrea pig L-asparagi	4.24e+02
C	388	14	1.4	1311	7	Q41469	CDNA encoding soluble	4.24e+02	C	461	14	1.4	1943	23	T48583	Human tub genomic seq	4.24e+02
C	389	14	1.4	1323	31	T60700	Rhodococcus rhodocho	4.24e+02	C	462	14	1.4	1969	29	T64531	Glutamate dehydrogen	4.24e+02
C	390	14	1.4	1341	15	Q90492	CDNA encoding soluble	4.24e+02	C	463	14	1.4	1981	10	O56705	Partial sequence of t	4.24e+02
C	391	14	1.4	1344	31	T60705	Human somatostatin re	4.24e+02	C	464	14	1.4	1983	22	T32235	Nutree Class II type	4.24e+02
C	392	14	1.4	1351	7	Q45655	Nutree Class II type	4.24e+02	C	465	14	1.4	2008	15	O94599	Enter enterotoxin enco	4.24e+02
C	393	14	1.4	1360	22	T33234	Hop latent virus coat	4.24e+02	C	466	14	1.4	2012	30	T68823	Cytosolic phospholipa	4.24e+02
C	394	14	1.4	1375	30	T67082	Cotton UDP glucose sy	4.24e+02	C	467	14	1.4	2019	29	T47706	Human ERX2 gene.	4.24e+02
C	395	14	1.4	1398	20	T63700	Human calcium channel	4.24e+02	C	468	14	1.4	2040	13	T63735	Human G-protein coupl	4.24e+02
C	396	14	1.4	1424	5	Q29273	Elm C10:O-acyl carrie	4.24e+02	C	469	14	1.4	2044	27	T13167	Rat interleukin-1 typ	4.24e+02
C	397	14	1.4	1433	11	O65397	Elm acyl-ACP thioeste	4.24e+02	C	470	14	1.4	2059	2	N60895	Sequence of plasmid p	4.24e+02
C	398	14	1.4	1433	22	T36108	C5A-like seven trans	4.24e+02	C	471	14	1.4	2070	8	O48515	Encodes rabbit HRI pr	4.24e+02
C	399	14	1.4	1433	14	O92306	Human CD20.4 antigen	4.24e+02	C	472	14	1.4	2070	12	O79199	Rat mu-subtype oploid	4.24e+02
C	400	14	1.4	1443	26	T45873	Zinc finger protein c	4.24e+02	C	473	14	1.4	2071	10	O56945	A. niger PH 2.5 acid	4.24e+02
C	401	14	1.4	1474	22	T14710	Human CD20.4 antigen	4.24e+02	C	474	14	1.4	2071	10	O58121	Mouse amyloid precurs	4.24e+02
C	402	14	1.4	1476	18	T08578	CD20 cDNA.	4.24e+02	C	475	14	1.4	2085	12	O69003	Mouse amyloid precurs	4.24e+02
C	403	14	1.4	1476	1	N90613	Human CD20 antigen cd	4.24e+02	C	476	14	1.4	2088	4	O27801	Mouse RXR-alpha codin	4.24e+02
C	404	14	1.4	1476	22	T14713	Resynthesised gluta	4.24e+02	C	477	14	1.4	2095	2	O13387	NADP-specific gluta	4.24e+02
C	405	14	1.4	1497	21	T06750	NADP-specific gluta	4.24e+02	C	478	14	1.4	2108	33	T64543	Human TRAF inhibitor	4.24e+02
C	406	14	1.4	1506	29	T64547	Homolox vector 443-8	4.24e+02	C	479	14	1.4	2110	7	T63726	Clone GP22 encoding m	4.24e+02
C	407	14	1.4	1507	28	T48511	Phytoene dehydrogenas	4.24e+02	C	480	14	1.4	2112	30	T68826	Cytosolic phospholipa	4.24e+02
C	408	14	1.4	1507	2	O68935	Phytoene dehydrogenas	4.24e+02	C	481	14	1.4	2117	22	T68826	Sf9 (suppressor of t	4.24e+02
C	409	14	1.4	1517	2	O13720	Phytoene dehydrogenas	4.24e+02	C	482	14	1.4	2130	14	T27050	Human H-2RIIP cDNA.	4.24e+02
C	410	14	1.4	1518	23	T40792	Phytoene dehydrogenas	4.24e+02	C	483	14	1.4	2137	29	T64542	NADP-specific gluta	4.24e+02
C	411	14	1.4	1522	23	T40793	Phytoene dehydrogenas	4.24e+02	C	484	14	1.4	2140	29	T64542	NADP-specific gluta	4.24e+02
C	412	14	1.4	1522	22	T37095	Phytoene dehydrogenas	4.24e+02	C	485	14	1.4	2160	15	O93102	Human mu opiate recep	4.24e+02
C	413	14	1.4	1525	8	Q45958	hRXR-beta3.	4.24e+02	C	486	14	1.4	2170	15	T04098	Mouse prostaglandin-F	4.24e+02
C	414	14	1.4	1525	8	Q45958	hRXR-beta3.	4.24e+02	C	487	14	1.4	2179	29	T63181	FSH receptor gene wil	4.24e+02
C	415	14	1.4	1540	2	N80917	Sequence of the 3'-en	4.24e+02	C	488	14	1.4	2180	5	O29377	FSHR DNA.	4.24e+02
C	416	14	1.4	1540	26	T28573	Bacterial antibiotic	4.24e+02	C	489	14	1.4	2196	1	O06815	Sequence encoding hea	4.24e+02
C	417	14	1.4	1558	31	T72721	Brassicin synthase fac	4.24e+02	C	490	14	1.4	2230	2	N81778	Sequence of porcine g	4.24e+02
C	418	14	1.4	1610	14	O89226	Human mu oploid recep	4.24e+02	C	491	14	1.4	2232	15	O96297	Human monocytic chema	4.24e+02
C	419	14	1.4	1618	14	O89223	Transcription regulat	4.24e+02	C	492	14	1.4	2236	1	N80604	Lambda APCR1614, amin	4.24e+02
C	420	14	1.4	1629	9	O54496	Alcaligenes bronchise	4.24e+02	C	493	14	1.4	2256	1	O20532	Sequence of clone lam	4.24e+02
C	421	14	1.4	1635	23	T37177	LKT-GNR fusion of pc	4.24e+02	C	494	14	1.4	2256	7	O42651	Lambda clone APC1681	4.24e+02
C	422	14	1.4	1642	8	Q45957	hRXR-beta2.	4.24e+02	C	495	14	1.4	2256	2	O100014	Clone lambda APC1681	4.24e+02
C	423	14	1.4	1642	8	Q45957	hRXR-beta2.	4.24e+02	C	496	14	1.4	2278	15	O27802	APP51.	4.24e+02
C	424	14	1.4	1642	8	Q45957	hRXR-beta2.	4.24e+02	C	497	14	1.4	2278	15	O27802	Rat 5HT transporter (4.24e+02
C	425	14	1.4	1642	8	Q45957	hRXR-beta2.	4.24e+02	C	498	14	1.4	2295	23	T31994	Nonense-mediated mRN	4.24e+02
C	426	14	1.4	1648	4	Q25532	Sequence of genomic c	4.24e+02	C	499	14	1.4	2297	23	T33949	Human Factor V cDNA P	4.24e+02
C	427	14	1.4	1674	17	T17846	Human lymphocyte PFA	4.24e+02	C	500	14	1.4	2297	23	T33949	Human Factor V heavy	4.24e+02
C	428	14	1.4	1679	13	O80522	Plasmid pSI4001 alpha	4.24e+02	C	501	14	1.4	2313	12	O74708	CDNA of App 770 gene	4.24e+02
C	429	14	1.4	1680	15	Q27150	Gutrea pig L-asparagi	4.24e+02	C	502	14	1.4	2333	11	O66637	Human Activin recepto	4.24e+02
C	430	14	1.4	1695	22	T36138	Human p1g L-asparagi	4.24e+02	C	503	14	1.4	2333	6	O37948	Sequence of a DNA iso	4.24e+02
C	431	14	1.4	1713	23	T36138	Human p1g L-asparagi	4.24e+02	C	504	14	1.4	2333	6	O37948	Human PH30 beta chain	4.24e+02
C	432	14	1.4	1717	14	O92299	Mango class II thioes	4.24e+02	C	505	14	1.4	2373	15	T72725	Herf-GM-CSF immuno	4.24e+02
C	433	14	1.4	1718	14	O90052	Melanoan differentiat	4.24e+02	C	506	14	1.4	2385	31	O70812	Protein Kinase (CKI)	4.24e+02
C	434	14	1.4	1721	15	O54257	APP-REP 751 amyloid p	4.24e+02	C	507	14	1.4	2385	12	O70812	Human HRR25-like case	4.24e+02
C	435	14	1.4	1721	15	O54257	SHR2 enterotoxin loc	4.24e+02	C	508	14	1.4	2385	15	O92947	Human HRR25-like case	4.24e+02
C	436	14	1.4	1722	15	O94598	Pepper Group 2 gene I	4.24e+02	C	509	14	1.4	2414	16	O65308	Wilson disease gene e	4.24e+02
C	437	14	1.4	1727	18	T16871	Fragment of plasmid p	4.24e+02	C	510	14	1.4	2415	7	O41056	Rat 5HT transporter c	4.24e+02
C	438	14	1.4	1738	18	T07280	Plasmid pSCM525 fragm	4.24e+02	C	511	14	1.4	2415	15	O94017	Rat 5HT transporter (4.24e+02
C	439	14	1.4	1738	22	T31616	Neurokinin-3 receptor	4.24e+02	C	512	14	1.4	2425	15	O11711	Shuttle vector pMW15	4.24e+02
C	440	14	1.4	1755	8	O49461	hRXR-beta1.	4.24e+02	C	513	14	1.4	2430	20	T08125	Human syndecan-1 gene	4.24e+02
C	441	14	1.4	1757	8	O45956	hRXR-beta1.	4.24e+02	C	514	14	1.4	2430	20	O73844	P. occultum DNA polym	4.24e+02
C	442	14	1.4	1757	8	O45956	hRXR-beta1.	4.24e+02	C	515	14	1.4	2439	31	T63354	Bacillus subtilis epr	4.24e+02
C	443	14	1.4	1762	5	Q28112	ETV HA (A2/suffolk/89	4.24e+02	C	516	14	1.4	2439	29	T53381	Extracellular protease	4.24e+02
C	444	14	1.4	1766	15	O97491	Plasmid pTSC22 + hmg	4.24e+02	C	517	14	1.4	2439	29	T53381	Epr gene encoding ext	4.24e+02
C	445	14	1.4	1767	21	T26580	Aspergillus oryzae ta	4.24e+02	C	518	14	1.4	2455	1	O04788	Rat D2 dopamine recep	4.24e+02
C	446	14	1.4	1767	21	T26580	Aspergillus oryzae ta	4.24e+02	C	519	14	1.4	2476	21	T18377	Plasmid pKMH1.	4.24e+02
C	447	14	1.4	1786	32	T71716	Human integrin-linked	4.24e+02	C	520	14	1.4	2492	12	O79480	Thai catfish GHRH/PAC	4.24e+02
C	448	14	1.4	1788	1	N71067	Sequence encoding equ	4.24e+02	C	521	14	1.4	2505	24	T45648	Mouse haematopoietic-	4.24e+02
C	449	14	1.4	1797	1	O04597	Equine hemagglutinin	4.24e+02	C	522	14	1.4	2521	28	T61926	Putative human cadher	4.24e+02
C	450	14	1.4	1800	2	Q14057	EIA gene from human a	4.24e+02	C	523	14	1.4	2521	31	T85404	Human cadherin-12 cod	4.24e+02
C	451	14	1.4	1816	24	T42315	Oilpalm ACP thioester	4.24e+02	C	524	14	1.4	2522	32	T47252	Bacillus subtilis ext	4.24e+02
C	452	14	1.4	1827	31	T63336	Human host cell prote	4.24e+02	C	525	14	1.4	2522	32	O11202	Plasmid pRW44d encod	4.24e+02
C	453	14	1.4	1849	15	O97716	Endoglucanase-II geno	4.24e+02	C	526	14	1.4	2539	3	Q15024	Rat prolactin poly A	4.24e+02

C	527	14	1.4	2555	2	011009	Fibulin B.	4.24e+02	C	600	14	1.4	3550	5	031623	p1RX-2 containing trlx	4.24e+02
C	528	14	1.4	2561	2	010400	D2 dopamine receptor	4.24e+02	C	601	14	1.4	3552	1	005875	p1rx-2 plasmid sequen	4.24e+02
C	530	14	1.4	2574	14	076019	Expression plasmid f1r	4.24e+02	C	602	14	1.4	3557	2	060801	Human pro-growth horn	4.24e+02
C	531	14	1.4	2577	6	036620	Expression plasmid po	4.24e+02	C	603	14	1.4	3565	14	084051	Sequence encoding mel	4.24e+02
C	532	14	1.4	2583	7	046606	Plasmid p1NT4ld codin	4.24e+02	C	604	14	1.4	3566	14	084051	Sequence encoding mel	4.24e+02
C	533	14	1.4	2600	28	T43624	Chromatin regulator p	4.24e+02	C	605	14	1.4	3600	22	T13227	Thermosable enzyme (4.24e+02
C	534	14	1.4	2623	32	T51715	cDNA for adenovirus E	4.24e+02	C	606	14	1.4	3621	21	N60847	Human pre-prolactin g	4.24e+02
C	535	14	1.4	2641	5	030970	Non-clonable, solubl	4.24e+02	C	607	14	1.4	3628	7	041297	BMP-2 expression vect	4.24e+02
C	536	14	1.4	2652	9	051114	Sequence encoding met	4.24e+02	C	608	14	1.4	3632	2	N60848	Plasmid sequence enc	4.24e+02
C	537	14	1.4	2717	2	N60381	Plasmid pASPCg-SV(10)	4.24e+02	C	609	14	1.4	3632	14	090770	E.coli thiredoxin-hu	4.24e+02
C	538	14	1.4	2719	2	N60572	Genomic sequence enco	4.24e+02	C	610	14	1.4	3632	15	093133	Thiredoxin/Des-Pro-1	4.24e+02
C	539	14	1.4	2755	5	030566	Vector pASPCg-SV(10)	4.24e+02	C	611	14	1.4	3632	10	027476	Vector for thiredoxi	4.24e+02
C	540	14	1.4	2755	5	030566	Vector pNN03	4.24e+02	C	612	14	1.4	3632	10	044670	pALTRxA/ER/IL1delta	4.24e+02
C	541	14	1.4	2761	4	026546	Encodes 5HTT serotoni	4.24e+02	C	613	14	1.4	3659	2	N60204	Thiredoxin-Interleuk	4.24e+02
C	542	14	1.4	2770	32	T78599	Vector pMT-Apo:9HS (H	4.24e+02	C	614	14	1.4	3659	2	N60204	Interferon-pseudo-ome	4.24e+02
C	543	14	1.4	2794	3	014238	AS-30D tumour Type II	4.24e+02	C	615	14	1.4	3664	11	062675	Plasmid pASK4s for ex	4.24e+02
C	544	14	1.4	2794	10	044760	IKT352 gene.	4.24e+02	C	616	14	1.4	3681	2	013578	Plasmid pKSR15.	4.24e+02
C	545	14	1.4	2794	7	043177	Recombinant leukotoxi	4.24e+02	C	617	14	1.4	3699	27	044179	Plasmid pge for clon	4.24e+02
C	546	14	1.4	2794	23	T37179	Leukotoxin 352 gene 1	4.24e+02	C	618	14	1.4	3699	27	T37237	Heavy chain mnlilocus	4.24e+02
C	547	14	1.4	2817	7	043122	P. haemolytica leukot	4.24e+02	C	619	14	1.4	3712	15	097490	Plasmid pPHTRA1.	4.24e+02
C	548	14	1.4	2817	7	043122	GnRH-leukotoxin gene	4.24e+02	C	620	14	1.4	3735	10	014452	Rat prolactin gene in	4.24e+02
C	549	14	1.4	2820	11	066454	Xenopus thrombospondi	4.24e+02	C	621	14	1.4	3754	10	057880	Intermediate plasmid	4.24e+02
C	550	14	1.4	2832	1	N81664	Denque virus type 3-d	4.24e+02	C	622	14	1.4	3754	13	084782	Protein-tyrosine-kin	4.24e+02
C	551	14	1.4	2838	7	041321	Somatostatin-leukotox	4.24e+02	C	623	14	1.4	3754	13	085420	Plasmid pTRCH2.	4.24e+02
C	552	14	1.4	2849	28	T48512	Homology vector 443-8	4.24e+02	C	624	14	1.4	3769	15	097492	Sequence encoding fis	4.24e+02
C	553	14	1.4	2849	12	070573	Homology vector 443-8	4.24e+02	C	625	14	1.4	3784	1	005326	Sequence of the chlor	4.24e+02
C	554	14	1.4	2849	12	068937	Fowlpox virus (FPV) g	4.24e+02	C	626	14	1.4	3803	1	003155	Parathyroid calcium r	4.24e+02
C	555	14	1.4	2861	7	043433	Rotavirus VP4-leukoto	4.24e+02	C	627	14	1.4	3809	27	T61382	Plasmid pFISH encodin	4.24e+02
C	556	14	1.4	2887	13	084589	AMM1 chromosome inv(1	4.24e+02	C	628	14	1.4	3820	1	003517	Sequence of plasmid p	4.24e+02
C	557	14	1.4	2935	30	T68827	Hamster cytosolic pho	4.24e+02	C	629	14	1.4	3826	10	045288	Sequence of plasmid p	4.24e+02
C	558	14	1.4	2935	24	T44578	Calcium-independent c	4.24e+02	C	630	14	1.4	3833	2	N91060	Sequence of new plasm	4.24e+02
C	559	14	1.4	2935	19	T05842	Calcium-independent c	4.24e+02	C	631	14	1.4	3850	1	N81634	Sequence of plasmid p	4.24e+02
C	560	14	1.4	2939	29	T59199	Ca-independent phosph	4.24e+02	C	632	14	1.4	3851	33	T99019	Yellow tail/fish tuna	4.24e+02
C	561	14	1.4	2949	1	087350	Plasmid BGJINV.	4.24e+02	C	633	14	1.4	3851	33	T99019	Yellow tail/fish tuna	4.24e+02
C	562	14	1.4	2949	1	005086	Sequence encodes NAP-	4.24e+02	C	634	14	1.4	3878	5	040299	Sequence of plasmid p	4.24e+02
C	563	14	1.4	2950	1	N91050	Sequence encoding nov	4.24e+02	C	635	14	1.4	3878	5	040299	Sequence of plasmid p	4.24e+02
C	564	14	1.4	2950	2	013672	SUP-B27 t(1;19) trans	4.24e+02	C	636	14	1.4	3879	7	046410	Leukotoxin genes hlyB	4.24e+02
C	565	14	1.4	3003	1	005745	Plasmid p_L-mu-smc(1e	4.24e+02	C	637	14	1.4	3887	8	051082	Plasmid pGCH4 which e	4.24e+02
C	566	14	1.4	3006	1	005085	Sequence encodes NAP	4.24e+02	C	638	14	1.4	3919	13	080418	Human mnlil3 cDNA.	4.24e+02
C	567	14	1.4	3033	22	T30192	Peripheral nervous nov	4.24e+02	C	639	14	1.4	3926	1	003736	Sequence of plasmid p	4.24e+02
C	568	14	1.4	3033	22	T30192	Peripheral nervous nov	4.24e+02	C	640	14	1.4	3933	16	T03885	Human mucosal lymphoc	4.24e+02
C	569	14	1.4	3068	19	T16274	Pyroclitium oculatum	4.24e+02	C	641	14	1.4	3944	5	028750	Human vector.	4.24e+02
C	570	14	1.4	3104	2	N90296	DNA target sequence a	4.24e+02	C	642	14	1.4	3957	18	T14077	Human dihydropyrimidi	4.24e+02
C	571	14	1.4	3138	2	017712	Shuttle vector pMOW16	4.24e+02	C	643	14	1.4	3962	14	092520	Human mammary carcino	4.24e+02
C	572	14	1.4	3141	32	T47556	Human cytomegalovirus	4.24e+02	C	644	14	1.4	3969	8	049757	Protein tyrosine-kin	4.24e+02
C	573	14	1.4	3194	10	058039	GM-CSF gene.	4.24e+02	C	645	14	1.4	3976	16	T03309	Expression vector pds	4.24e+02
C	574	14	1.4	3213	25	T42119	M-lates gene encoding	4.24e+02	C	646	14	1.4	3977	8	051081	Plasmid pGCH5 which e	4.24e+02
C	575	14	1.4	3215	8	048933	MOSF-2.	4.24e+02	C	647	14	1.4	3977	12	087704	Plasmid pDS56/RBSII,S	4.24e+02
C	576	14	1.4	3229	9	054213	Bovine IFNgamma/LKT	4.24e+02	C	648	14	1.4	3977	12	087707	Plasmid pDS56/RBSII,S	4.24e+02
C	577	14	1.4	3249	14	082748	PRB2 retinoblastoma t	4.24e+02	C	649	14	1.4	3977	12	074431	Plasmid pDS56/RBSII,S	4.24e+02
C	578	14	1.4	3266	18	T11192	Plasmid pASK75 compri	4.24e+02	C	650	14	1.4	3977	12	087683	Plasmid pDS56/RBSII,S	4.24e+02
C	579	14	1.4	3275	3	N97129	Partial sequence of m	4.24e+02	C	651	14	1.4	3977	12	087706	Plasmid pDS56/RBSII,S	4.24e+02
C	580	14	1.4	3311	33	T02771	Bovine IL-2 - LKT chl	4.24e+02	C	652	14	1.4	3977	12	087706	Plasmid pDS56/RBSII,S	4.24e+02
C	581	14	1.4	3311	33	T02771	Cytoshesin 1	4.24e+02	C	653	14	1.4	3977	12	087700	Plasmid pDS56/RBSII,S	4.24e+02
C	582	14	1.4	3327	22	T34620	P. vivax BSE-1 blood	4.24e+02	C	654	14	1.4	3977	12	087705	Plasmid pDS56/RBSII,S	4.24e+02
C	583	14	1.4	3343	1	004635	Plasmid p10169 encodi	4.24e+02	C	655	14	1.4	3977	12	087705	Plasmid pDS56/RBSII,S	4.24e+02
C	584	14	1.4	3353	9	054258	Amyloid precursor pro	4.24e+02	C	656	14	1.4	3977	12	087705	Plasmid pDS56/RBSII,S	4.24e+02
C	585	14	1.4	3353	9	054258	Amyloid precursor pro	4.24e+02	C	657	14	1.4	3977	12	087705	Plasmid pDS56/RBSII,S	4.24e+02
C	586	14	1.4	3353	3	014097	Sequence of gene enco	4.24e+02	C	658	14	1.4	3977	12	087709	Plasmid pDS56/RBSII,S	4.24e+02
C	587	14	1.4	3403	15	092573	Nucleotide sequence	4.24e+02	C	659	14	1.4	3977	12	087711	Plasmid pDS56/RBSII,S	4.24e+02
C	588	14	1.4	3415	5	092573	Human placenta deriv	4.24e+02	C	660	14	1.4	3977	12	087711	Plasmid pDS56/RBSII,S	4.24e+02
C	589	14	1.4	3415	5	092573	Human placenta deriv	4.24e+02	C	661	14	1.4	3977	12	087711	Plasmid pDS56/RBSII,S	4.24e+02
C	590	14	1.4	3416	2	012783	Expression plasmid pd	4.24e+02	C	662	14	1.4	3977	12	087684	Plasmid pDS56/RBSII,S	4.24e+02
C	591	14	1.4	3416	5	034607	pDS56/RBSII-1 sequen	4.24e+02	C	663	14	1.4	3977	12	087684	Plasmid pDS56/RBSII,S	4.24e+02
C	592	14	1.4	3423	17	T00771	Expression plasmid pd	4.24e+02	C	664	14	1.4	3977	12	087689	Plasmid pDS56/RBSII,S	4.24e+02
C	593	14	1.4	3423	17	T00771	Expression plasmid pd	4.24e+02	C	665	14	1.4	3977	12	087689	Plasmid pDS56/RBSII,S	4.24e+02
C	594	14	1.4	3440	2	013728	GST-SEP Fusion gene f	4.24e+02	C	666	14	1.4	3977	12	087689	Plasmid pDS56/RBSII,S	4.24e+02
C	595	14	1.4	3440	2	013728	GST-SEP Fusion gene f	4.24e+02	C	667	14	1.4	3977	12	087689	Plasmid pDS56/RBSII,S	4.24e+02
C	596	14	1.4	3440	2	013728	GST-SEP Fusion gene f	4.24e+02	C	668	14	1.4	3984	15	T07310	Plasmid pDS56/RBSII,S	4.24e+02
C	597	14	1.4	3457	8	048468	Sequence of plasmid p	4.24e+02	C	669	14	1.4	3984	15	T07310	Plasmid pDS56/RBSII,S	4.24e+02
C	598	14	1.4	3474	5	029146	Nitrate reductase N1a	4.24e+02	C	670	14	1.4	3993	20	T82277	Human plasmid pPOPE-	4.24e+02
C	599	14	1.4	3495	28	T48237	pMTN-MPH plasmid for	4.24e+02	C	671	14	1.4	4003	1	006305	Plasmid pX306 sequen	4.24e+02
C	599	14	1.4	3546	22	T40235	Neuronal nicotinic ac	4.24e+02	C	672	14	1.4	4004	1	006306	Sequence of plasmid p	4.24e+02

673	1.4	4009 12	070219	Plasmid pIG2 for TME	4.24e+02	746	14	1.4	4792 15	Q84696	Plasmid GS contg. N.	4.24e+02
674	1.4	4020 2	N71016	Sequence of LAV/HPLV	4.24e+02	747	14	1.4	4824 20	T08975	Shortened C1 gene in	4.24e+02
675	1.4	4045 12	Q70942	Plasmid pND211 contai	4.24e+02	748	14	1.4	4864 16	Q74207	Expression vector V17	4.24e+02
676	1.4	4046 7	Q42525	Cardiac adenyllyl cycl	4.24e+02	749	14	1.4	4864 16	T01114	Expression vector V17	4.24e+02
677	1.4	4054 2	Q11888	Collagenase gene.	4.24e+02	750	14	1.4	4866 14	O83848	p-selectin gene 5' fl	4.24e+02
678	1.4	4059 17	T03875	Eukaryotic expression	4.24e+02	751	14	1.4	4883 8	O51192	pDEL10; plasmid DNA r	4.24e+02
679	1.4	4059 24	T41899	Vector pAPEX-1.	4.24e+02	752	14	1.4	4883 4	Q25709	pDEL10.	4.24e+02
680	1.4	4059 17	T12239	Eucaryotic (CMV) expr	4.24e+02	753	14	1.4	4893 13	O81069	Plasmid pKSI nucleoti	4.24e+02
681	1.4	4067 10	Q63192	Human adeno-associate	4.24e+02	754	14	1.4	4896 20	T08970	PTS256 contg. p35S-ba	4.24e+02
682	1.4	4068 1	N90730	Sequence of plasmid p	4.24e+02	755	14	1.4	4906 1	N95081	Plasmid pCIB709 confe	4.24e+02
683	1.4	4080 23	T31933	Nonsense-mediated mRN	4.24e+02	756	14	1.4	4909 32	T47558	42K promoted cytomega	4.24e+02
684	1.4	4114 14	Q90727	Thiodioxin/Tr-11 gen	4.24e+02	757	14	1.4	4909 32	T518924	Plasmid pAI261.	4.24e+02
685	1.4	4120 29	T64421	Plasmid pMW206.	4.24e+02	758	14	1.4	4910 33	T84569	Plasmid pT889P encod	4.24e+02
686	1.4	4120 3	Q21502	Vector pMV206 for clo	4.24e+02	759	14	1.4	4916 3	Q22982	Synthetic human growt	4.24e+02
687	1.4	4151 8	Q51524	Rabbit sodium ion/hyd	4.24e+02	760	14	1.4	4928 22	T33656	Plasmid encoding huma	4.24e+02
688	1.4	4161 5	Q32349	Templat clone Fab NQ	4.24e+02	761	14	1.4	4933 15	T04569	Plasmid pAR-2 sequenc	4.24e+02
689	1.4	4164 15	T04575	Plasmid pAR-1 sequenc	4.24e+02	762	14	1.4	4963 17	T066873	pHCW**1 promoter and	4.24e+02
690	1.4	4171 18	Q74082	Oncostatin M receptor	4.24e+02	763	14	1.4	4963 13	Q76270	pHCW**1-controlled p	4.24e+02
691	1.4	4176 3	N90709	Sequence of plasmid p	4.24e+02	764	14	1.4	4965 13	Q75973	pHLA-B7/beta-2 microg	4.24e+02
692	1.4	4181 5	Q25345	MCC gene of chromosom	4.24e+02	765	14	1.4	4977 10	Q44359	Plasmid pE18C123CCS.	4.24e+02
693	1.4	4189 2	Q05397	Secretion Vector pSEC	4.24e+02	766	14	1.4	4977 33	T84570	Plasmid pE18C-123 enc	4.24e+02
694	1.4	4203 2	Q14000	Leukotoxin genes.	4.24e+02	767	14	1.4	4977 10	Q44358	Parathyroid calcium r	4.24e+02
695	1.4	4204 2	Q10279	Sequence of plasmid p	4.24e+02	768	14	1.4	5006 27	T61381	Plasmid pE18C-123.	4.24e+02
696	1.4	4207 1	N92031	Sequence of clone pS2	4.24e+02	769	14	1.4	5015 1	Q04672	Plasmid pJI446 contg.	4.24e+02
697	1.4	4237 6	Q40380	Receptor type tyrosin	4.24e+02	770	14	1.4	5033 12	Q74695	pPH1406 vector contg	4.24e+02
698	1.4	4290 22	T18394	Receptor type tyrosin	4.24e+02	771	14	1.4	5056 1	N90795	Plasmid pCIB709.	4.24e+02
699	1.4	4290 26	T51235	Receptor-type tyrosin	4.24e+02	772	14	1.4	5092 1	N90643	Entire sequence of cI	4.24e+02
700	1.4	4290 24	T42593	Coding sequence for r	4.24e+02	773	14	1.4	5098 10	Q44356	Plasmid pIat70PE.	4.24e+02
701	1.4	4294 14	Q92325	Plasmid pBGC646.	4.24e+02	774	14	1.4	5099 4	Q24672	DNA encoding B-Hdg-T	4.24e+02
702	1.4	4296 20	T28272	Plasmid pMR28 sequenc	4.24e+02	775	14	1.4	5110 14	O83834	Plasmid pCM-p1208.	4.24e+02
703	1.4	4320 32	T73388	DNA encoding HSP72 an	4.24e+02	776	14	1.4	5110 14	O83833	Plasmid pCM-B64.	4.24e+02
704	1.4	4341 10	Q62391	Vector pVact.	4.24e+02	777	14	1.4	5110 14	O83828	Plasmid pCM-p1160.	4.24e+02
705	1.4	4368 17	T03133	Human dThydropyrimidi	4.24e+02	778	14	1.4	5110 14	O83836	Plasmid pCM-T221.	4.24e+02
706	1.4	4369 17	T03143	Human dThydropyrimidi	4.24e+02	779	14	1.4	5110 14	O83835	Plasmid pCM-p1031.	4.24e+02
707	1.4	4403 8	Q48899	BrabtkoxinA-TRIP fusi	4.24e+02	780	14	1.4	5140 4	Q24977	DNA encoding soluble	4.24e+02
708	1.4	4421 28	T58319	DNA sequence of hepat	4.24e+02	781	14	1.4	5141 16	Q94114	Expression vector pSV	4.24e+02
709	1.4	4432 12	Q74205	Expression vector V17	4.24e+02	782	14	1.4	5168 1	Q03516	Plasmid pKRG3 encodi	4.24e+02
710	1.4	4432 16	T01113	Expression vector V17	4.24e+02	783	14	1.4	5169 17	T06001	Streptomycies vedmoren	4.24e+02
711	1.4	4443 2	N70627	Encodes ampicillin re	4.24e+02	784	14	1.4	5178 27	T49876	PreT-Splice.	4.24e+02
712	1.4	4450 1	N81025	Sequence of peplomer	4.24e+02	785	14	1.4	5186 15	O84967	E. coli PEPC gene (wt	4.24e+02
713	1.4	4454 30	T66462	Plasmid pCEML.8 conta	4.24e+02	786	14	1.4	5211 12	Q77789	Pre-pro-cobra C3 codi	4.24e+02
714	1.4	4466 1	N90286	Plasmid pTP104-4.	4.24e+02	787	14	1.4	5233 2	N70644	Sequence of plasmid p	4.24e+02
715	1.4	4477 3	Q22962	Sequence of pHCV-34 e	4.24e+02	788	14	1.4	5238 1	Q04654	Plasmid pPH11 encodi	4.24e+02
716	1.4	4481 6	Q38265	HCV CKS-Core fusion g	4.24e+02	789	14	1.4	5248 17	T08489	Plasmid pBT Trc S05/N	4.24e+02
717	1.4	4481 3	Q21677	pHCV-34 - recombinant	4.24e+02	790	14	1.4	5278 1	Q05168	Plasmid pPR1H4 with g	4.24e+02
718	1.4	4481 6	Q38250	HCV CKS-Core expressi	4.24e+02	791	14	1.4	5292 19	T13391	Hybrid vector pSF3.	4.24e+02
719	1.4	4482 11	Q62662	pJO200 expression vec	4.24e+02	792	14	1.4	5294 14	T13391	Hybrid vector pSF3.	4.24e+02
720	1.4	4515 8	Q46823	PLISC-se vector.	4.24e+02	793	14	1.4	5299 2	N70600	Plasmid pMW1 contain	4.24e+02
721	1.4	4519 14	O87347	Plasmid pINVI.	4.24e+02	794	14	1.4	5314 2	Q13576	Plasmid pMW1 contain	4.24e+02
722	1.4	4555 1	Q04077	Human 32k alveolar su	4.24e+02	795	14	1.4	5323 19	T13390	Hybrid vector pSF1.	4.24e+02
723	1.4	4577 33	T72813	Mouse SP6 cDNA.	4.24e+02	796	14	1.4	5356 25	T43797	Plasmid pPR1HAT (rat	4.24e+02
724	1.4	4599 22	T27052	KRP3 telomerase-assoc	4.24e+02	797	14	1.4	5364 19	T13393	Hybrid vector pMT1.	4.24e+02
725	1.4	4608 2	N81407	Sequence of new recom	4.24e+02	798	14	1.4	5379 1	N91151	Perdue strain of tran	4.24e+02
726	1.4	4608 1	N90288	Plasmid pTP70-1	4.24e+02	799	14	1.4	5379 21	T31895	TGE virus gp195 gene.	4.24e+02
727	1.4	4621 31	T69889	Human cyclin D1-human	4.24e+02	800	14	1.4	5393 5	Q42755	S-PRY-055 TGE virus g	4.24e+02
728	1.4	4645 1	N92023	Recombinant plasmid p	4.24e+02	801	14	1.4	5393 5	Q34611	Plasmid pPR3.	4.24e+02
729	1.4	4648 2	Q12770	Alpha-glucosidase-Arg	4.24e+02	802	14	1.4	5406 2	N70872	Growth hormone releas	4.24e+02
730	1.4	4648 2	Q12756	Alpha-glucosidase/Arg	4.24e+02	803	14	1.4	5421 14	Q85678	Wilson's disease gene	4.24e+02
731	1.4	4651 1	N92044	Sequence of recombina	4.24e+02	804	14	1.4	5472 6	Q41050	Sequence of plasmid p	4.24e+02
732	1.4	4655 4	Q25108	DHFR-APP fusion prote	4.24e+02	805	14	1.4	5511 24	T41853	cDNA encoding Plasmid	4.24e+02
733	1.4	4660 1	N90266	DHFR-APP fusion prote	4.24e+02	806	14	1.4	5519 13	Q76040	Retrovirus vector pPO	4.24e+02
734	1.4	4668 1	Q04519	Recombinant plasmid p	4.24e+02	807	14	1.4	5574 10	Q44361	Plasmid pIATdeltaTacs-	4.24e+02
735	1.4	4673 4	Q25100	DHFR-APP fusion prote	4.24e+02	808	14	1.4	5585 29	T61430	Interleukin-2 express	4.24e+02
736	1.4	4690 5	Q29910	RBI, PDI coexpression	4.24e+02	809	14	1.4	5600 6	Q38451	Plasmid pMP6-112.	4.24e+02
737	1.4	4691 16	Q92546	pCmb3 expression vec	4.24e+02	810	14	1.4	5600 6	Q38451	HCV CKS-33-BCD fusion	4.24e+02
738	1.4	4715 1	Q05083	Plasmid pSG1-12 of E.	4.24e+02	811	14	1.4	5600 3	Q22963	Sequence of pHCV-31 e	4.24e+02
739	1.4	4715 1	N90284	Plasmid pGRF2-15 cont	4.24e+02	812	14	1.4	5600 11	Q62663	pHCV-31 plasmid expre	4.24e+02
740	1.4	4732 1	Q00576	Recombinant plasmid p6	4.24e+02	813	14	1.4	5600 6	Q38266	HCV CKS-33-BCD fusion	4.24e+02
741	1.4	4762 1	Q003700	Portion of plasmid p6	4.24e+02	814	14	1.4	5618 15	O88310	Plasmid pRC/CNV-HBS c	4.24e+02
742	1.4	4760 1	Q005204	Plasmid pBSFOLEK1 con	4.24e+02	815	14	1.4	5642 8	Q51193	pDE4; plasmid DNA rep	4.24e+02
743	1.4	4762 1	N81675	Plasmid pBIAK1 stably	4.24e+02	816	14	1.4	5653 33	T76802	REV tar Rev m10 retro	4.24e+02
744	1.4	4774 1	N81424		4.24e+02	817	14	1.4	5658 22	T14616	C. pneumoniae antigen	4.24e+02
745	1.4	4788 13	Q85367		4.24e+02	818	14	1.4				

C	819	14	1.4	5690 15	086902	Sat receptor type-pro	4.24e+02	C	892	14	1.4	7298 7	047192	Plasmid pHCY-162 codi	4.24e+02
C	820	14	1.4	5703 22	T34110	Anti-IL-5 humanised a	4.24e+02	C	893	14	1.4	7330 1	N9.856	Plasmid pBNA-1.	4.24e+02
C	821	14	1.4	5727 7	014435	PKA6 sequence.	4.24e+02	C	894	14	1.4	7356 30	T69982	Canarypox virus DNA c	4.24e+02
C	822	14	1.4	5770 7	043814	puD3D4 construct.	4.24e+02	C	895	14	1.4	7351 32	T47529	Canarypox virus DNA c	4.24e+02
C	823	14	1.4	5779 1	005367	Recombinant plasmid p	4.24e+02	C	896	14	1.4	7360 18	T15930	DHFR/Inticon (WTRASD)	4.24e+02
C	824	14	1.4	5836 33	T84444	Human prostate-specific	4.24e+02	C	897	14	1.4	7399 5	033479	HDPACK1.	4.24e+02
C	825	14	1.4	5856 15	096296	Human SP16 cDNA.	4.24e+02	C	898	14	1.4	7436 2	010686	Plasmid pBNA-1.	4.24e+02
C	826	14	1.4	5864 33	T72812	Human SP16 cDNA.	4.24e+02	C	899	14	1.4	7474 31	T71320	Plasmid pBNA-1.	4.24e+02
C	827	14	1.4	5885 33	T90659	Sequence of the human	4.24e+02	C	900	14	1.4	7533 1	N70491	Butire sequence of hi	4.24e+02
C	828	14	1.4	5931 7	043701	Plasmid pBdelPRDSAF c	4.24e+02	C	901	14	1.4	7533 1	N81970	Plasmid pBNA-1.	4.24e+02
C	829	14	1.4	6010 28	T59676	Plasmid pPR14129 cod	4.24e+02	C	902	14	1.4	7566 7	042160	Plasmid pPS0212 contg	4.24e+02
C	830	14	1.4	6020 1	006548	Plasmid pPR14129 cod	4.24e+02	C	903	14	1.4	7607 16	T03097	Protein tyrosine-Kina	4.24e+02
C	831	14	1.4	6028 33	T90659	Plasmid pBdelPRDSAF c	4.24e+02	C	904	14	1.4	7607 16	T03097	Hybrid activation vec	4.24e+02
C	832	14	1.4	6044 30	T28280	Plasmid pBdelPRDSAF c	4.24e+02	C	905	14	1.4	7625 31	T71323	Stroilimus effector pr	4.24e+02
C	833	14	1.4	6061 33	T90659	Plasmid pBdelPRDSAF c	4.24e+02	C	906	14	1.4	7633 17	T00770	Stroilimus effector pr	4.24e+02
C	834	14	1.4	6062 3	020732	Plasmid pBdelPRDSAF c	4.24e+02	C	907	14	1.4	7653 17	T00770	Stroilimus effector pr	4.24e+02
C	835	14	1.4	6096 2	N70871	Plasmid pBdelPRDSAF c	4.24e+02	C	908	14	1.4	7653 17	T00770	Stroilimus effector pr	4.24e+02
C	836	14	1.4	6115 29	T63235	Plasmid pBdelPRDSAF c	4.24e+02	C	909	14	1.4	7653 17	T00770	Stroilimus effector pr	4.24e+02
C	837	14	1.4	6156 29	092547	Plasmid pBdelPRDSAF c	4.24e+02	C	910	14	1.4	7653 17	T00770	Stroilimus effector pr	4.24e+02
C	838	14	1.4	6170 18	098829	Plasmid pBdelPRDSAF c	4.24e+02	C	911	14	1.4	7653 17	T00770	Stroilimus effector pr	4.24e+02
C	839	14	1.4	6171 20	098829	Plasmid pBdelPRDSAF c	4.24e+02	C	912	14	1.4	7653 17	T00770	Stroilimus effector pr	4.24e+02
C	840	14	1.4	6176 27	T49226	Plasmid pBdelPRDSAF c	4.24e+02	C	913	14	1.4	7653 17	T00770	Stroilimus effector pr	4.24e+02
C	841	14	1.4	6207 7	043813	Plasmid pBdelPRDSAF c	4.24e+02	C	914	14	1.4	7653 17	T00770	Stroilimus effector pr	4.24e+02
C	842	14	1.4	6229 20	T29320	Plasmid pBdelPRDSAF c	4.24e+02	C	915	14	1.4	7653 17	T00770	Stroilimus effector pr	4.24e+02
C	843	14	1.4	6231 30	T66737	Plasmid pBdelPRDSAF c	4.24e+02	C	916	14	1.4	7653 17	T00770	Stroilimus effector pr	4.24e+02
C	844	14	1.4	6231 30	T70309	Plasmid pBdelPRDSAF c	4.24e+02	C	917	14	1.4	7653 17	T00770	Stroilimus effector pr	4.24e+02
C	845	14	1.4	6244 13	076269	Plasmid pBdelPRDSAF c	4.24e+02	C	918	14	1.4	7653 17	T00770	Stroilimus effector pr	4.24e+02
C	846	14	1.4	6254 18	098916	Plasmid pBdelPRDSAF c	4.24e+02	C	919	14	1.4	7653 17	T00770	Stroilimus effector pr	4.24e+02
C	847	14	1.4	6254 18	098916	Plasmid pBdelPRDSAF c	4.24e+02	C	920	14	1.4	7653 17	T00770	Stroilimus effector pr	4.24e+02
C	848	14	1.4	6254 18	098916	Plasmid pBdelPRDSAF c	4.24e+02	C	921	14	1.4	7653 17	T00770	Stroilimus effector pr	4.24e+02
C	849	14	1.4	6254 18	098916	Plasmid pBdelPRDSAF c	4.24e+02	C	922	14	1.4	7653 17	T00770	Stroilimus effector pr	4.24e+02
C	850	14	1.4	6274 7	043812	Plasmid pBdelPRDSAF c	4.24e+02	C	923	14	1.4	7653 17	T00770	Stroilimus effector pr	4.24e+02
C	851	14	1.4	6285 22	T34109	Plasmid pBdelPRDSAF c	4.24e+02	C	924	14	1.4	7653 17	T00770	Stroilimus effector pr	4.24e+02
C	852	14	1.4	6312 20	T03696	Plasmid pBdelPRDSAF c	4.24e+02	C	925	14	1.4	7653 17	T00770	Stroilimus effector pr	4.24e+02
C	853	14	1.4	6312 20	T03696	Plasmid pBdelPRDSAF c	4.24e+02	C	926	14	1.4	7653 17	T00770	Stroilimus effector pr	4.24e+02
C	854	14	1.4	6312 20	T03696	Plasmid pBdelPRDSAF c	4.24e+02	C	927	14	1.4	7653 17	T00770	Stroilimus effector pr	4.24e+02
C	855	14	1.4	6330 23	T35198	Plasmid pBdelPRDSAF c	4.24e+02	C	928	14	1.4	7653 17	T00770	Stroilimus effector pr	4.24e+02
C	856	14	1.4	6330 23	T35198	Plasmid pBdelPRDSAF c	4.24e+02	C	929	14	1.4	7653 17	T00770	Stroilimus effector pr	4.24e+02
C	857	14	1.4	6330 23	T35198	Plasmid pBdelPRDSAF c	4.24e+02	C	930	14	1.4	7653 17	T00770	Stroilimus effector pr	4.24e+02
C	858	14	1.4	6330 23	T35198	Plasmid pBdelPRDSAF c	4.24e+02	C	931	14	1.4	7653 17	T00770	Stroilimus effector pr	4.24e+02
C	859	14	1.4	6330 23	T35198	Plasmid pBdelPRDSAF c	4.24e+02	C	932	14	1.4	7653 17	T00770	Stroilimus effector pr	4.24e+02
C	860	14	1.4	6330 23	T35198	Plasmid pBdelPRDSAF c	4.24e+02	C	933	14	1.4	7653 17	T00770	Stroilimus effector pr	4.24e+02
C	861	14	1.4	6330 23	T35198	Plasmid pBdelPRDSAF c	4.24e+02	C	934	14	1.4	7653 17	T00770	Stroilimus effector pr	4.24e+02
C	862	14	1.4	6330 23	T35198	Plasmid pBdelPRDSAF c	4.24e+02	C	935	14	1.4	7653 17	T00770	Stroilimus effector pr	4.24e+02
C	863	14	1.4	6330 23	T35198	Plasmid pBdelPRDSAF c	4.24e+02	C	936	14	1.4	7653 17	T00770	Stroilimus effector pr	4.24e+02
C	864	14	1.4	6330 23	T35198	Plasmid pBdelPRDSAF c	4.24e+02	C	937	14	1.4	7653 17	T00770	Stroilimus effector pr	4.24e+02
C	865	14	1.4	6330 23	T35198	Plasmid pBdelPRDSAF c	4.24e+02	C	938	14	1.4	7653 17	T00770	Stroilimus effector pr	4.24e+02
C	866	14	1.4	6330 23	T35198	Plasmid pBdelPRDSAF c	4.24e+02	C	939	14	1.4	7653 17	T00770	Stroilimus effector pr	4.24e+02
C	867	14	1.4	6330 23	T35198	Plasmid pBdelPRDSAF c	4.24e+02	C	940	14	1.4	7653 17	T00770	Stroilimus effector pr	4.24e+02
C	868	14	1.4	6330 23	T35198	Plasmid pBdelPRDSAF c	4.24e+02	C	941	14	1.4	7653 17	T00770	Stroilimus effector pr	4.24e+02
C	869	14	1.4	6330 23	T35198	Plasmid pBdelPRDSAF c	4.24e+02	C	942	14	1.4	7653 17	T00770	Stroilimus effector pr	4.24e+02
C	870	14	1.4	6330 23	T35198	Plasmid pBdelPRDSAF c	4.24e+02	C	943	14	1.4	7653 17	T00770	Stroilimus effector pr	4.24e+02
C	871	14	1.4	6330 23	T35198	Plasmid pBdelPRDSAF c	4.24e+02	C	944	14	1.4	7653 17	T00770	Stroilimus effector pr	4.24e+02
C	872	14	1.4	6330 23	T35198	Plasmid pBdelPRDSAF c	4.24e+02	C	945	14	1.4	7653 17	T00770	Stroilimus effector pr	4.24e+02
C	873	14	1.4	6330 23	T35198	Plasmid pBdelPRDSAF c	4.24e+02	C	946	14	1.4	7653 17	T00770	Stroilimus effector pr	4.24e+02
C	874	14	1.4	6330 23	T35198	Plasmid pBdelPRDSAF c	4.24e+02	C	947	14	1.4	7653 17	T00770	Stroilimus effector pr	4.24e+02
C	875	14	1.4	6330 23	T35198	Plasmid pBdelPRDSAF c	4.24e+02	C	948	14	1.4	7653 17	T00770	Stroilimus effector pr	4.24e+02
C	876	14	1.4	6330 23	T35198	Plasmid pBdelPRDSAF c	4.24e+02	C	949	14	1.4	7653 17	T00770	Stroilimus effector pr	4.24e+02
C	877	14	1.4	6330 23	T35198	Plasmid pBdelPRDSAF c	4.24e+02	C	950	14	1.4	7653 17	T00770	Stroilimus effector pr	4.24e+02
C	878	14	1.4	6330 23	T35198	Plasmid pBdelPRDSAF c	4.24e+02	C	951	14	1.4	7653 17	T00770	Stroilimus effector pr	4.24e+02
C	879	14	1.4	6330 23	T35198	Plasmid pBdelPRDSAF c	4.24e+02	C	952	14	1.4	7653 17	T00770	Stroilimus effector pr	4.24e+02
C	880	14	1.4	6330 23	T35198	Plasmid pBdelPRDSAF c	4.24e+02	C	953	14	1.4	7653 17	T00770	Stroilimus effector pr	4.24e+02
C	881	14	1.4	6330 23	T35198	Plasmid pBdelPRDSAF c	4.24e+02	C	954	14	1.4	7653 17	T00770	Stroilimus effector pr	4.24e+02
C	882	14	1.4	6330 23	T35198	Plasmid pBdelPRDSAF c	4.24e+02	C	955	14	1.4	7653 17	T00770	Stroilimus effector pr	4.24e+02
C	883	14	1.4	6330 23	T35198	Plasmid pBdelPRDSAF c	4.24e+02	C	956	14	1.4	7653 17	T00770	Stroilimus effector pr	4.24e+02
C	884	14	1.4	6330 23	T35198	Plasmid pBdelPRDSAF c	4.24e+02	C	957	14	1.4	7653 17	T00770	Stroilimus effector pr	4.24e+02
C	885	14	1.4	6330 23	T35198	Plasmid pBdelPRDSAF c	4.24e+02	C	958	14	1.4	7653 17	T00770	Stroilimus effector pr	4.24e+02
C	886	14	1.4	6330 23	T35198	Plasmid pBdelPRDSAF c	4.24e+02	C	959	14	1.4	7653 17	T00770	Stroilimus effector pr	4.24e+02
C	887	14	1.4	6330 23	T35198	Plasmid pBdelPRDSAF c	4.24e+02	C	960	14	1.4	7653 17	T00770	Stroilimus effector pr	4.24e+02
C	888	14	1.4	6330 23	T35198	Plasmid pBdelPRDSAF c	4.24e+02	C	961	14	1.4	7653 17	T00770	Stroilimus effector pr	4.24e+02
C	889	14	1.4	6330 23	T35198	Plasmid pBdelPRDSAF c	4.24e+02	C	962	14	1.4	7653 17	T00770	Stroilimus effector pr	4.24e+02
C	890	14	1.4	6330 23	T35198	Plasmid pBdelPRDSAF c	4.24e+02	C	963	14	1.4	7653 17	T00770	Stroilimus effector pr	4.24e+02
C	891	14	1.4	6330 23	T35198	Plasmid pBdelPRDSAF c	4.24e+02	C	964	14	1.4	7653 17	T00770	Stroilimus effector pr	4.24e+02

C	965	14	1.4	10241	18	T10690	Expression vector pBI	4.24e+02
C	966	14	1.4	10288	31	T71322	Plasmid pCB51 encodin	4.24e+02
C	967	14	1.4	10366	12	O67401	Huntingtin DNATRTS 9	4.24e+02
C	968	14	1.4	10367	33	T80057	Sequence of plasmid p	4.24e+02
C	969	14	1.4	10367	10	O58701	PURB332.	4.24e+02
C	970	14	1.4	10433	31	T71319	Plasmid pTR72 encodin	4.24e+02
C	971	14	1.4	10558	18	O98914	TGF-beta responsive e	4.24e+02
C	972	14	1.4	10569	18	O98913	TGF-beta responsive e	4.24e+02
C	973	14	1.4	10704	7	O43846	Plasmid pAH4625.	4.24e+02
C	974	14	1.4	10723	31	T49303	CDNA sequence encodin	4.24e+02
C	975	14	1.4	10733	31	T49304	CDNA sequence encodin	4.24e+02
C	976	14	1.4	10844	7	O43848	Plasmid pAH4602.	4.24e+02
C	977	14	1.4	10930	20	O81326	Plasmid pM16-1.	4.24e+02
C	978	14	1.4	10950	12	O81325	Plasmid pM16.	4.24e+02
C	979	14	1.4	10970	12	O73735	Retro virus vector p5	4.24e+02
C	980	14	1.4	11093	27	T50855	DNA cassette for amph	4.24e+02
C	981	14	1.4	11529	7	O43844	Plasmid pAH4602.	4.24e+02
C	982	14	1.4	11616	12	O67390	Construct pHEBO-DR-RE	4.24e+02
C	983	14	1.4	12283	2	O10353	Nucleotide sequence o	4.24e+02
C	984	14	1.4	12537	24	T41705	Lymphocyte specific i	4.24e+02
C	985	14	1.4	12923	3	N90338	Sequence of human mus	4.24e+02
C	986	14	1.4	13206	1	O05243	Rat acyl peptide hydr	4.24e+02
C	987	14	1.4	13414	31	T71321	Plasmid pCB50 encodin	4.24e+02
C	988	14	1.4	13747	7	O47342	Myotonic dystrophy ge	4.24e+02
C	989	14	1.4	13939	7	O43845	Plasmid pSV4611.	4.24e+02
C	990	14	1.4	14311	24	T38744	Plasmid pSV4611.	4.24e+02
C	991	14	1.4	14704	3	O20685	PKS 741 insert conng.	4.24e+02
C	992	14	1.4	15328	13	O81139	HPLA-8 gene.	4.24e+02
C	993	14	1.4	16566	21	T30787	Alphavirus-based euka	4.24e+02
C	994	14	1.4	18318	24	T41418	RCMV Toledo strain no	4.24e+02
C	995	14	1.4	19307	20	T27558	Shuttle vector pAdel	4.24e+02
C	996	14	1.4	19307	20	T27558	Shuttle vector pAdel	4.24e+02
C	997	14	1.4	37885	24	T34137	Gene for biosynthetic	4.24e+02
C	998	14	1.4	46899	9	O54386	T. niwem Cyclosporin	4.24e+02
C	999	14	1.4	53577	28	T18551	Human polyomycin kidn	4.24e+02
C	1000	14	1.4	134525	1	O04525	Total base sequence o	4.24e+02

ALIGNMENTS

RESULT 1
ID Q75931 standard; DNA; 1000 BP.
AC Q75931;
18-NOV-1995 (first entry)
DE Human kappa opioid receptor partial cDNA fragment.
KW Mouse; kappa; delta; mu; opioid receptor; brain; primer; PCR; amplify;
KW Transmembrane domain; somatostatin; receptor; human; expression vector;
KW truncate; chimeric; assay; probe; ss.
OS Homo sapiens.
FH key Location/Qualifiers
FT CDS 102..989
FT /*tag= 2
FT /product= partial human kappa opioid receptor
FT WO9428132-A.
PN 08-DEC-1994.
PF 20-MAY-1994; U05747.
PR 20-MAY-1993; US-066296.
PR 30-JUL-1993; US-100694.
PR 05-NOV-1993; US-147592.
PA (ARCH-) ARCH DEV CORP.
PI Bell GI, Reisine T, Yasuda K;
PI MPI: 95-022804/03.
DR P-PSDB; R67672.
PT Polynucleotides and peptides derived from opioid receptor
PT screening assays for useful therapeutic compositions and in
PS Claim 10; Page 236-239; 300pp; English.
CC The partial nucleotide sequence of the novel human kappa opioid receptor
CC gene. The gene was isolated from a human brain hippocampus cDNA library
CC using a probe from the mouse kappa opioid receptor gene (Q75926). The
CC gene is missing the N-terminal sequence. The C-terminal sequence is
CC very similar to the mouse kappa opioid receptor sequence. Of the
CC C-terminal 293 amino acids, 281 residues are identical and 6 residues

CC have conservative substitutions. The gene encoding the human opioid
CC receptor can be placed in a suitable expression vector for production of
CC the protein in a cell. The opioid receptors thus produced are useful for
CC the development of novel assays designed to select or improve substances,
CC capable of interacting with the opioid receptor proteins, for use in
CC diagnosis, drug design and therapeutic applications.
SQ Sequence 1000 BP; 238 A; 253 C; 225 G; 278 T;

Query Match 96.9%; Score 963; DB 13; Length 1000;
Best Local Similarity 99.9%; Pred. No. 0.00e+00;
Matches 999; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 aagaagcaaaatccatataccaaagagctatccaaacattccattctgggtttgac 60
1 AAGAGCAAAATCCGTAATCCAAAGGCTATCCAAACATTCCTTATGAGGATTTGAC 60
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61 tgaagaaatgagaggaatgctatcttcttctcttttagatatacaagaagaagacg 120
61 TGAAGAAATGAGAGGAATGCTATCTTCTTCTTTAGATATACAAAGATGAGACAG 120
|||||
121 gaaccaaatattacatatattaacctggctttggcagatgcttagtactaaacatgc 180
121 GAACCAAAATTAACATATTAACTGCTTTGGCAGATGCTTAGTACTAAACCATATC 180
|||||
181 cctttcagaagatcaggtctactctgatacattccctggccttttggggatgctgtgaaga 240
181 CCTTTAGAGTACGGTCTACTCTGATGATTAATCCTGGCTTTGGGAGATGCTGTGAAGA 240
|||||
241 tagtaattccatltatlaactaacaatgttaccagaatcttcaacttgaacatgatga 300
241 TAGTAATTCGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTA 300
|||||
301 gggatgacccgtacattgcgtgtgtccaccocggtgaagctttggaattccgacaacct 360
301 GGGATGACCCGTCACATTGCGGTGTGTCCACCOCGGTGAAGCTTTGGAATTCGACACCT 360
|||||
361 tgaagcaaaatgcatatcatatcgtatcgtctgtgtcgtatcgtatctgttgcattctgc 420
361 TGAAGCAAAATGCAATATCATATCTGATCTGGTGTGTCGATCTGATCTGATCTGTCG 420
|||||
421 caatagtccttggagagcaacaagtcaaggaagtgctgattgattgattgctgttcg 480
421 CAATAGTCCTTGGAGGACCAAGTCAAGGAGGATGCTGATGATGATGATGATGATGATG 480
|||||
481 agttccagaatgatactactctcgttggagaccttcaatgaagatcgtgcttcatct 540
481 AGTTCAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 540
|||||
541 ttgccttgatccttccctgtccatcatatcgtctgtcgaacccctgagatccctgcgtc 600
541 TTGCCTTGATCCTTCCCTGTCCATCATATCATGCTGTCTGATCAACCTGATGATCTGCTGC 600
|||||
601 tcaagaaatccgagctccttcttgcctccgagagaagaatncaacctgcgttagagata 660
601 TCAAGAAATCCGAGCTCCTTCTTGCCTCCGAGAGAAATNCAACCTGCCTGAGATCA 660
|||||
661 ccaagatgctcctgtgtgtgtgtgagcagcttctgtgtgtgtgtgtgtgtgtgtgtgt 720
661 CCAAGATGCTCCTGT 720
|||||
721 tcatcctgtgtgagctctggggagagacctcccaagacagctgtctctcccaagctatc 780
721 TCATCCTGTGTGAGCTCTGGGAGAGACCTCCCAAGACAGCTGTCTCTCCAGCTATT 780
|||||
781 actctgtcatcgccttaggctataccaagaagtagccttgatccattctctacgctttc 840
781 ACTCTGTCATCGCCTTAGGCTATACCAAGATAGCTGATCCATTCCTACGCTTTC 840
|||||
841 ttgatgaaacttaagcgggtgtttccggagactctgctttcaactgaagatgagatgag 900
841 TTGATGAAACTTAAGCGGTTGTTCGGGAGACTCTGCTTTCACCTGAGATGAGATGAG 900
|||||
901 agcgcagagcagcattagcagagctcgaataacagtttagatctctgttcccttgaggaga 960


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QY 901 ACCGCNAGAGCACTAGCAAGTCCGAATACACTTASGATCTCTTACTGAGGAGA 960
DB 961 tcatgggatgatgaataaaccagatgactagtcgtgga 1000
QY 961 TGATGGGATGATGATATACACAGATGACTAGTGTGGA 1000

RESULT 2
ID T12550 standard; cDNA; 1142 BP.
AC T12550;
DI 03-SEP-1996 (first entry)
DE Human kappa opioid receptor cDNA.
KM Human; kappa opioid receptor; psychiatric disorder; cardiovascular;
OS neurology; diagnosis; ds.
FH Homo sapiens.
FH Key Location/Qualifiers
FT CDS 1..1142
FT /product= kappa-opioid-receptor
FT /note= "Incomplete termination codon"
FN WO9601898-A1.
PD 25-JAN-1996.
PR 07-JUL-1995; F00912.
PR 11-JUL-1994; FR-008531.
PA (UNST-) UNIV PASTEUR STRASBOURG LOUIS.
PI Kieffer B; Simonin F;
DR WPI; 96-097628/10.
DR P-PSDB; R88722.
PT New nucleic acid encoding the human Kappa opioid receptor - useful
PT in diagnosis and therapy, and for isolating receptor ligands and
PT modulators
PS Claim 5; Page 13-15; 30pp; French.
CC This sequence codes for the human kappa opioid receptor and was
CC obtained from two overlapping cDNA fragments isolated from a
CC human placental cDNA library. The fragments were amplified from
CC the library using PCR primers based on the sequence of human
CC genomic clones which hybridised with a murine delta receptor cDNA
CC probe. Nucleotide probes derived from the kappa opioid receptor
CC coding sequence are useful for diagnosis of neurological, cardio-
CC vascular and psychiatric disorders associated with opioid
CC receptors.
SQ Sequence 1142 BP; 236 A; 337 C; 283 G; 286 T;

Query Match 73.3%; Score 729; DB 20; Length 1142;
Best Local Similarity 98.8%; Pred. No. 0.00e+00;
Matches 849; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

DB 257 gatacaaaagtgtagagcagcaaccacattatataatttaacctgttgagcagatg 316
QY 100 GATACACAAGATGAGACAGCAACCAACATTATATTAACCTGGCTTGGCAGATG 159
DB 317 cttagtactacaaccatgccccttcagagtagcgttactgtagtgaattcctgacct 376
QY 160 CTTTGTACTACTACACCATGCCCTTTCAGAGTACGGTCTACTTGTATGATTTCTT6CCTT 219
DB 377 ttggggatgctgctgtgcaagatagtaatttcattgattactacaacatggtacacagca 436
QY 220 TTGGGAGATGCTGTGCAAGATAGTAATTTCATTGATTACTACAAACATGTTACACAGCA 279
DB 437 tcttacttgaacctgtagtgagcgtgagccgttaacatgcccgtgtgccaaccccgtagag 496
QY 260 TCTTACCTTGACCACTGATGAGCGTGAGCCGCTACATTGCCCTGTGCCACCCCGTAGAGG 339
DB 437 cttagtactcgcacacccctgtaggcaagaatcatcatatctgcatctgctgctgct 556
QY 340 CTTTGGACTTCCGCACACCTTGAAGGCAAGATATCATATTCGCACTGCGCTGCTGT 399
DB 557 cgtcatctgttggcaactctctgcaatagatccttggagagcaaccaagtcaaggagaagctcg 616
QY 400 CGTCACTGTTGGCAGATCTGCAATAGTCCCTTGAGGGCACCAGATGACAGGAGGATGCG 459
DB 617 atgtatattgagtgctcccttgcagttcccaagatgatactactcctcgtgtggacctcttca 676

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QY 460 ATGTCAATTGAGTGCCTGGTTCAGATTCCAGATGATGATACCTCCGCTGAGGACCTCTTCA 519
DB 677 tgaagatcgcgtctcaatccttgctcctgctgctgctgctcctcctcctcctcctcctcct 736
QY 520 TGAATATCTGCTCTTCACTCTTCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 579
DB 737 aacacctgatactcctgctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcct 796
QY 580 ACACCTGATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 639
DB 737 atcgcaacctgcgttagagatcaccagactgctcgtgctgctgctgctgctgctgctgctgct 856
QY 640 ATNNCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 699
DB 857 gctgaccccaattacataatcctcctgctgctgctgctgctgctgctgctgctgctgctgct 916
QY 700 GCTGAGCTCCCACTTCAATTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 759
DB 917 cagctgctctctcagctattactctcctcctcctcctcctcctcctcctcctcctcctcctcct 976
QY 760 CAGTGCCTCTCTCCAGCTATTAATCTCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 819
DB 977 atccattctctagccttcttctgataaacttaacgcgtgttccgggactctctgct 1036
QY 820 ATCCATCTCTACCCCTTCTTGTATGAAACTTCACAGCGGTTCGGGCACTTCTGCT 879
DB 1037 tttccactaagatgtagtgtagcgagcagagcactagcagagtcgcaataaagttcagg 1096
QY 880 TTCCACTGAAGATGAGNATGGAGCGCAGACNAGACNATGAGAGTCCGAATATACAGTTCAAG 939
DB 1097 atcccttactcctgagga 1115
QY 940 ATCTGCTTACTGAGGA 958

RESULT 3
ID 056702 standard; DNA; 2447 BP.
AC 056702;
DI 15-SEP-1994 (first entry)
DE Partial sequence of the human kappa opioid receptor
DE genomic clone H14 (KORa).
KM Opioid receptor; morphine; opiate; ss.
OS Homo sapiens.
PN WO9404552-A.
PD 03-MAR-1994.
PR 13-AUG-1993; U07665.
PR 13-AUG-1992; US-929200.
PA (REGC ) UNIV CALIFORNIA.
PI Edwards RH, Evans CJ, Kaufman D, Keith DE;
DR WPI; 94-083099/10.
PT DNA encoding opioid receptors and antibodies against this
PT receptor - used to express and locate these receptors, and screen
PT cDNAs for opioid (ant)agonist activity
PS Example; Fig 8b; 74pp; English.
CC To isolate opiate receptor genomic clones, 300,000 human genomic
CC clones and a similar number of mouse genomic clones were probed
CC with the 1.1 kb mouse delta opioid receptor clone DOR-1 Pst/XbaI
CC fragment. One mouse clone and three human genomic clones were
CC isolated. The 3 human clones had very different EcoRI patterns
CC which indicated that three different genes were represented by the
CC human genomic clones which were designated H3, H14 and H20. H14 maps
CC to chromosome 8. It encodes the human kappa opioid receptor.
SQ Sequence 2447 BP; 683 A; 512 C; 498 G; 747 T;

Query Match 24.6%; Score 245; DB 10; Length 2447;
Best Local Similarity 100.0%; Pred. No. 1.31e-231;
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 cctggcctttggggatgctgtgcaagatagatattcattatgatacaacatgt 60
QY 211 CTTGGCCTTTGGGATGCTGTGCAAGATGATTAATTCATTGATTACTACACATGT 270

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Dh 61 tcacagcatcttcacacctgaccatgatgaagcgtgaccgcctacattgcccgtgtccaccc 120
Oy 271 TCACCAAGCATCTTCACCTTGACCATGATGAGCGTGACCGCTACATTGCGTGCCACCC 330
Dh 121 ccgtgaagccttcttgacttcgcacacaccttgaagcacaagatcacaatcatctgcatct 180
Oy 331 CCGTGAAGCGCTTGTGACTTCCGACACACCTTGAGGCAANAAGATCATCAATATCTGCATCT 390
Dh 181 ggcctcgtctgcacactgtttgcatctctgcaatagtctcttgaggacaccaaagtcaggg 240
Oy 391 GCGTGTCTGCGTCATCTGTGTGGCATCTCTGCAATAGTCTCTTGAGGACCAAGAATCAGGG 450
Dh 241 aagct 245
Oy 451 AAGCT 455

RESULT 4
ID Q75925 standard; DNA: 1410 BP.
AC Q75925:
DE 17-AUG-1995 (first entry)
KW Mouse kappa opioid receptor MORK1 cDNA.
KW Mouse: kappa; delta; mu; opioid receptor; brain; primer; PCR; amplify;
KW transmembrane domain; somatostatin; receptor; human; expression vector;
KW truncate; chimaeric; assay; probe; ss.
OS Mus musculus.
PH Key Location/Qualifiers
FT CDS 186..1338
FT /*tag= a
FT /product= mouse kappa opioid receptor
PN MO9423132-A.
PD 08-DEC-1994.
PF 20-MAY-1994; U05747.
PR 20-MAR-1993; US-066296.
PR 30-JUL-1993; US-100694.
PR 05-NOV-1993; US-147592.
PA (ARCH-) ARCH DEV CORP.
PI Bell GI, Reisine T, Yasuda K;
DR WPI: 95-022804/03.
DR P-PSDB; R67669.
DE Polynucleotides and peptides derived from opioid receptor
DE polypeptides - for use in therapeutic compositions and in
DE screening assays for useful drug substances.
PS Claim 10: Page 207-211; 300pp; English.
CC The nucleotide sequence of the novel mouse kappa opioid receptor gene
CC MORK1. The gene was isolated from a mouse brain cDNA library using a
CC fragment (amplified from the cDNA library with primers Q75929-30) as a
CC probe. The primers are based on the conserved sequences present in the
CC second and third transmembrane domains of somatostatin (SRI) receptor
CC subtypes SSTR1, SSTR2 and SSTR3. The 1.2 kb PstI fragment from the mouse
CC kappa opioid receptor clone, lambda msl-1, was subcloned into the CMV
CC promoter-based expression vector PCMV-6b. The resultant construct
CC PCMV-msl-1 was transfected into COS-1 cells for protein production. The
CC gene encoding the opioid receptor can be used to produce complete,
CC truncated or chimaeric opioid receptor proteins. The opioid receptors
CC thus produced are useful for the development of novel assays designed to
CC select or improve substances, capable of interacting with the opioid
CC receptor proteins, for use in diagnosis, drug design and therapeutic
CC applications.
CC Sequence 1410 BP; 322 A; 360 C; 337 G; 391 T;
SQ
Query Match 3.2%; Score 32; DB 13; Length 1410;
Best Local Similarity 100.0%; Pred. No. 1.52e-11;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DT 01-DEC-1995 (first entry)
DE Mammalian kappa opioid receptor protein cDNA.
KW Mammalian kappa opioid receptor; mouse delta opioid receptor; analgesic;
KW amplification; primer; rat; probe; E.coli; RT-PCR; hypnotic compound; ds.
OS Rattus rattus.
FH Key Location/Qualifiers
FT CDS 111..1253
FT /*tag= a
FT /product= kappa opioid receptor
PN J07070191-A.
PD 14-MAR-1995.
PF 30-JUL-1993; 190261.
PR 09-JUL-1993; JP-170591.
PR (TAKE) TAKEDA CHEM IND LTD.
PA WPI: 95-144857/19.
DR P-PSDB; R72591.
DE Kappa opioid receptor protein and cells expressing it - useful
DE for the screening of compounds for analgesic and hypnotic
DE properties
PS Claim 2; Page 9-10; 15pp; Japanese.
CC The nucleotide sequence of the novel mammalian kappa opioid receptor
CC cDNA. The gene was isolated by amplifying a fragment from rat brain mRNA
CC by reverse transcriptase-PCR (RT-PCR) using primers Q86726-7 derived from
CC the mouse delta-opioid receptor gene. This fragment was cloned into the
CC plasmid pCRIT to produce pRII. The plasmid pRII was used to probe a rat
CC brain DNA library in lambda ZAPIT to obtain a clone of the rat kappa
CC opioid receptor gene, designated PKOPR2. This clone was introduced into
CC E.coli JM109 for production of the receptor protein. The receptor protein
CC is useful for screening of analgesic and hypnotic compounds including
CC peptides and proteins.
SQ Sequence 2481 BP; 629 A; 588 C; 544 G; 720 T;

Query Match 3.2%; Score 32; DB 15; Length 2481;
Best Local Similarity 100.0%; Pred. No. 1.52e-11;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Dh 399 tacatattaacctgcttgacagatgcttt 430
Oy 132 TACATATTAACTGCTTGGACAGATGCTTT 163

RESULT 6
ID Q56700 standard; cDNA; 1821 BP.
AC Q56700:
DE 15-SEP-1994 (first entry)
DE Sequence of murine delta opioid receptor in the DOR-1 cDNA clone.
KW Opioid receptor; morphine; opiate; ss.
OS Mus musculus.
FH Key Location/Qualifiers
FT CDS 29..1139
FT /*tag= a
FT MO9404552-A.
PN 03-MAR-1994.
PD 13-AUG-1993; U07665.
PR 13-AUG-1992; US-929200.
PA (REGC) UNIV CALIFORNIA.
PI Edwards RH, Evans CJ, Kaufman D, Keith DE;
DR WPI: 94-083099/10.
DR P-PSDB; R48629.
DE DNA encoding opioid receptors and antibodies against this
DE receptor - used to express and locate these receptors, and screen
DE pcps. for opioid (ant)agonist activity
PS Claim 1; Fig 5; 74pp; English.
CC A cDNA library was constructed using mRNA isolated from the NG109-15
CC cell line. A single clone, named the DOR-1 clone was isolated.
CC Comparisons with known sequences in Genbank showed highest homology
CC between DOR-1 and the G-protein-coupled somatostatin receptor. Other
CC features of the DOR-1 clone AA sequence deduced from the cDNA
CC sequence include 3 consensus glycosylation sites at residues 18 and
CC 33 (predicted to be in the extracellular N-terminal domain), and at
CC residue 310 (close to the C-terminus and predicted to be
CC intracellular). Phosphokinase C consensus sites are present within
CC predicted intracellular domains, at residues 242,255, 344 & 352.

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CC Seven putative membrane-spanning regions were identified. The DOR-1
CC clone produces a delta receptor with a predicted mol. wt. of 40,558
CC kDatons prior to post-translational modifications.
CC Sequence 1821 BP; 339 A; 539 C; 541 G; 382 T;

Query Match 2.9%; Score 29; DB 10; Length 1821;
Best Local Similarity 100.0%; Pred. No. 5.30e-09;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 446 accatgatgagcgtgacgcctacattgc 474
Qy 291 ACCATGATGAGCGGTGACCGCTACATTGC 319

RESULT 7
ID Q66656 standard; cDNA; 2216 BP.
AC Q66656;
DT 19-JAN-1995 (first entry)
DE Murine delta opioid receptor coding sequence.
KW delta opioid; enkephalin; receptor; mouse; murine; analgesic; pain;
KM drug addiction; neurological disorder; psychiatric; disorder;
OS cardiovascular disorder; ds.
FH Mus musculus.
FH Key Location/Qualifiers
FT CDS 59..1174
ET /tag= a
ET /product= opioid_receptor
FN FR897850-A.
PN 13-MAY-1994.
PF 10-NOV-1992; 013526.
PR 10-NOV-1992; FR-013526.
PA (UNST-) UNITV PASTEUR STRASBOURG LOUIS.

PI Kieffer B; 178255/22.
DR WPI; 94-178255/22.
DR P-PSDB; R65503.
PT New nucleic acid encoding opioid receptor - and related
PT polypeptide, antisense nucleic acid, probes, recombinant cells
PT and ligands, useful in diagnosis and treatment of e.g.
PT neurological disorders
PS Claim 3; Page 16-18; 29pp; French.
CC A cDNA bank constructed from hybridoma N6108-15, was used to
CC transfect COS-1 cells. The cells were tested for ability to bind
CC tritium-labelled Tyr-D-Phe-Gly-Phe-Leu-Thr, in the presence or
CC absence of the opioid antagonist naloxone. Clone K56 was isolated
CC from a positive colony and found to contain a 2216bp insert. This
CC cDNA encodes a delta opioid (enkephalin) receptor with apparent
CC dissociation constant 1.4nM and Bmax 3.9-6.4 pmole/mg protein.
SQ Sequence 2216 BP; 460 A; 647 C; 649 G; 460 T;

Query Match 2.9%; Score 29; DB 11; Length 2216;
Best Local Similarity 100.0%; Pred. No. 5.30e-09;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 476 accatgatgagcgtgacgcctacattgc 504
Qy 291 ACCATGATGAGCGGTGACCGCTACATTGC 319

RESULT 8
ID Q75927 standard; DNA; 2272 BP.
AC Q75927;
DT 17-AUG-1995 (first entry)
DE Mouse delta opioid receptor MOR1 cDNA.
KW Mouse; kappa; delta; mu; opioid receptor; brain; primer; PCR; amplify;
KW transmembrane domain; somatostatin; receptor; human; expression vector;
KW truncate; chimeric; assay; probe; ss.
OS Mus musculus.
FH Key Location/Qualifiers
FT CDS 12..1130
ET /tag= a
ET /product= mouse delta opioid receptor
FN WO9428132-A.
PD 08-DEC-1994.

PR 20-MAY-1994; U05747.
PR 20-MAY-1993; US-066296.
PR 30-JUL-1993; US-100694.
PR 05-NOV-1993; US-147592.
PA (ARCH-) ARCH DEV CORP.
PI Bell GI, Reisine T, Yasuda K;
DR WPI; 95-022804/03.
DR P-PSDB; R67670.

PT Polynucleotides and peptides derived from opioid receptor
PT polypeptides - for use in therapeutic compositions and in
PT screening assays for useful drug substances.
PS Claim 6; Page 215-221; 300pp; English.

CC The nucleotide sequence of the novel mouse delta opioid receptor gene
CC MOR1. The gene was isolated from a mouse brain cDNA library using a
CC fragment (amplified from the cDNA library with primers Q75929-30) as a
CC probe. The primers are based on the conserved sequences present in the
CC second and third transmembrane domains of somatostatin (SRIF) receptor
CC subtypes SSTR1, SSTR2 and SSTR3. The 1.3 kb EcoRI-SacI fragment from the
CC mouse delta opioid receptor clone, lambda msl-2, was subcloned into the
CC CMV promoter-based expression vector pCMV-6c. The resultant construct
CC pCMV-msl-2 was transfected into COS-1 cells for protein production. The
CC gene encoding the opioid receptor can be used to produce complete,
CC truncated or chimeric opioid receptor proteins. The opioid receptors
CC thus produced are useful for the development of novel assays designed to
CC select or improve substances, capable of interacting with the opioid
CC receptor proteins, for use in diagnosis, drug design and therapeutic
CC applications.
SQ Sequence 2272 BP; 485 A; 665 C; 650 G; 472 T;

Query Match 2.9%; Score 29; DB 13; Length 2272;
Best Local Similarity 100.0%; Pred. No. 5.30e-09;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 429 accatgatgagcgtgacgcctacattgc 457
Qy 291 ACCATGATGAGCGGTGACCGCTACATTGC 319

RESULT 9
ID Q89223 standard; cDNA; 1618 BP.
AC Q89223;
DT 20-OCT-1995 (first entry)
DE Transcription regulatory protein cDNA.
KW Mu opioid receptor; MOR-1; gene therapy; diagnostic;
KW transcription regulatory protein; ss.
OS Rattus sp.
FH Key Location/Qualifiers
FT CDS 339..1235
ET /tag= a
ET WO9507983-A.
PN 23-MAR-1995.
PD 13-SEP-1994; U10358.
PR 13-SEP-1993; US-120601.
PA (INDV) UNITV INDIANA FOUND.

PI Yu L; 95-131351/17.
DR WPI; 95-131351/17.
DR P-PSDB; R71965.
PT New nucleic acid encoding new human mu opioid receptor - and
PT related vectors, transformed cells, antibodies etc., useful in
PT diagnosis, treatment and drug screening.
PS Disclosure; Page 199-203; 266pp; English.
CC A 365 bp fragment of the mouse delta opioid receptor was used to
CC screen a rat brain cDNA library under low stringency conditions.
CC One positive clone included the sequence given in Q89222, encoding a
CC mu opioid receptor, MOR-1 (R71964). Sequence analysis revealed an
CC alternative reading frame (Q89223) encoding a zinc
CC finger-containing transcription regulatory protein (R71965).
SQ Sequence 1618 BP; 390 A; 486 C; 370 G; 372 T;

Query Match 2.6%; Score 26; DB 14; Length 1618;
Best Local Similarity 100.0%; Pred. No. 1.52e-06;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


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Db      652 gattactacacatgttcaccagcat 677
      |||
QY      255 GATTACTACACATGTTCACACAGCAT 280

RESULT 10
ID      089222 standard; cDNA; 1618 BP.
AC      089222;
DE      20-OCT-1995 (first entry)
KW      Rat mu opioid receptor cDNA.
OS      Mu opioid receptor; MOR-1; gene therapy; diagnostic; ss.
FH      Rattus sp.
PI      Key
PI      CDS      Location/Qualifiers
          214..1410
          /*tag= a
          WO9507983-A.
          PD      23-MAR-1995.
          PF      13-SEP-1994; U10358.
          PR      13-SEP-1993; US-120601.
          PA      (INDV ) UNIV INDIANA FOUND.
          PY      Yu L;
          DR      WPI: 95-131351/17.
          P-PSDB; R71966.
          PT      New nucleic acid encoding new human mu opioid receptor - and
          PI      related vectors, transformed cells, antibodies etc., useful in
          PS      diagnosis, treatment and drug screening.
          PS      Disclosure: Page 190-194; 266pp; English.
          CC      A 365 bp fragment of the mouse delta opioid receptor was used to
          CC      screen a rat brain cDNA library under low stringency conditions.
          CC      One positive clone included the sequence given in 089222, encoding a
          CC      mu opioid receptor, MOR-1 (R71964). MOR-1 was stably expressed in
          CC      transfected CHO cells.
          SQ      Sequence 1618 BP; 390 A; 486 C; 370 G; 372 T;

Query Match
Best Local Similarity 100.0%; Score 26; DB 14; Length 1618;
Pred. No. 1.52e-06;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db      652 gattactacacatgttcaccagcat 677
      |||
QY      255 GATTACTACACATGTTCACACAGCAT 280

RESULT 11
ID      079199 standard; cDNA; 2070 BP.
AC      079199;
DE      19-APR-1995 (first entry)
KW      Rat mu-subtype opioid receptor cDNA.
OS      Mu-subtype opioid receptor; MSOR; drug addiction; ds.
FH      Rattus rattus.
PI      Key
PI      CDS      Location/Qualifiers
          83..1154
          /*tag= a
          /product= Mu-subtype_opioid_receptor
          FT      BP-612845-A.
          PD      31-AUG-1994.
          PF      09-FEB-1994; 101368.
          PR      26-FEB-1993; US-026140.
          PA      (AMCJ ) AMERICAN CYANAMID CO.
          PI      Corbett MJ, Eppler CM, Snieh H, Zysk JR;
          DR      P-PSDB; R65188.
          PT      Pure mu-type opioid receptor protein - and nucleic acid coding
          PT      for it
          PS      Claim 1; Fig 11; 39pp; English.
          CC      R65188 is the rat mu-subtype opioid receptor protein purified
          CC      from rat brain membranes, with biotinyl-b-endorphin (B56665)
          CC      as its ligand. It is encoded by the nucleotide sequence 079199
          CC      which was synthesised using 071022 and 071023 as PCR primers.
          CC      R65188 is useful for identifying other receptor subtypes, for
          CC      screening new opioid ligands, and for studying mechanisms of
          CC      opioid action, e.g. drug addiction.
          SQ      Sequence 2070 BP; 526 A; 564 C; 423 G; 557 T;

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Query Match
Best Local Similarity 100.0%; Score 26; DB 12; Length 2070;
Pred. No. 1.52e-06;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db      404 gattactacacatgttcaccagcat 429
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QY      255 GATTACTACACATGTTCACACAGCAT 280

RESULT 12
ID      056703 standard; DNA; 829 BP.
AC      056703;
DE      15-SEP-1994 (first entry)
DE      Partial sequence of the human mu opioid receptor
DE      genomic clone H20 (MORA).
KW      Opioid receptor; morphine; opiate; ss.
OS      Homo sapiens.
PI      WO9404552-A.
PI      03-MAR-1994.
PF      13-AUG-1993; U07665.
PR      13-AUG-1992; US-929200.
PA      (RESC ) UNIV CALIFORNIA.
PI      Edwards RH, Evans CJ, Kaufman D, Keith DE;
PI      WPI: 94-083099/10.
PT      DNA encoding opioid receptors and antibodies against this
PT      receptor - used to express and locate these receptors, and screen
PT      cpgs. for opioid (ant)agonist activity
PS      Example; Fig 8c; 74pp; English.
CC      To isolate opiate receptor genomic clones, 300,000 human genomic
CC      clones and a similar number of mouse genomic clones were probed
CC      with the 1.1 kb mouse delta opioid receptor clone DOR-1 Pst/XbaI
CC      fragment. One mouse clone and three human genomic clones were
CC      isolated. The 3 human clones had very different EcoRI patterns
CC      which indicated that three different genes were represented by the
CC      human genomic clones which were designated H3, H14 and H20. H20 maps
CC      to chromosome 6. It encodes the human mu receptor. In addition, H20
CC      appears to contain a CACACA marker (056704) which provides a means
CC      to track the inheritance of this gene.
          SQ      Sequence 829 BP; 182 A; 205 C; 134 G; 214 T;

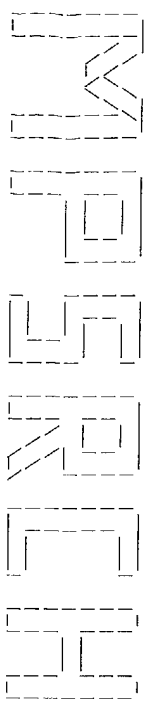
Query Match
Best Local Similarity 100.0%; Score 25; DB 10; Length 829;
Pred. No. 9.56e-06;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db      600 tgcctcgtcgtgacctccattccacat 624
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QY      694 TCGCTCGTGTGACATCCCATTCACAT 718

RESULT 13
ID      089226 standard; cDNA; 1610 BP.
AC      089226;
DE      20-OCT-1995 (first entry)
DE      Human mu opioid receptor cDNA.
KW      Mu opioid receptor; MOR; gene therapy; diagnostic; ss.
OS      Homo sapiens.
PI      Key
PI      CDS      Location/Qualifiers
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          WO9507983-A.
          PD      23-MAR-1995.
          PF      13-SEP-1994; U10358.
          PR      13-SEP-1993; US-120601.
          PA      (INDV ) UNIV INDIANA FOUND.
          PY      Yu L;
          DR      WPI: 95-131351/17.
          P-PSDB; R71966.
          PT      New nucleic acid encoding new human mu opioid receptor - and
          PT      related vectors, transformed cells, antibodies etc., useful in
          PT      diagnosis, treatment and drug screening.
          PS      Claim 5; Page 208-210; 266pp; English.
          CC      A cDNA library constructed from human caudate nucleus mRNA was

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(TM)

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Run on: Tue Apr 21 01:09:36 1998; MasPar time 715.34 Seconds
Tabular output not generated. 1177.303 Million cell updates/sec

Title: >US-08-292-694A-11
Description: (1-1000) from US08292694A.seq
Perfect Score: 994
N.A. Sequence: 1 AAGAGCAAAATCATATC.....CCAGTATGACTAGTGTGGA 1000
Comp: TTTCTGTTTATGTCATTAG.....GCTCATCTGATCAGACACCT

Scoring table: TABLE jmetric
Gap 60

Match STD : Dbase 0; Query 0

Searched: 1126798 seqs, 421087984 bases x 2

Post-processing: Minimum Match 0%
Listing first 1000 summaries

Database:

emb1_est
1:em_est1 2:em_est2 3:em_est3 4:em_est4 5:em_est5
6:em_est6 7:em_est8 8:em_gss

Database: genbank_est
9:gb_est1 10:gb_est2 11:gb_est3 12:gb_est4 13:gb_est5
14:gb_est6 15:gb_est7 16:gb_est8 17:gb_est9 18:gb_est10
19:gb_est11 20:gb_est12 21:gb_est13 22:gb_est14 23:gb_est15

Statistics: Mean 9.203; Variance 1.229; scale 7.491

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query	Match	Length	ID	Description	Pred. No.
1	137	13.8	153	10	R31984	Yb62c10.r1 Homo sapien	0.00e+00	
2	112	11.3	183	10	R81583	Vj04b04.r1 Homo sapien	2.36e-256	
3	19	1.9	206	18	AA317847	EST19840 Retina II Hom	6.71e-06	
4	19	1.9	360	21	B50520	CIT-HSP-45B23-TV CIT-	6.71e-06	
5	19	1.9	360	22	CELRK096D7F	C.elegans CDNA clone y	6.71e-06	
6	19	1.9	415	9	M75869	CELRK096D7F	6.71e-06	
7	19	1.9	521	23	AA447244	zw93c04.r1 Soares tota	6.71e-06	
8	18	1.8	187	13	HSAAADHMH	H. sapiens putatively	3.21e-04	
9	18	1.8	224	12	H74768	313 Brassica napus CDN	3.21e-04	
10	18	1.8	261	18	AA331167	EST13211 Embryo, 8 wee	3.21e-04	
11	18	1.8	261	11	H36470	yp69b06.r1 Homo sapien	3.21e-04	
12	18	1.8	316	18	AA296456	EST11038 Umbilical vei	3.21e-04	
13	18	1.8	337	17	AA361360	EST170628 T-cell lympho	3.21e-04	
14	18	1.8	364	21	FR0019360	F.rubripes GSS sequenc	3.21e-04	
15	18	1.8	367	9	T01065	WEST1786 Caenorhabdit	3.21e-04	

16	18	1.8	433	10	R81332	Yj04b04.r1 Homo sapien	3.21e-04
17	18	1.8	440	15	W76111	cd65c03.r1 Soares feta	3.21e-04
18	18	1.8	447	9	T94320	Yb37h04.s1 Homo sapien	3.21e-04
19	18	1.8	447	20	G29478	human SRS SHGC-33760.	3.21e-04
20	18	1.8	466	10	R15256	human SRS SHGC-33760.	3.21e-04
21	18	1.8	630	13	W22330	5SH12 Human retina CDN	3.21e-04
22	17	1.7	127	20	H0WC5577	Human chromosome 5 LAN	1.25e-02
23	17	1.7	168	15	AA093468	KK4722.seq.F fetal hea	1.25e-02
24	17	1.7	198	18	AA322475	EST25114 Cerebellum II	1.25e-02
25	17	1.7	238	10	R39553	yc95e11.s1 Homo sapien	1.25e-02
26	17	1.7	242	12	N21596	Yx60b06.s1 Homo sapien	1.25e-02
27	17	1.7	259	20	H0WUT466A	human SRS SHGC-33760.	1.25e-02
28	17	1.7	274	11	T31698	EST13206 Homo sapiens	1.25e-02
29	17	1.7	300	22	T16896	NIB1978 Normalized inf	1.25e-02
30	17	1.7	320	22	C11273	C.elegans CDNA clone y	1.25e-02
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33	17	1.7	327	10	R40686	Yf73c09.s1 Homo sapien	1.25e-02
34	17	1.7	331	20	G07052	human SRS WI-8958.	1.25e-02
35	17	1.7	344	16	AA158837	z058f04.r1 StrataGene	1.25e-02
36	17	1.7	352	17	AA073530	mm84f08.r1 StrataGene	1.25e-02
37	17	1.7	352	17	AA073530	mm84f08.r1 StrataGene	1.25e-02
38	17	1.7	352	9	T55579	Yb39409.s1 Homo sapien	1.25e-02
39	17	1.7	354	14	R85458	Yq26h04.s1 Soares feta	1.25e-02
40	17	1.7	357	14	R75136	MDH1081 Mouse brain, S	1.25e-02
41	17	1.7	357	9	T83796	Yd65e10.r1 Homo sapien	1.25e-02
42	17	1.7	358	13	N85608	J4165F Homo sapiens CD	1.25e-02
43	17	1.7	359	10	R55445	Yj79e06.r1 Homo sapien	1.25e-02
44	17	1.7	361	18	AA324050	EST12615 Cerebellum II	1.25e-02
45	17	1.7	363	9	T93658	ye05f09.r1 Homo sapien	1.25e-02
46	17	1.7	373	23	M0573E04	Mouse embryonal carcin	1.25e-02
47	17	1.7	381	11	R86041	Yp12h05.r1 Homo sapien	1.25e-02
48	17	1.7	398	16	N43613	SW31CA11798K Brugia ma	1.25e-02
49	17	1.7	399	9	T86078	Yd76e10.r1 Homo sapien	1.25e-02
50	17	1.7	400	20	G14676	human SRS SHGC-11837.	1.25e-02
51	17	1.7	405	11	T31706	EST13356 Homo sapiens	1.25e-02
52	17	1.7	417	15	AA147259	z038f05.r1 StrataGene	1.25e-02
53	17	1.7	429	12	N21161	Yx47d06.s1 Homo sapien	1.25e-02
54	17	1.7	430	11	R94666	Yq42e10.r1 Homo sapien	1.25e-02
55	17	1.7	439	13	N74629	z455c07.s1 Homo sapien	1.25e-02
56	17	1.7	440	22	AA431600	zw70c08.r1 Soares test	1.25e-02
57	17	1.7	451	10	R24706	Yq43e01.r1 Homo sapien	1.25e-02
58	17	1.7	451	15	W56291	zdl5b03.s1 Soares feta	1.25e-02
59	17	1.7	454	15	AA156452	z151f07.s1 Soares prey	1.25e-02
60	17	1.7	455	21	B60908	T19D2F TNAV Arabidops	1.25e-02
61	17	1.7	463	15	AA118221	MBARCE607m3 Brugia ma	1.25e-02
62	17	1.7	463	16	N59403	Yf51d05.s1 Soares feta	1.25e-02
63	17	1.7	476	9	T62904	Yc70g06.r1 Homo sapien	1.25e-02
64	17	1.7	478	12	H67558	Yf46c06.r1 Homo sapien	1.25e-02
65	17	1.7	489	23	AA500746	Vf96e12.r1 Soares mous	1.25e-02
66	17	1.7	502	13	W37077	zb20g09.r1 Soares feta	1.25e-02
67	17	1.7	513	16	W85753	zh55c03.s1 Soares feta	1.25e-02
68	17	1.7	536	17	AA029713	ze95c03.s1 Soares feta	1.25e-02
69	17	1.7	553	17	AA144197	mr75b01.r1 StrataGene	1.25e-02
70	17	1.7	559	17	AA239704	my15c07.r1 Barstead mo	1.25e-02
71	17	1.7	582	19	W87636	zh67b10.s1 Soares feta	1.25e-02
72	17	1.7	584	19	W87635	zh67b10.r1 Soares feta	1.25e-02
73	17	1.7	588	21	FR00222800	F.rubripes GSS sequenc	1.25e-02
74	17	1.7	598	21	FR00222800	F.rubripes GSS sequenc	1.25e-02
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76	17	1.7	608	16	AA166869	F.rubripes GSS sequenc	1.25e-02
77	17	1.7	610	21	FR00222812	F.rubripes GSS sequenc	1.25e-02
78	17	1.7	619	17	AA184382	37h3 Human retina CDNA	1.25e-02
79	17	1.7	654	13	W27800	54f1 Human retina CDNA	1.25e-02
80	17	1.7	858	16	AA0303200	me62g05.r1 Soares mous	1.25e-02
81	17	1.7	938	13	W28981	me62g07.r1 Soares mous	1.25e-02
82	17	1.7	987	14	W34891	Yz31f06.r1 Homo sapien	3.92e-01
83	17	1.7	105	13	N77425	Yx47d05.s1 Homo sapien	3.92e-01
84	17	1.7	115	12	N21160	C.elegans CDNA clone y	3.92e-01
85	16	1.6	147	22	N97330	0012M7 gmbfFHB3.1, G.	3.92e-01
86	16	1.6	152	23	N97330	Mouse embryonal carcin	3.92e-01
87	16	1.6	152	23	N97330	Mouse embryonal carcin	3.92e-01
88	16	1.6	183	23	M05A6E08	Mouse embryonal carcin	3.92e-01

89	1.6	191 21	B60346	CIT-HSP-2007624.TFB.CT	3.92e-01	162	1.6	355 15	CHES1742	C.hircus mRNA for EST1	3.92e-01
90	1.6	192 21	B34966	HS-1026-A1-F09-MR.ab1	3.92e-01	163	1.6	356 11	H41632	yo09h09.r1 Homo sapien	3.92e-01
91	1.6	205 14	R75166	MDR107R Mouse brain,	3.92e-01	164	1.6	357 12	AA063697	T33r1 MVA14 Bloodstrea	3.92e-01
92	1.6	208 20	G18171	human STS SHGC-4711.c1	3.92e-01	165	1.6	359 22	C06950	similar to insulin.1	3.92e-01
93	1.6	216 22	C02941	Human Heart cDNA, clone	3.92e-01	166	1.6	360 22	C13438	C.elegans cDNA clone Y	3.92e-01
94	1.6	224 16	R62395	y153e11.s1 Homo sapien	3.92e-01	167	1.6	360 22	CEIK06287F	C.elegans cDNA clone Y	3.92e-01
95	1.6	225 15	AA053301	z1f7g03.r1 Soares feta	3.92e-01	168	1.6	360 22	CEIK069A5F	C.elegans cDNA clone Y	3.92e-01
96	1.6	225 22	C02820	Human Heart cDNA, clone	3.92e-01	169	1.6	360 22	CEIK088A6F	C.elegans cDNA clone Y	3.92e-01
97	1.6	226 16	AA369627	EST181350 Prostate glan	3.92e-01	170	1.6	362 12	AA170972	ms45f05.r1 Life Tech m	3.92e-01
98	1.6	233 14	AA078862	EST191608 Synovial sarc	3.92e-01	171	1.6	364 9	T49458	ya75f05.r1 Homo sapien	3.92e-01
99	1.6	234 19	W06754	SMEST0390 Schistosoma	3.92e-01	172	1.6	366 19	AA375808	EST18141 HSC172 cells	3.92e-01
100	1.6	237 20	G05485	human STS WI-9955	3.92e-01	173	1.6	369 14	W68150	mg13f01.r1 Soares mous	3.92e-01
101	1.6	238 22	C16936	Human placenta cDNA, 5'	3.92e-01	174	1.6	370 12	H0MBS3F9	Homo sapiens thymus MR	3.92e-01
102	1.6	242 21	B44234	HS-1059-A1-C04-ME.ab1	3.92e-01	175	1.6	370 9	I82209	yo09g09.r1 Homo sapien	3.92e-01
103	1.6	243 20	G02858	human STS WI-2295.	3.92e-01	176	1.6	371 15	N76768	1015C3 czpPFpD2.1, De	3.92e-01
104	1.6	246 21	RN082592	Rattus norvegicus geno	3.92e-01	177	1.6	372 9	T80290	yo03h05.r1 Homo sapien	3.92e-01
105	1.6	247 19	AA374773	EST186965 HSC172 cells	3.92e-01	178	1.6	373 12	H58782	yr36c07.s1 Homo sapien	3.92e-01
106	1.6	250 22	C05799	similar to none.	3.92e-01	179	1.6	374 9	T09212	EST07105 Homo sapien	3.92e-01
107	1.6	252 20	AA066812	Astatotrochomys allua	3.92e-01	180	1.6	374 15	AA156009	zo48a08.s1 Stratagene	3.92e-01
108	1.6	265 10	R34687	yh87c07.s1 Homo sapien	3.92e-01	181	1.6	378 11	H09467	y197g05.r1 Homo sapien	3.92e-01
109	1.6	269 22	CE15C7	C. elegans cDNA clone	3.92e-01	182	1.6	381 12	H98953	yx11a02.s1 Homo sapien	3.92e-01
110	1.6	270 19	AA369228	EST180608 Placenta II H	3.92e-01	183	1.6	382 10	R63334	y107e12.r1 Homo sapien	3.92e-01
111	1.6	270 20	HSA061YF9	H.sapiens (D2S2372) DN	3.92e-01	184	1.6	383 23	AA133701	z192a05.r1 Stratagene	3.92e-01
112	1.6	276 9	T06272	EST04161 Homo sapiens	3.92e-01	185	1.6	383 13	ATPMS1121	A. thaliana transcribe	3.92e-01
113	1.6	278 12	H84554	YV87b08.s1 Homo sapien	3.92e-01	186	1.6	383 21	B73858	T255222TF TAMU Arabidop	3.92e-01
114	1.6	280 14	W18754	mc02a07.r1 Soares mous	3.92e-01	187	1.6	386 17	AA227125	zr21g11.r1 Stratagene	3.92e-01
115	1.6	280 17	AA47973	K1160.seq.F Human feta	3.92e-01	188	1.6	386 15	AA112396	zn68h10.s1 Stratagene	3.92e-01
116	1.6	283 13	N80275	za96f04.s1 Homo sapien	3.92e-01	189	1.6	386 23	R1CIS14569A	Rice cDNA, partial seq	3.92e-01
117	1.6	288 23	AA640020	zx49h11.s1 Soares test	3.92e-01	190	1.6	388 11	H38475	yp66g06.r1 Homo sapien	3.92e-01
118	1.6	289 12	H64514	YU67e12.s1 Homo sapien	3.92e-01	191	1.6	389 9	T83468	yp46g03.r1 Homo sapien	3.92e-01
119	1.6	290 10	R04706	PK27g04.r1 Caenorhabdi	3.92e-01	192	1.6	391 10	R65823	y127d01.s1 Homo sapien	3.92e-01
120	1.6	292 18	AA325123	EST128075 Cerebellum II	3.92e-01	193	1.6	391 15	W91217	wf72d10.r1 Soares mous	3.92e-01
121	1.6	294 22	C06971	similar to insulin.1	3.92e-01	194	1.6	392 14	W65945	me08a07.r1 Soares mous	3.92e-01
122	1.6	294 9	T79088	Yd69d01.r1 Homo sapien	3.92e-01	195	1.6	393 16	AA161077	zo58f07.r1 Stratagene	3.92e-01
123	1.6	294 20	G07280	human STS WI-9426.	3.92e-01	196	1.6	395 13	AA270719	va67d01.r1 Soares mous	3.92e-01
124	1.6	294 14	HSC0WC062	H. sapiens partial cDN	3.92e-01	197	1.6	396 22	C06976	similar to insulin.1	3.92e-01
125	1.6	296 10	R72114	y187b02.r1 Homo sapien	3.92e-01	198	1.6	397 22	C06806	similar to insulin.1	3.92e-01
126	1.6	298 18	AA317371	EST19335 Retina II Hom	3.92e-01	199	1.6	397 19	AA374186	EST86230 HSC172 cells	3.92e-01
127	1.6	300 22	C07250	C.elegans cDNA clone Y	3.92e-01	200	1.6	398 23	AA447097	zw91b10.s1 Soares tota	3.92e-01
128	1.6	305 18	AA313062	EST183859 Pancreas tum	3.92e-01	201	1.6	399 10	R53690	YX84h07.r1 Homo sapien	3.92e-01
129	1.6	307 23	AA455834	zx96f11.r1 Soares ovar	3.92e-01	202	1.6	401 15	W24831	yo65g05.r1 Soares feta	3.92e-01
130	1.6	307 17	AA073611	mm84a09.r1 Stratagene	3.92e-01	203	1.6	402 16	N64091	YV60a04.r1 Soares feta	3.92e-01
131	1.6	308 17	AA248148	cs90618.seq.F Human fe	3.92e-01	204	1.6	403 22	CEIK00562F	C.elegans cDNA clone Y	3.92e-01
132	1.6	309 13	HSC1H011	H. sapiens partial cDN	3.92e-01	205	1.6	404 14	T27030	N1EP11A09r Infant bra	3.92e-01
133	1.6	311 9	T05855	EST03744 Homo sapiens	3.92e-01	206	1.6	404 11	H46264	YOL5e02.s1 Homo sapien	3.92e-01
134	1.6	311 9	T07687	EST05577 Homo sapiens	3.92e-01	207	1.6	405 18	AA325631	EST18649 Cerebellum II	3.92e-01
135	1.6	311 13	ATRS1673	A. thaliana transcribe	3.92e-01	208	1.6	405 15	R55659	YX88b09.r1 Homo sapien	3.92e-01
136	1.6	315 18	AA333726	EST37843 Embryo, 9 wee	3.92e-01	209	1.6	405 11	BNAF0090E	Brassicica rapa (clone F	3.92e-01
137	1.6	321 14	W34984	mc34a03.r1 Soares mous	3.92e-01	210	1.6	405 15	AA335531	EST79941 Epiddymus Ho	3.92e-01
138	1.6	322 23	R1CIC10405A	Rice cDNA, partial seq	3.92e-01	211	1.6	405 18	AA325531	EST79941 Epiddymus Ho	3.92e-01
139	1.6	323 10	R41926	YV04d09.s1 Homo sapien	3.92e-01	212	1.6	405 11	T24256	crs1346 Ricinus commun	3.92e-01
140	1.6	324 16	AA308937	EST179938 Retina I Hom	3.92e-01	213	1.6	405 17	AA183954	mo96c07.r1 Stratagene	3.92e-01
141	1.6	325 23	M0588F06	Mouse embryonal carcino	3.92e-01	214	1.6	409 21	FR0003406	F.rubripes GSS sequenc	3.92e-01
142	1.6	326 21	B70905	CIT-HSP-2063E16.WR.CIT	3.92e-01	215	1.6	409 17	AA214731	PMY0121 Kc1a Lambda za	3.92e-01
143	1.6	327 16	AA158048	zo57f09.r1 Stratagene	3.92e-01	216	1.6	412 22	C06600	similar to insulin.1	3.92e-01
144	1.6	329 13	HSC2WC011	H. sapiens partial cDN	3.92e-01	217	1.6	413 11	H18119	YNA17g07.s1 Homo sapien	3.92e-01
145	1.6	333 9	T91903	YEO2a05.r1 Homo sapien	3.92e-01	218	1.6	414 16	AA191778	zs06a04.r1 Sommer Firs	3.92e-01
146	1.6	336 23	AA459169	zx86e09.r1 Soares ovar	3.92e-01	219	1.6	415 22	C06513	similar to insulin.1	3.92e-01
147	1.6	336 12	H84942	YV88b07.s1 Homo sapien	3.92e-01	220	1.6	416 10	R79893	y186d01.r1 Homo sapien	3.92e-01
148	1.6	337 22	C06608	similar to insulin.1	3.92e-01	221	1.6	416 21	B35568	HS-1029-A2-C11-MR.ab1	3.92e-01
149	1.6	337 22	CEIK129E4R	C.elegans cDNA clone Y	3.92e-01	222	1.6	418 22	C06840	similar to insulin.1	3.92e-01
150	1.6	338 21	B57948	CIT-HSP-2011A22.WF.CIT	3.92e-01	223	1.6	420 18	AA277411	vb06d10.r1 Barstead mo	3.92e-01
151	1.6	340 22	AA442600	zV57h02.r1 Soares test	3.92e-01	224	1.6	420 14	W97618	mg01g07.r1 Soares mous	3.92e-01
152	1.6	341 22	C06750	similar to insulin.1	3.92e-01	225	1.6	421 22	C07149	similar to insulin.1	3.92e-01
153	1.6	341 18	T81386	Yd24f11.r1 Homo sapien	3.92e-01	226	1.6	421 14	W98374	mg13g08.r1 Soares mous	3.92e-01
154	1.6	341 18	AA337075	EST142014 Endometrial t	3.92e-01	227	1.6	422 10	R82066	y106g01.s1 Homo sapien	3.92e-01
155	1.6	342 19	HSPD06937	H.sapiens EST sequence	3.92e-01	228	1.6	423 15	AA331897	zk11f06.r1 Soares preg	3.92e-01
156	1.6	344 19	AA125750	z123c08.r1 Soares preg	3.92e-01	229	1.6	423 15	H96129	YV13b06.r1 Soares feta	3.92e-01
157	1.6	346 21	B76141	RPC111-J3L24.IP RPC111	3.92e-01	230	1.6	423 22	C06514	similar to insulin.1	3.92e-01
158	1.6	350 11	R30456	Y124f05.s1 Homo sapien	3.92e-01	231	1.6	426 22	AA053065	z171f05.r1 Stratagene	3.92e-01
159	1.6	351 23	HIC0456	Rice cDNA, partial seq	3.92e-01	232	1.6	428 22	C06536	similar to insulin.1	3.92e-01
160	1.6	352 10	R11811	YF53a02.r1 Homo sapien	3.92e-01	233	1.6	428 22	C03237	Human Heart cDNA, clone	3.92e-01
161	1.6	354 9	T63811	Yc21f08.r1 Homo sapien	3.92e-01	234	1.6	429 18	AA313020	EST183859 Pancreas tum	3.92e-01

C	235	16	1.6	429 22	C06642	similar to insulin 1.	3	92e-01	C	308	16	1.6	470 14	W59193	mg79d03.r1	Soares	mous	3	92e-01	
C	236	16	1.6	431 12	H85699	ys68e04.r1	Homo sapien	3	92e-01	C	309	16	1.6	470 12	AA18697	mg40b10.r1	Barstead	MP	3	92e-01
C	237	15	1.6	432 19	AA151154	z10a12.r1	Soares preg	3	92e-01	C	310	16	1.6	471 17	H66735	ys83f11.r1	Homo sapien		3	92e-01
C	238	16	1.6	433 14	W80352	me90e12.r1	Soares mous	3	92e-01	C	311	16	1.6	471 16	R28157	y655d11.r1	Homo sapien		3	92e-01
C	239	16	1.6	433 16	AA212412	mb78a10.r1	Stratagene	3	92e-01	C	312	16	1.6	472 10	AA410475	z380g01.r1	Homo sapien		3	92e-01
C	240	16	1.6	434 9	T61622	yb6gq11.r1	Homo sapien	3	92e-01	C	313	16	1.6	473 17	AA15039	mg53f05.r1	Soares	ovar	3	92e-01
C	241	16	1.6	434 22	C06831	similar to insulin 1.	3	92e-01	C	314	16	1.6	474 16	AA213580	z939b05.r1	Stratagene		3	92e-01	
C	242	16	1.6	435 9	T72706	y419c09.r1	Homo sapien	3	92e-01	C	315	16	1.6	474 23	AA510608	v337a05.r1	Soares	mous	3	92e-01
C	243	16	1.6	435 15	W94191	zd77d07.r1	Soares feta	3	92e-01	C	316	16	1.6	475 10	PA1996	ml14c09.r1	Soares	mous	3	92e-01
C	244	16	1.6	435 20	G00423	fruit fly Strs Dm0021	c	3	92e-01	C	317	16	1.6	475 14	R81264	ml99a10.r1	Soares	mous	3	92e-01
C	245	16	1.6	436 12	N24446	mb14g02.r1	Soares mous	3	92e-01	C	318	16	1.6	475 14	W29439	ml99a10.r1	Soares	mous	3	92e-01
C	246	16	1.6	436 21	FR0004011	F.rubripes GSS sequenc	3	92e-01	C	319	16	1.6	475 14	W29439	ml99a10.r1	Soares	mous	3	92e-01	
C	247	16	1.6	436 21	FR0004011	F.rubripes GSS sequenc	3	92e-01	C	320	16	1.6	475 14	W29439	ml99a10.r1	Soares	mous	3	92e-01	
C	248	16	1.6	437 11	H50250	Y289g05.r1	Homo sapien	3	92e-01	C	321	16	1.6	479 17	AA231224	me40d01.r1	Soares	mous	3	92e-01
C	249	16	1.6	437 11	H50250	Y289g05.r1	Homo sapien	3	92e-01	C	322	16	1.6	480 20	G34598	me37e03.r1	Soares	mous	3	92e-01
C	250	16	1.6	437 15	W53233	md19e08.r1	Soares mous	3	92e-01	C	323	16	1.6	480 14	AA008796	human Strs STGC-51939			3	92e-01
C	251	16	1.6	437 15	W73089	zds4c09.r1	Soares feta	3	92e-01	C	324	16	1.6	480 14	AA008796	mg98h04.r1	Soares	mous	3	92e-01
C	252	16	1.6	437 12	N53398	Y223f06.r1	Homo sapien	3	92e-01	C	325	16	1.6	481 15	AA063788	ml16b03.r1	Soares	mous	3	92e-01
C	253	16	1.6	439 9	T83089	Y404f05.r1	Homo sapien	3	92e-01	C	326	16	1.6	481 15	AA063788	ml16b03.r1	Soares	mous	3	92e-01
C	254	16	1.6	440 18	AA350536	BS57858 Infant brain	3	92e-01	C	327	16	1.6	484 14	W34494	ma98e09.r1	Soares	mous	3	92e-01	
C	255	16	1.6	440 10	R53955	Y899d09.r1	Homo sapien	3	92e-01	C	328	16	1.6	486 14	W78469	me79a01.r1	Soares	mous	3	92e-01
C	256	16	1.6	440 14	W36672	mb89b02.r1	Soares mous	3	92e-01	C	329	16	1.6	486 22	C06154	similar to none.			3	92e-01
C	257	16	1.6	441 11	H18211	Y474712.r1	Homo sapien	3	92e-01	C	330	16	1.6	487 17	AA242327	mg26c09.r1	Soares	mous	3	92e-01
C	258	16	1.6	442 14	AA050021	mj39b10.r1	Soares mous	3	92e-01	C	331	16	1.6	488 22	AA415137	zw76h09.r1	Soares	test	3	92e-01
C	259	16	1.6	442 14	AA050021	mm26h10.r1	Stratagene	3	92e-01	C	332	16	1.6	488 15	H96502	Y888e10.r1	Soares	mela	3	92e-01
C	260	16	1.6	443 15	AA153386	zoz8a07.r1	Homo sapien	3	92e-01	C	333	16	1.6	489 10	R55683	Y888e10.r1	Soares	mela	3	92e-01
C	261	16	1.6	443 13	N66818	za09b12.r1	Homo sapien	3	92e-01	C	334	16	1.6	491 21	B35459	HS-1029-r1	-M02-MR	abl	3	92e-01
C	262	16	1.6	444 14	W58917	md50a09.r1	Soares mous	3	92e-01	C	335	16	1.6	491 22	C07167	similar to insulin 1.			3	92e-01
C	263	16	1.6	444 19	AA136777	zK99d05.r1	Soares preg	3	92e-01	C	336	16	1.6	491 17	AA218221	mw61b08.r1	Soares	mous	3	92e-01
C	264	16	1.6	444 12	N41001	Y880a04.r1	Homo sapien	3	92e-01	C	337	16	1.6	491 17	W89617	mw61b08.r1	Soares	mous	3	92e-01
C	265	16	1.6	444 17	W61555	mm90e09.r1	Stratagene	3	92e-01	C	338	16	1.6	492 18	AA271368	v471f03.r1	Soares	mous	3	92e-01
C	266	16	1.6	445 16	W73194	zds4c09.r1	Soares feta	3	92e-01	C	339	16	1.6	492 10	R37636	v61a108.r1	Homo sapien		3	92e-01
C	267	16	1.6	446 23	AA462647	vF90h06.r1	Soares mous	3	92e-01	C	340	16	1.6	493 17	AA189661	mt63b09.r1	Soares	2NB4	3	92e-01
C	268	16	1.6	447 10	RA5064	Y838c04.r1	Soares sapien	3	92e-01	C	341	16	1.6	493 17	T91051	YD59c03.r1	Homo sapien		3	92e-01
C	269	16	1.6	447 17	AA261490	me87a01.r1	Soares mous	3	92e-01	C	342	16	1.6	493 17	PA154487	mr94f08.r1	Stratagene		3	92e-01
C	270	16	1.6	448 13	N78731	zB05a11.r1	Homo sapien	3	92e-01	C	343	16	1.6	494 17	AA166132	ms24h07.r1	Stratagene		3	92e-01
C	271	16	1.6	448 15	W16211	mb63f04.r1	Soares mous	3	92e-01	C	344	16	1.6	495 15	W89252	mf3b07.r1	Soares	mous	3	92e-01
C	272	16	1.6	449 15	W31611	zB91d12.r1	Soares para	3	92e-01	C	345	16	1.6	496 21	B47607	CIT-HSP-215111	TVB	CIT	3	92e-01
C	273	16	1.6	449 12	AA542347	Y999a02.r1	Homo sapien	3	92e-01	C	346	16	1.6	496 14	AA002949	mg40a10.r1	Soares	mous	3	92e-01
C	274	16	1.6	449 12	H72129	vH81d10.r1	Knowles Sol	3	92e-01	C	347	16	1.6	497 16	AA188808	zP77e03.r1	Stratagene		3	92e-01
C	275	16	1.6	449 13	AA517756	VB10h04.r1	Soares mous	3	92e-01	C	348	16	1.6	497 14	W54315	mg40a10.r1	Soares	mous	3	92e-01
C	276	16	1.6	449 18	AA542236	VX28b05.r1	Soares mous	3	92e-01	C	349	16	1.6	498 16	AA017858	md44d11.r1	Soares	mous	3	92e-01
C	277	16	1.6	449 23	AA517756	mg66g06.r1	Soares mous	3	92e-01	C	350	16	1.6	498 23	AA473478	V977g02.r1	Stratagene		3	92e-01
C	278	16	1.6	450 23	AA542236	Y999e06.r1	Homo sapien	3	92e-01	C	351	16	1.6	499 16	AA106437	ml94e07.r1	Barstead	MP	3	92e-01
C	279	16	1.6	450 14	AA007961	Y993e07.r1	Homo sapien	3	92e-01	C	352	16	1.6	501 14	AA028699	ml12f11.r1	Soares	mous	3	92e-01
C	280	16	1.6	451 11	H38486	Y993e07.r1	Homo sapien	3	92e-01	C	353	16	1.6	501 23	AA499000	v187g09.r1	Stratagene		3	92e-01
C	281	16	1.6	451 10	R56374	Y993e07.r1	Homo sapien	3	92e-01	C	354	16	1.6	502 17	AA170314	mg10e09.r1	Barstead	MP	3	92e-01
C	282	16	1.6	452 16	AA186879	zP74e05.r1	Stratagene	3	92e-01	C	355	16	1.6	502 21	FR0024232	mg26f01.r1	Soares	mous	3	92e-01
C	283	16	1.6	452 22	C06788	similar to insulin 1.	3	92e-01	C	356	16	1.6	502 14	AA039651	F.rubripes GSS sequenc			3	92e-01	
C	284	16	1.6	453 18	AA308826	BS1179643 Retina II Ho	3	92e-01	C	357	16	1.6	503 14	AA017596	zF08e12.r1	Soares	feta	3	92e-01	
C	285	16	1.6	453 14	AA008047	mg68f04.r1	Soares mous	3	92e-01	C	358	16	1.6	503 23	AA449922	zX37f07.r1	Soares	tota	3	92e-01
C	286	16	1.6	454 19	AA045756	zK68c10.r1	Soares preg	3	92e-01	C	359	16	1.6	504 14	AA032474	ml20f10.r1	Soares	mous	3	92e-01
C	287	16	1.6	454 14	AA032302	MTA-A01.088-A MTA adu1	3	92e-01	C	360	16	1.6	504 17	AA153053	mr84b07.r1	Stratagene		3	92e-01	
C	288	16	1.6	455 23	AA456816	zw28f03.r1	Soares ovar	3	92e-01	C	361	16	1.6	504 14	AA033416	ml31c11.r1	Soares	mous	3	92e-01
C	289	16	1.6	456 9	T81772	Y430d03.r1	Homo sapien	3	92e-01	C	362	16	1.6	505 18	AA273335	vc03b01.r1	Barstead	MP	3	92e-01
C	290	16	1.6	456 23	AA537909	VJ35e05.r1	Stratagene	3	92e-01	C	363	16	1.6	506 12	N83767	Y64f05.r1	Homo sapien		3	92e-01
C	291	16	1.6	457 14	W25114	zB68b08.r1	Soares feta	3	92e-01	C	364	16	1.6	507 14	AA049553	mg35g04.r1	Soares	mous	3	92e-01
C	292	16	1.6	457 14	W78259	mb79g10.r1	Soares mous	3	92e-01	C	365	16	1.6	508 23	AA449921	mx87i02.r1	Soares	tota	3	92e-01
C	293	16	1.6	457 11	H24554	ym65f102.r1	Soares mous	3	92e-01	C	366	16	1.6	508 23	FR0022519	F.rubripes GSS sequenc			3	92e-01
C	294	16	1.6	457 11	H24554	Y423c02.r1	Homo sapien	3	92e-01	C	367	16	1.6	509 14	W97879	v202f06.r1	Soares	mous	3	92e-01
C	295	16	1.6	459 17	AA071753	mm70c03.r1	Stratagene	3	92e-01	C	368	16	1.6	510 14	AA049553	mg98b04.r1	Soares	mous	3	92e-01
C	296	16	1.6	460 11	H06968	Y184g09.r1	Homo sapien	3	92e-01	C	369	16	1.6	512 14	AA003317	mg47a10.r1	Soares	mous	3	92e-01
C	297	16	1.6	462 16	AA198155	mw46b07.r1	Soares mous	3	92e-01	C	370	16	1.6	513 13	MUS6800532	Mouse 3'-directed CDN			3	92e-01
C	298	16	1.6	463 14	AA008206	mg75f02.r1	Soares mous	3	92e-01	C	371	16	1.6	514 16	AA067929	Y44012.r1	Homo sapien		3	92e-01
C	299	16	1.6	465 19	AA387504	CPBSTR.283	unizAPCPTOMA	3	92e-01	C	372	16	1.6	514 16	AA067929	Y44012.r1	Homo sapien		3	92e-01
C	300	16	1.6	466 17	AA218901	Z415e05.r1	Stratagene	3	92e-01	C	373	16	1.6	518 15	AA086107					

C 381	16	522 17	AA239498	my21b12.r1 Barstead mo	3.92e-01	C 484	15	107 18	AA301891	EST14873 Aorta endoth	9.51e+00
C 382	16	523 22	C18799	Human placenta cDNA 5'	3.92e-01	C 485	15	117 14	HSAPAAATM	H. sapiens putatively	9.51e+00
C 383	16	524 23	AA530040	vj15c10.r1 Barstead mo	3.92e-01	C 486	15	139 11	H43697	y080c03.s1 Homo sapien	9.51e+00
C 384	16	533 19	AA397494	CPEST.299 unizAPC10MA	3.92e-01	C 487	15	1.5	R06040	y089e08.r1 Homo sapien	9.51e+00
C 385	16	538 16	N57857	yy60b04.s1 Soares feta	3.92e-01	C 488	15	157 14	w70486	me21b06.r1 Soares mous	9.51e+00
C 386	16	545 9	T78443	yv68b07.s1 Homo sapien	3.92e-01	C 489	15	1.5	N89054	k7549F Fetal heart, Ia	9.51e+00
C 387	16	548 10	R39446	yc95c07.s1 Homo sapien	3.92e-01	C 490	15	165 15	w20689	mc21f05.r1 Soares mous	9.51e+00
C 388	16	549 22	AA434056	zw24d01.r1 Soares ovit	3.92e-01	C 491	15	1.5	AA021420	ze66f08.r1 Soares reti	9.51e+00
C 389	16	549 21	B71032	CIT-HSP-2065L11.TP CIT	3.92e-01	C 492	15	169 16	AA091361	zr39g02.r1 Soares NHHM	9.51e+00
C 390	16	550 16	AA089086	mm51d12.r1 Stratagene	3.92e-01	C 493	15	175 19	AA368456	EST17377 Placenta, I Ho	9.51e+00
C 391	16	551 16	AA193799	rs03f12.r1 Sommer pris	3.92e-01	C 494	15	201 18	G21490	human STS wt-16697.	9.51e+00
C 392	16	553 23	AA530381	xy74804.r1 Stratagene	3.92e-01	C 495	15	201 18	AA338945	EST14394 Fetal brain I	9.51e+00
C 393	16	554 22	AA436968	xy72g05.r1 Soares tota	3.92e-01	C 496	15	204 18	AA331175	EST35220 Embryo, 8 wee	9.51e+00
C 394	16	555 22	C07148	similar to insulin 1.	3.92e-01	C 497	15	204 9	T77882	y620d07.s1 Homo sapien	9.51e+00
C 395	16	556 21	B27940	T2216TFC TAMU Arabidop	3.92e-01	C 498	15	206 16	AA055181	z120d07.r1 Soares feta	9.51e+00
C 396	16	563 22	AA115663	z189g11.r1 Stratagene	3.92e-01	C 499	15	208 17	AA174802	mt13b11.r1 Soares mous	9.51e+00
C 397	16	564 22	C06914	similar to insulin 1.	3.92e-01	C 470	15	208 9	T59648	yc13d12.s1 Homo sapien	9.51e+00
C 398	16	564 16	AA025822	ze85h09.s1 Soares feta	3.92e-01	C 471	15	211 20	HS067Xa9	H.sapiens DNA segment	9.51e+00
C 399	16	568 22	C05975	similar to glia-derivate	3.92e-01	C 472	15	215 16	AA209150	zq58c10.r1 Stratagene	9.51e+00
C 400	16	574 17	AA125071	mg63g09.r1 Stratagene	3.92e-01	C 473	15	219 18	AA329889	EST33572 Embryo, 12 we	9.51e+00
C 401	16	576 21	FR0022372	F.rubripes GSS sequenc	3.92e-01	C 474	15	222 10	R10761	y132g08.s1 Homo sapien	9.51e+00
C 402	16	579 9	T24127	SME8T0325 Schistosoma	3.92e-01	C 475	15	224 20	G04713	human STS wt-4876.	9.51e+00
C 403	16	583 21	B54513	CIT-HSP-345111.TP CIT	3.92e-01	C 476	15	227 23	AA512493	y17f904.r1 Barstead mo	9.51e+00
C 404	16	583 23	AA467314	vg99c03.r1 Soares mous	3.92e-01	C 477	15	228 18	AA347554	EST33879 Homo sapiens	9.51e+00
C 405	16	584 16	AA214938	mu83h05.r1 Stratagene	3.92e-01	C 478	15	233 11	T27616	EST01569 Homo sapiens	9.51e+00
C 406	16	587 16	AA176131	zp23g03.s1 Stratagene	3.92e-01	C 479	15	233 10	R30701	EST01209 Homo sapiens	9.51e+00
C 407	16	588 21	FR0011370	F.rubripes GSS sequenc	3.92e-01	C 480	15	235 10	C24922	yf60g12.s1 Homo sapien	9.51e+00
C 408	16	588 10	R39054	y088c10.s1 Homo sapien	3.92e-01	C 481	15	237 23	R30701	Rice cDNA, partial seq	9.51e+00
C 409	16	591 17	AA230508	mw26g11.r1 GuayWoodfor	3.92e-01	C 482	15	243 22	CELK006A4F	C.elegans cDNA clone y	9.51e+00
C 410	16	595 16	AA180962	zp41d01.r1 Stratagene	3.92e-01	C 483	15	248 18	AA345297	EST51559 Gall bladder	9.51e+00
C 411	16	597 21	B66083	CIT-HSP-2023021.TP CIT	3.92e-01	C 484	15	253 18	AA033802	zk19h12.r1 Soares preg	9.51e+00
C 412	16	600 14	AA050410	mt11d02.r1 Soares mous	3.92e-01	C 485	15	256 19	AA327842	EST31230 Embryo, 12 we	9.51e+00
C 413	16	601 16	AA105934	ml180e01.r1 Stratagene	3.92e-01	C 486	15	257 12	H84068	y594b11.r1 Homo sapien	9.51e+00
C 414	16	603 21	FR0016200	F.rubripes GSS sequenc	3.92e-01	C 487	15	260 18	HSP01099	H.sapiens EST sequenc	9.51e+00
C 415	16	603 15	w82950	me80b10.r1 Soares mous	3.92e-01	C 488	15	261 18	AA319360	EST12573 Adrenal gland	9.51e+00
C 416	16	608 17	AA122594	mc09e08.r1 Barstead MP	3.92e-01	C 489	15	261 23	R1CS2108A	Rice cDNA, partial seq	9.51e+00
C 417	16	609 17	AA122639	mc09h07.r1 Barstead MP	3.92e-01	C 490	15	261 11	T28704	EST52396 Homo sapiens	9.51e+00
C 418	16	609 13	w47910	mc84a10.r1 Soares mous	3.92e-01	C 491	15	262 9	T39149	y901b10.r2 Homo sapien	9.51e+00
C 419	16	612 17	AA184420	mt52a02.r1 Stratagene	3.92e-01	C 492	15	263 23	AA444191	vc34c02.r1 Ko mouse em	9.51e+00
C 420	16	612 17	AA268193	va97a03.r1 Soares mous	3.92e-01	C 493	15	264 22	HUM00TPB025	Human HepG2 3'-directe	9.51e+00
C 421	16	613 17	AA167997	me66c06.r1 Stratagene	3.92e-01	C 494	15	264 23	AA511356	y127c09.r1 Soares mous	9.51e+00
C 422	16	617 21	AA500275	v197f02.r1 Barstead mo	3.92e-01	C 495	15	266 12	H59171	y03f02.r1 Homo sapien	9.51e+00
C 423	16	615 14	AA030625	mt10d02.r1 Soares mous	3.92e-01	C 496	15	267 18	AA327319	EST30631 Colon I Homo	9.51e+00
C 424	16	616 14	w78285	me18d12.r1 Soares mous	3.92e-01	C 497	15	267 19	HSP01177	H.sapiens EST sequenc	9.51e+00
C 425	16	616 16	w97809	mg02e08.r1 Soares mous	3.92e-01	C 498	15	270 18	AA361252	EST70552 T-cell lympho	9.51e+00
C 426	16	618 23	AA541868	vy54g01.r1 Knowles Sol	3.92e-01	C 499	15	271 14	AA017271	z336c03.r1 Soares reti	9.51e+00
C 427	16	619 21	FR0007535	F.rubripes GSS sequenc	3.92e-01	C 500	15	272 18	AA344949	EST50925 Gall bladder	9.51e+00
C 428	16	619 21	FR0022373	F.rubripes GSS sequenc	3.92e-01	C 501	15	273 19	AA385950	EST99654 Thyroid Homo	9.51e+00
C 429	16	619 21	FR0019372	F.rubripes GSS sequenc	3.92e-01	C 502	15	274 19	AA355638	EST64065 Jurkat T-cell	9.51e+00
C 430	16	619 17	AA167925	me25a05.r1 Stratagene	3.92e-01	C 503	15	275 23	R1CR2587A	Rice cDNA, partial seq	9.51e+00
C 431	16	620 15	w74645	zq77d07.s1 Soares feta	3.92e-01	C 504	15	276 11	T29473	EST81189 Homo sapiens	9.51e+00
C 432	16	621 16	AA024369	mh93b06.r1 Soares mous	3.92e-01	C 505	15	276 14	MMTE8T44	M.musculus expressed s	9.51e+00
C 433	16	621 17	AA242331	mw26d09.r1 Soares mous	3.92e-01	C 506	15	278 14	HSCNCO021	H.sapiens partial cDN	9.51e+00
C 434	16	623 17	AA220088	mx98f01.r1 Barstead mo	3.92e-01	C 507	15	278 18	AA008986	mg99e02.r1 Soares mous	9.51e+00
C 435	16	624 14	AA034016	z106c12.s1 Soares feta	3.92e-01	C 508	15	278 18	AA317792	EST17979 Retina II Hom	9.51e+00
C 436	16	625 13	w22409	6665 Human retina cDNA	3.92e-01	C 509	15	280 10	R17354	y613f04.r1 Homo sapien	9.51e+00
C 437	16	625 13	B17760	347J12.TVB C179785XAI	3.92e-01	C 510	15	281 19	AA384025	EST97576 Thyroid Homo	9.51e+00
C 438	16	629 17	AA221400	my15a12.r1 Barstead mo	3.92e-01	C 511	15	282 11	H21432	y7f6f08.r1 Homo sapien	9.51e+00
C 439	16	630 21	B08043	TZB21-Sp6.1 TAMU Arabi	3.92e-01	C 512	15	282 22	HUM00TPB037	Human HepG2 3'-directe	9.51e+00
C 440	16	632 17	AA142395	ms08c04.r1 Stratagene	3.92e-01	C 513	15	286 9	T01318	EST02039 Caenorhadit	9.51e+00
C 441	16	632 17	AA12537	FLM21-Sp6.1 IGF Arabid	3.92e-01	C 514	15	287 22	HUM519B03B	Human placenta cDNA 5'	9.51e+00
C 442	16	632 17	AA188657	mt33g09.r1 Soares 2NBK	3.92e-01	C 515	15	290 17	AA361255	EST70555 T-cell lympho	9.51e+00
C 443	16	632 17	AA195034	zt35b09.s1 Soares NHHM	3.92e-01	C 516	15	293 17	AA078562	EST70555 T-cell lympho	9.51e+00
C 444	16	632 17	AA220007	mx97d12.r1 Barstead mo	3.92e-01	C 517	15	294 12	H64992	y666c10.r1 Homo sapien	9.51e+00
C 445	16	633 14	w89520	mx78g10.r1 Soares mous	3.92e-01	C 518	15	296 16	AA333091	EST183888 Prostate gla	9.51e+00
C 446	16	634 17	AA220007	mx78g10.r1 Soares mous	3.92e-01	C 519	15	296 19	T73404	y34g06.r1 Homo sapien	9.51e+00
C 447	16	634 17	B08401	TAP6-T7 TAMU Arabidops	3.92e-01	C 520	15	297 19	AA380840	z696c08.r1 Soares preg	9.51e+00
C 448	16	634 17	B11053	human STS wt-9078.	3.92e-01	C 521	15	297 19	AA377854	EST93859 Activated T-c	9.51e+00
C 449	16	634 17	B11053	human STS wt-9078.	3.92e-01	C 522	15	297 19	AA377854	EST93859 Activated T-c	9.51e+00
C 450	16	634 17	B11053	human STS wt-9078.	3.92e-01	C 523	15	297 19	AA377854	EST93859 Activated T-c	9.51e+00
C 451	16	634 17	B11053	human STS wt-9078.	3.92e-01	C 524	15	297 19	AA377854	EST93859 Activated T-c	9.51e+00
C 452	16	634 17	B11053	human STS wt-9078.	3.92e-01	C 525	15	297 19	AA377854	EST93859 Activated T-c	9.51e+00
C 453	16	634 17	B11053	human STS wt-9078.	3.92e-01	C 526	15	297 19	AA377854	EST93859 Activated T-c	9.51e+00

527	15	1.5	303	9	T10587	hbc455 Homo sapiens cd	9.51e+00	600	15	1.5	360	22	CEIK101BZF	C.elegans cDNA clone y	9.51e+00
528	15	1.5	303	19	HSPD6151	H.sapiens EST sequence	9.51e+00	601	15	1.5	360	22	C09430	C.elegans cDNA clone y	9.51e+00
529	15	1.5	304	9	T81273	Y24c10.s1 Homo sapien	9.51e+00	602	15	1.5	360	22	C13375	C.elegans cDNA clone y	9.51e+00
530	15	1.5	304	10	R26732	yh1f01.s1 Homo sapien	9.51e+00	603	15	1.5	361	14	K56983	md18e10.r1 Soares mous	9.51e+00
531	15	1.5	304	10	R03918	pk13a12.s1 Caenorhabdi	9.51e+00	604	15	1.5	361	10	R21192	yh2f01.s1 Homo sapien	9.51e+00
532	15	1.5	305	17	AA254064	va10e07.r1 Soares mous	9.51e+00	605	15	1.5	362	12	N20859	yx5b009.s1 Homo sapien	9.51e+00
533	15	1.5	305	18	AA300819	ESF13767 Testis tumor	9.51e+00	606	15	1.5	362	19	AA400942	z5b0b08.s1 Soares ovar	9.51e+00
534	15	1.5	307	23	AA447704	aa20b04.s1 Soares Nhm	9.51e+00	607	15	1.5	362	11	R85068	y062b04.r1 Homo sapien	9.51e+00
535	15	1.5	307	20	G30052	human STR SHGC-36062.	9.51e+00	608	15	1.5	363	16	AA2211705	pk06a03.s1 Caenorhabdi	9.51e+00
536	15	1.5	307	13	HSC22B112	H. sapiens partial cDN	9.51e+00	609	15	1.5	363	10	R03397	z064f09.r1 Stratagene	9.51e+00
537	15	1.5	308	16	AA166358	mt75a05.r1 Soares mous	9.51e+00	610	15	1.5	365	14	N24669	z063f02.r1 Soares feta	9.51e+00
538	15	1.5	312	18	AA309678	EST180578 Jurkat T-cell	9.51e+00	611	15	1.5	365	15	W42674	j0643F Fetal heart, La	9.51e+00
539	15	1.5	316	22	C00065	HMG5004676, Human Ge	9.51e+00	612	15	1.5	365	14	N86137	z062a11.s1 Soares sene	9.51e+00
540	15	1.5	316	22	W96396	zet0e11.r1 Soares feta	9.51e+00	613	15	1.5	365	17	AA223481	cp3025.seq.F Fetal hea	9.51e+00
541	15	1.5	317	19	HSPD04747	H.sapiens EST sequence	9.51e+00	614	15	1.5	365	15	AA095150	zx35f11.s1 Soares tota	9.51e+00
542	15	1.5	317	19	R94387	y03c06.s1 Homo sapien	9.51e+00	615	15	1.5	366	23	AA422556	F0312 Fetal heart Homo	9.51e+00
543	15	1.5	318	10	R06620	yf10h01.r1 Homo sapien	9.51e+00	616	15	1.5	367	13	R57037	me64e07.r1 Stratagene	9.51e+00
544	15	1.5	318	10	W85548	mf47c09.r1 Soares mous	9.51e+00	617	15	1.5	368	23	AA530207	me64e07.r1 Soares mous	9.51e+00
545	15	1.5	319	23	AA532125	TENF0189 T. cruzi opima	9.51e+00	618	15	1.5	369	14	W77405	yn48g08.r1 Homo sapien	9.51e+00
546	15	1.5	321	19	W90544	zh75d10.r1 Soares feta	9.51e+00	619	15	1.5	371	12	H63162	yx50a02.r1 Homo sapien	9.51e+00
547	15	1.5	321	19	T37447	EST102572 Saccharomyce	9.51e+00	620	15	1.5	371	10	R09690	yf23b11.r1 Homo sapien	9.51e+00
548	15	1.5	323	13	N98942	yy71b01.r1 Homo sapien	9.51e+00	621	15	1.5	373	15	AA115387	y105b09.s1 Soares preg	9.51e+00
549	15	1.5	326	17	AA253795	mw03q03.r1 Soares mous	9.51e+00	622	15	1.5	373	22	HUMG500579	EST74556 Pitneal gland	9.51e+00
550	15	1.5	327	23	R1C34235A	Rice cDNA, partial seq	9.51e+00	623	15	1.5	374	18	AA316545	EST188233 HCC cell lin	9.51e+00
551	15	1.5	328	19	AA115741	EST044779 Homo sapiens	9.51e+00	624	15	1.5	374	18	AA316545	mt12h12.r1 Soares mous	9.51e+00
552	15	1.5	328	19	AA115741	zK96b07.s1 Soares preg	9.51e+00	625	15	1.5	375	16	AA085722	SM31CA1568K Bruglia ma	9.51e+00
553	15	1.5	321	19	AA365311	EST76039 Pitneal gland	9.51e+00	626	15	1.5	376	15	AA085722	zn33f06.s1 Stratagene	9.51e+00
554	15	1.5	331	9	T94160	ye28g11.r1 Homo sapien	9.51e+00	627	15	1.5	377	18	AA340603	EST74864 Fetal kidney	9.51e+00
555	15	1.5	332	9	T59780	yc13d12.r1 Homo sapien	9.51e+00	628	15	1.5	380	14	AA103011	mo16e10.r1 Soares mous	9.51e+00
556	15	1.5	332	12	H99055	yv9d008.s1 Homo sapien	9.51e+00	629	15	1.5	380	14	W59014	md61d11.r1 Soares mous	9.51e+00
557	15	1.5	332	12	CEIK076C2R	C.elegans cDNA clone y	9.51e+00	630	15	1.5	381	13	HSC1DE101	H. sapiens partial cDN	9.51e+00
558	15	1.5	333	9	T94945	yE38b06.r1 Homo sapien	9.51e+00	631	15	1.5	381	13	N76815	Y461b08.r1 Homo sapien	9.51e+00
559	15	1.5	333	9	T27762	EST15391 Homo sapiens	9.51e+00	632	15	1.5	381	13	N76815	EST101292 Homo sapiens	9.51e+00
560	15	1.5	335	9	T02531	0144c3 Plasmodium falc	9.51e+00	633	15	1.5	381	13	N76815	Y719c11.s1 Homo sapien	9.51e+00
561	15	1.5	337	19	AA363732	EST97152 Testis I Homo	9.51e+00	634	15	1.5	381	12	H78329	Yy19c11.s1 Homo sapien	9.51e+00
562	15	1.5	339	12	H56449	yq98g10.s1 Homo sapien	9.51e+00	635	15	1.5	383	10	R41724	Yy11b01.s1 Homo sapien	9.51e+00
563	15	1.5	340	18	AA346234	EST53345 Greater oment	9.51e+00	636	15	1.5	383	11	H44210	yn58d09.r1 Homo sapien	9.51e+00
564	15	1.5	341	13	N67367	y250g01.s1 Homo sapien	9.51e+00	637	15	1.5	385	15	H89879	mf77e02.r1 Soares mous	9.51e+00
565	15	1.5	342	18	AA329709	EST33379 Embryo, 12 we	9.51e+00	638	15	1.5	385	15	AA351728	EST55579 Infant Brain	9.51e+00
566	15	1.5	344	16	W87550	yE64b09.s1 Homo sapien	9.51e+00	639	15	1.5	386	10	R24590	Yh39e07.r1 Homo sapien	9.51e+00
567	15	1.5	344	16	W87550	zH55b06.r1 Soares feta	9.51e+00	640	15	1.5	387	10	R24590	Yh39e07.r1 Homo sapien	9.51e+00
568	15	1.5	344	16	AA099716	zK86g09.r1 Soares preg	9.51e+00	641	15	1.5	388	22	AA122403	z188a01.r1 Stratagene	9.51e+00
569	15	1.5	345	11	H27803	y158g08.r1 Homo sapien	9.51e+00	642	15	1.5	388	22	AA122403	HS-1051-A2-B04-MR-ab1	9.51e+00
570	15	1.5	346	18	HSP003798	H.sapiens EST sequence	9.51e+00	643	15	1.5	389	17	AA267354	mz91b12.r1 Soares mous	9.51e+00
571	15	1.5	347	10	R34610	Yh87f03.r1 Homo sapien	9.51e+00	644	15	1.5	391	15	AA111054	zn53g09.r1 Stratagene	9.51e+00
572	15	1.5	347	10	C24311	Citrus cDNA, partial s	9.51e+00	645	15	1.5	391	17	AA098210	mc74a05.r1 Soares mous	9.51e+00
573	15	1.5	348	18	AA317393	EST19366 Retina II Hom	9.51e+00	646	15	1.5	392	17	T66345	yc78b11.r1 Homo sapien	9.51e+00
574	15	1.5	349	19	AA365285	EST76007 Pitneal gland	9.51e+00	647	15	1.5	392	13	W44082	mc73e11.r1 Soares mous	9.51e+00
575	15	1.5	349	9	T09707	mp55g07.r1 Soares 2NDX	9.51e+00	648	15	1.5	392	13	W44082	yp72e10.r1 Homo sapien	9.51e+00
576	15	1.5	350	17	AA118862	zr48g07.s1 Soares Nhm	9.51e+00	649	15	1.5	393	11	H48037	Yr11h06.r1 Homo sapien	9.51e+00
577	15	1.5	350	17	AA233748	yq31e08.s1 Homo sapien	9.51e+00	650	15	1.5	394	12	H59986	Yr11h06.r1 Homo sapien	9.51e+00
578	15	1.5	350	17	AA233748	yc30g01.r1 Homo sapien	9.51e+00	651	15	1.5	394	12	H59986	Yr11h06.r1 Homo sapien	9.51e+00
579	15	1.5	351	11	R68949	H. sapiens partial cDN	9.51e+00	652	15	1.5	394	12	H59986	Yr11h06.r1 Homo sapien	9.51e+00
580	15	1.5	351	13	HSC36C111	mz77f03.r1 Soares mous	9.51e+00	653	15	1.5	396	18	AA311024	Ym44a02.r1 Homo sapien	9.51e+00
581	15	1.5	351	17	AA255246	Yw18h01.r1 Homo sapien	9.51e+00	654	15	1.5	396	18	AA311024	Ym44a02.r1 Homo sapien	9.51e+00
582	15	1.5	351	12	H88001	aa20b03.s1 Soares Nhm	9.51e+00	655	15	1.5	397	22	AA053704	z173d10.r1 Stratagene	9.51e+00
583	15	1.5	351	23	AA447860	EST10123 Adipose tissu	9.51e+00	656	15	1.5	397	12	H69141	Yr99d10.s1 Homo sapien	9.51e+00
584	15	1.5	353	18	AA302423	zq87a07.r1 Stratagene	9.51e+00	657	15	1.5	397	12	H69141	Yr99d10.s1 Homo sapien	9.51e+00
585	15	1.5	355	16	AA211199	ze35f02.r1 Soares reti	9.51e+00	658	15	1.5	397	12	H69141	Yr99d10.s1 Homo sapien	9.51e+00
586	15	1.5	355	14	AA013060	ye82c12.r1 Homo sapien	9.51e+00	659	15	1.5	397	22	AA053616	z173g02.r1 Stratagene	9.51e+00
587	15	1.5	356	9	R02014	Yr71a03.s1 Homo sapien	9.51e+00	660	15	1.5	398	11	T29902	EST93693 Homo sapiens	9.51e+00
588	15	1.5	356	11	H47726	Yr26f05.r1 Homo sapien	9.51e+00	661	15	1.5	400	10	R26849	Yh53b01.s1 Soares para	9.51e+00
589	15	1.5	357	12	H63611	CIT-HSP-2009P16, rR CIT	9.51e+00	662	15	1.5	401	15	W60498	zr1e604.s1 Stratagene	9.51e+00
590	15	1.5	358	21	B57550	Human aorta cDNA 5'-en	9.51e+00	663	15	1.5	402	23	AA055218	T4233 WYAT Bloodstrea	9.51e+00
591	15	1.5	358	22	HUM230A068	z03b06.s1 Soares feta	9.51e+00	664	15	1.5	402	23	AA055218	mn96g09.r1 Stratagene	9.51e+00
592	15	1.5	359	14	W68393	mj12b07.r1 Soares mous	9.51e+00	665	15	1.5	402	11	H15707	Ym28d01.s1 Homo sapien	9.51e+00
593	15	1.5	359	14	AA050307	Yr71f01.r1 Homo sapien	9.51e+00	666	15	1.5	402	11	H15707	Ym28d01.s1 Homo sapien	9.51e+00
594	15	1.5	359	12	H66908	z069b02.r1 Soares reti	9.51e+00	667	15	1.5	403	18	N63673	zai1h09.s1 Homo sapien	9.51e+00
595	15	1.5	360	16	AA021640	z069b02.r1 Soares reti	9.51e+00	668	15	1.5	403	18	N63673	zai1h09.s1 Homo sapien	9.51e+00
596	15	1.5	360	16	AA433938	CEIK119GZF	9.51e+00	669	15	1.5	403	21	B22940	F2422IF IGF Arabidopsi	9.51e+00
597	15	1.5	360	22	CEIK119GZF	C.elegans cDNA clone y	9.51e+00	670	15	1.5	404	10	AA105629	ym66d06.r1 Stratagene	9.51e+00
598	15	1.5	360	22	CEIK072AXF	C.elegans cDNA clone y	9.51e+00	671	15	1.5	404	10	R22816	yh20g06.s1 Homo sapien	9.51e+00
599	15	1.5	360	22	CEIK100DXF	C.elegans cDNA clone y	9.51e+00	672	15	1.5	404	15	AA125091	mo37c01.r1 Life Tech m	9.51e+00

673	15	1.5	405	9	T66212	yc40b06.r1 Homo sapien	9.51e+00	746	15	1.5	438	16	AA199554	mw40b03.r1 Soares mus	9.51e+00
674	15	1.5	405	15	AA116934	mm22f03.r1 Beddington	9.51e+00	747	15	1.5	438	12	H71879	yr62d07.s1 Homo sapien	9.51e+00
675	15	1.5	405	21	FR0026122	F.rubripes Gss sequenc	9.51e+00	748	15	1.5	439	23	RI053450A	Rice cdna, partial seq	9.51e+00
676	15	1.5	407	22	AA142927	z149c03.s1 Soares preg	9.51e+00	749	15	1.5	439	14	AA051063	ng72c11.r1 Soares mus	9.51e+00
677	15	1.5	407	16	AA157736	z034d08.r1 Stratagene	9.51e+00	750	15	1.5	440	17	AA226817	zr20a03.r1 Stratagene	9.51e+00
678	15	1.5	407	13	HSAAPPLB	H. sapiens putatively	9.51e+00	751	15	1.5	440	11	H23226	ym55b12.r1 Homo sapien	9.51e+00
679	15	1.5	408	9	T70939	yc49b05.r1 Homo sapien	9.51e+00	752	15	1.5	440	10	R72285	yf89b05.s1 Homo sapien	9.51e+00
680	15	1.5	408	22	AA126067	z185b08.r1 Stratagene	9.51e+00	753	15	1.5	440	13	N66599	yy77a01.s1 Homo sapien	9.51e+00
681	15	1.5	410	12	H72999	yu28f09.r1 Homo sapien	9.51e+00	754	15	1.5	441	15	W79463	yy77a06.r1 Soares feta	9.51e+00
682	15	1.5	410	16	AA157703	z034d06.r1 Stratagene	9.51e+00	755	15	1.5	441	16	AA009739	ze82e08.s1 Soares feta	9.51e+00
683	15	1.5	411	17	AA183664	mt20h04.r1 Soares mus	9.51e+00	756	15	1.5	441	10	R24306	yg32c05.r1 Homo sapien	9.51e+00
684	15	1.5	411	21	B66415	CTT-HSP-2011B15.TRB.c1	9.51e+00	757	15	1.5	441	17	AA230981	mm30b04.r1 Soares mus	9.51e+00
685	15	1.5	412	11	H39085	yp65b11.r1 Homo sapien	9.51e+00	758	15	1.5	442	11	H02797	yf44f01.r1 Homo sapien	9.51e+00
686	15	1.5	412	12	H63392	yr53b04.r1 Homo sapien	9.51e+00	759	15	1.5	442	16	AA187406	zp69f04.r1 Stratagene	9.51e+00
687	15	1.5	412	16	N43212	SW3ICAI134SK.Brugia.ma	9.51e+00	760	15	1.5	443	17	AA163643	mt24d04.r1 Soares mus	9.51e+00
688	15	1.5	412	12	N47629	yy54d05.r1 Homo sapien	9.51e+00	761	15	1.5	443	17	W82105	mf02b12.r1 Soares mus	9.51e+00
689	15	1.5	413	20	GA051775	mj54h12.r1 Soares mus	9.51e+00	762	15	1.5	443	15	W56183	zdl4b10.r1 Soares feta	9.51e+00
690	15	1.5	413	20	G21142	human SMS WT-11774.	9.51e+00	763	15	1.5	443	14	W30458	mc20c11.r1 Soares mus	9.51e+00
691	15	1.5	414	23	AA448393	zw68b10.r1 Soares test	9.51e+00	764	15	1.5	443	15	W78004	zd78b06.s1 Soares feta	9.51e+00
692	15	1.5	414	14	W24110	zb48f02.r1 Soares feta	9.51e+00	765	15	1.5	444	17	AA111136	mp65b12.r1 Soares 2NM	9.51e+00
693	15	1.5	415	16	AA197211	zq11e12.s1 Stratagene	9.51e+00	766	15	1.5	444	10	R80279	y192c01.r1 Homo sapien	9.51e+00
694	15	1.5	415	15	T71700	yc64b04.r1 Homo sapien	9.51e+00	767	15	1.5	444	10	R82626	y119f09.r1 Homo sapien	9.51e+00
695	15	1.5	415	13	N62526	yz74g05.s1 Homo sapien	9.51e+00	768	15	1.5	444	17	AA110949	mp56f10.r1 Soares 2NM	9.51e+00
696	15	1.5	416	17	AA218734	zg97b05.s1 Stratagene	9.51e+00	769	15	1.5	444	10	R36011	yg69a02.r1 Homo sapien	9.51e+00
697	15	1.5	417	14	AA035540	ze24c01.s1 Soares feta	9.51e+00	770	15	1.5	445	15	AA136178	zk93f05.r1 Soares preg	9.51e+00
698	15	1.5	417	9	T68143	yc28f02.r1 Homo sapien	9.51e+00	771	15	1.5	445	17	AA242288	mx12g10.r1 Soares mus	9.51e+00
699	15	1.5	417	15	W47240	zc39d04.r1 Soares sene	9.51e+00	772	15	1.5	446	15	W60969	zd31f05.s1 Soares feta	9.51e+00
700	15	1.5	417	17	AA231091	mm11g09.r1 Soares mus	9.51e+00	773	15	1.5	446	14	W36380	mb83d05.r1 Soares mus	9.51e+00
701	15	1.5	418	17	AA223775	zr10c04.r1 Stratagene	9.51e+00	774	15	1.5	446	22	N30233	yy64d02.s1 Homo sapien	9.51e+00
702	15	1.5	418	17	R02514	ye70b08.r1 Homo sapien	9.51e+00	775	15	1.5	448	22	AA100479	z181e09.s1 Stratagene	9.51e+00
703	15	1.5	419	20	HS2842F5	H. sapiens (D3S1587) D	9.51e+00	776	15	1.5	448	15	W74705	zd57e08.s1 Soares feta	9.51e+00
704	15	1.5	419	17	AA280740	mm02f11.r1 Soares mus	9.51e+00	777	15	1.5	448	20	G23141	human SMS WT-12652.	9.51e+00
705	15	1.5	419	10	R63590	Y109g05.r1 Homo sapien	9.51e+00	778	15	1.5	449	14	AA007917	mg76e07.r1 Soares mus	9.51e+00
706	15	1.5	420	22	HUM178D08B	Human fetal brain CDNA	9.51e+00	779	15	1.5	449	13	T26418	AB20068r.Homo sapiens	9.51e+00
707	15	1.5	420	10	R18056	Yg15c09.r1 Homo sapien	9.51e+00	780	15	1.5	450	12	N40785	yy62a07.r1 Homo sapien	9.51e+00
708	15	1.5	421	23	AA459294	zx89b08.r1 Soares ovar	9.51e+00	781	15	1.5	450	18	ATU74163	Arabidopsis thaliana c	9.51e+00
709	15	1.5	421	11	M78870	EST01018.Homo sapiens	9.51e+00	782	15	1.5	450	18	AA277654	va80e04.r1 Soares mus	9.51e+00
710	15	1.5	421	15	AA013164	ze35e12.s1 Soares ret1	9.51e+00	783	15	1.5	450	10	R40502	yf72f05.r1 Homo sapien	9.51e+00
711	15	1.5	421	12	N24350	yx14e04.r1 Homo sapien	9.51e+00	784	15	1.5	450	23	AA472873	vd59f05.r1 Knowles Sol	9.51e+00
712	15	1.5	423	15	W78044	zdf72d02.r1 Soares feta	9.51e+00	785	15	1.5	451	18	AA285861	vb86a01.r1 Soares mus	9.51e+00
713	15	1.5	423	19	HSP004660	H.sapiens EST sequence	9.51e+00	786	15	1.5	451	21	H98788	yx16f10.s1 Homo sapien	9.51e+00
714	15	1.5	423	15	W51830	zc37e02.s1 Soares sene	9.51e+00	787	15	1.5	451	21	B39564	HS-1049-B2-c08-MR.ab1	9.51e+00
715	15	1.5	424	15	AA126890	z116f02.s1 Soares preg	9.51e+00	788	15	1.5	451	15	AA016257	ze33d01.s1 Soares ret1	9.51e+00
716	15	1.5	424	16	AA080206	mm34g08.r1 Stratagene	9.51e+00	789	15	1.5	452	10	R82864	y125e10.r1 Homo sapien	9.51e+00
717	15	1.5	424	16	AA273921	vb99c03.r1 Soares mus	9.51e+00	790	15	1.5	452	12	N51279	yz14e01.s1 Homo sapien	9.51e+00
718	15	1.5	425	17	AA224247	zr15g11.s1 Stratagene	9.51e+00	791	15	1.5	452	11	H43549	yo70g02.r1 Homo sapien	9.51e+00
719	15	1.5	425	11	H21515	Y132a10.s1 Homo sapien	9.51e+00	792	15	1.5	452	10	R34600	yh85f09.s1 Homo sapien	9.51e+00
720	15	1.5	426	10	R08878	yf21f06.s1 Homo sapien	9.51e+00	793	15	1.5	452	10	R23647	yh35f01.r1 Homo sapien	9.51e+00
721	15	1.5	426	22	AA406421	zvf10c01.r1 Soares NbhM	9.51e+00	794	15	1.5	452	10	R06173	yg94f03.r1 Homo sapien	9.51e+00
722	15	1.5	427	13	N66594	yy69h01.s1 Homo sapien	9.51e+00	795	15	1.5	454	15	W69557	zd47g04.r1 Soares feta	9.51e+00
723	15	1.5	428	23	AA505216	T4280.WVMT4.Bloodstrea	9.51e+00	796	15	1.5	455	13	N34509	yy55d02.s1 Homo sapien	9.51e+00
724	15	1.5	428	20	G10179	human SMS CHIC.ATCOC03	9.51e+00	797	15	1.5	455	9	T60158	yz22c11.s1 Homo sapien	9.51e+00
725	15	1.5	428	20	T60083	yb68b01.s1 Homo sapien	9.51e+00	798	15	1.5	455	10	R10278	yf36c11.r1 Homo sapien	9.51e+00
726	15	1.5	428	22	AA404373	zw35b04.s1 Soares tota	9.51e+00	799	15	1.5	455	14	W97648	mt199f11.r1 Soares mus	9.51e+00
727	15	1.5	428	16	AA025823	ze85b10.s1 Soares feta	9.51e+00	800	15	1.5	457	17	AA183812	mt21e02.r1 Soares mus	9.51e+00
728	15	1.5	428	15	AA0377104	zc51a10.r1 Soares sene	9.51e+00	801	15	1.5	457	15	AA123454	mm30c06.r1 Beddington	9.51e+00
729	15	1.5	429	14	N88454	K3433F.Fetal heart, La	9.51e+00	802	15	1.5	458	16	AA192167	zg03a11.s1 Stratagene	9.51e+00
730	15	1.5	429	23	AA500939	vg01g01.r1 Soares mus	9.51e+00	803	15	1.5	459	16	W86540	yz62c01.r1 Soares feta	9.51e+00
731	15	1.5	429	15	W82700	mf07d03.r1 Soares mus	9.51e+00	804	15	1.5	459	16	N55180	yz44c08.s1 Soares feta	9.51e+00
732	15	1.5	431	9	T50411	yb30d01.s1 Homo sapien	9.51e+00	805	15	1.5	459	12	N20491	yx40b09.s1 Homo sapien	9.51e+00
733	15	1.5	431	22	AA437330	yy66f05.r1 Homo sapien	9.51e+00	806	15	1.5	459	15	W95318	ze05h01.r1 Soares feta	9.51e+00
734	15	1.5	432	20	G30467	human SMS SHGC-37116.	9.51e+00	807	15	1.5	460	13	W17039	zb17g01.r1 Soares feta	9.51e+00
735	15	1.5	432	19	AA131911	z139c12.s1 Soares preg	9.51e+00	808	15	1.5	460	12	N24016	yr87g12.s1 Homo sapien	9.51e+00
736	15	1.5	432	11	H42471	yo64b02.s1 Homo sapien	9.51e+00	809	15	1.5	461	17	AA238916	mx92c02.r1 Soares mus	9.51e+00
737	15	1.5	433	12	N30229	yy64c06.s1 Homo sapien	9.51e+00	810	15	1.5	461	21	B58795	CTT-HSP-201AA10.TF.CIT	9.51e+00
738	15	1.5	433	22	AA437330	zw30a06.r1 Soares ovar	9.51e+00	811	15	1.5	461	12	N25241	yt74c03.s1 Homo sapien	9.51e+00
739	15	1.5	434	15	AA091317	ccbn2660.seg.F.fetal.h	9.51e+00	812	15	1.5	462	14	W96387	ze10a09.r1 Soares 2NM	9.51e+00
740	15	1.5	434	13	W45354	zc60b10.s1 Pantoacetic	9.51e+00	813	15	1.5	462	17	AA199020	ml16b06.r1 Soares 2NM	9.51e+00
741	15	1.5	435	12	N49098	yy79f02.s1 Homo sapien	9.51e+00	814	15	1.5	463	23	AA474362	vs57a02.r1 Knowles Sol	9.51e+00
742	15	1.5	435	18	AA340312	EST45500.Fetal brain I	9.51e+00	815	15	1.5	464	14	W31655	zb92d09.r1 Soares para	9.51e+00
743	15	1.5	435	18	AA340312	yy89b12.s1 Homo sapien	9.51e+00	816	15	1.5	464	14	W05284	ze83e05.s1 Soares feta	9.51e+00
744	15	1.5	437	14	W62539	md63e06.r1 Soares mus	9.51e+00	817	15	1.5	464	23	RI0C23332A	Rice cdna, partial seq	9.51e+00
745	15	1.5	438	12	N55698	J0618F.Homo sapiens cd	9.51e+00	818	15	1.5	465	14	AA034875	ml53a04.r1 Soares mus	9.51e+00

IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality.

FEATURES

location/Qualifiers

1.183
/organism="Homo sapiens"

BASE COUNT 31 a 56 c 40 g 46 t 10 others

ORIGIN

Query Match 11.3%; Score 112; DB 10; Length 183;
Best Local Similarity 91.1%; Pred. No. 2.36e-256;
Matches 112; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

DB 19 CCGCTCCATCATCATCATGCTGCTACACCTTATGATCTGCGCTCTCAAGAGCTCNG 78
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QY 554 CCTCTCTCATCATCATCATGCTGCTACACCTGATGATCTGCTCTCAAGAGCTCNG 613
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DB 79 GNTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 138
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QY 614 GCTCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 673
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DB 139 GGT 141
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QY 674 GGT 676

RESULT 3
LOCUS AA317847 206 bp mRNA EST 19-APR-1997
DEFINITION AA317847 Retina II Homo sapiens CDNA 5' end.
ACCESSION AA317847
NID g1970173
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homiidae;
Homo.
1 (bases 1 to 206)

REFERENCE

AUTHORS Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
Burt,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-
Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,T., Fine,L.D.,
Fitzgerald,L.M., Fitzhugh,W.M., Frichman,J.L., Georgagen,N.S.,
Glodet,A., Gnehm,C.L., Hanna,M.C., Heddon,E., Hinkle,P.S., Jr.,
Kelsey,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
Moresco-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
Phillips,C.A., Ryder,S.E., Scott,J.L., Saudex,D.M., Shirley,R.,
Small,K.V., Spriggs,T.A., Uterback,T.R., Weidman,J.F., Li,Y.,
Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
Dimke,D., Feng,D.-F., Ferris,A., Fischer,C., Hastings,G.A.,
He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Melsner,P.S., Olsen,H.,
Rozmund,L., Welty,F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M.,
Dillon,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
Fraser,C.M. and Venter,J.C.

TITLE Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cDNA sequence
JOURNAL Nature 377 (6547 Suppl.), 3-174 (1995)
MEDLINE 96026280
COMMENT

Contact: Kerlavage, AR

Bioinformatics

The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056

Fax: 3018699423

Email: arkerlav@tigr.org

For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (<http://www.tigr.org/tdb/ngi/ngi.html>)
Seq primer: M13 Reverse.
Location/Qualifiers

1..206

/organism="Homo sapiens"
/note="Organ: retina; Vector: pBluescript SK-; Site:1;
ECORI; Site:2; XhoI"
/db_xref="ATCC (inhost):118310"
/db_xref="taxon:9606"
/clone_id="Retina II"
/sex="mixed"
/dev_stage="adult"
<1..>206
BASE COUNT 50 a 48 c 65 g 41 t 2 others
ORIGIN

Query Match 1.9%; Score 19; DB 18; Length 206;
Best Local Similarity 100.0%; Pred. No. 6.71e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 48 CCGTGGAGGCTCTGGGG 66
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QY 725 CCGTGGAGGCTCTGGGG 743
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RESULT 4
LOCUS B50520 360 bp DNA GSS 10-NOV-1997
DEFINITION CIT-HSP-459E23.TV CIT-HSP Homo sapiens genomic clone 459E23.
ACCESSION B50520
NID g2602757
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 360)
AUTHORS Kim,U.-J., Adams,M.D. and Simon,M.I.
TITLE Determination of clone end sequences of human Bacterial Artificial
Chromosomes
JOURNAL Unpublished (1997)
COMMENT Other_GSSs: CIT-HSP-459E23.TP
Contact: Ung-Jin Kim
Caltech Genome Research Lab
California Institute of Technology
Division of Biology, MS 147-75, Pasadena, CA 91125, USA
Tel: 626 796 7066
Fax: 626 395 4901
Email: ung@ash.tree.caltech.edu
For clone availability, please contact ung-jin kim
(ung@ash.tree.caltech.edu)
Seq primer: T7
Class: BAC ends.

FEATURES

location/Qualifiers

1..360
/organism="Homo sapiens"
/note="Vector: pBluescript, Site:1: HindIII; Site:2:
HindIII"
/db_xref="taxon:9606"
/clone_id="459E23"
/clone_lib="CIT-HSP"
/sex="Male"
/cell_type="sperm"
BASE COUNT 93 a 102 c 80 g 85 t

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 6.71e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 90 GTTACACGACATCTACAC 108
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QY 269 GTTACACGACATCTACAC 287
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RESULT 5
LOCUS CELK096D7F 360 bp mRNA EST 06-JAN-1997
DEFINITION C.elegans cDNA clone yk96d7 : 5' end, single read.

ACCESSION D75109
 MID 91120893
 KEYWORDS EST; EST/expressed sequence tag;
 SOURCE Caenorhabditis elegans (strain:N2) embryo Hermaprodite embryo cDNA
 to mRNA, clone lib:Yuji Kohara unpublished cDNA.
 ORGANISM Caenorhabditis elegans
 Eukaryotes; Mitochondrial eukaryotes; Metazoa; Nematoda;
 Secernentea; Rhabdillia; Rhabdillidae; Rhabdillidae;
 Rhabdillidae; Pelodierinae; Caenorhabditis.
 REFERENCE 1 (bases 1 to 360)
 AUTHORS Kohara,Y., Motohashi,T., Tabara,H., Sugimoto,A., Watanabe,H. and Nishiyaki,A.
 TITLE Toward an expression map of the C.elegans genome
 JOURNAL Unpublished (1995)
 REFERENCE 2 (bases 1 to 360)
 AUTHORS Kohara,Y.
 TITLE Direct Submission
 JOURNAL Submitted (23-AUG-1995) to the DDBJ/EMBL/Genbank databases. Yuji Kohara, National Institute of Genetics, Gene Library Lab; Yata 1111, Mishima, Shizuoka 411, Japan (E-mail:YKohara@lab.nig.ac.jp, Tel:0559-81-6854, Fax:0559-81-6855)
 FEATURES
 source
 1..360
 /organism="Caenorhabditis elegans"
 /strain="N2"
 /db_xref="taxon:6239"
 /clone_id="Yuji Kohara unpublished cDNA"
 /dev_stage="embryo"
 /sex="Hermaprodite"
 /tissue_type="embryo"
 BASE COUNT 98 a 120 c 64 g 74 t 4 others
 ORIGIN
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 Best Local Similarity 100.0%; Pred. No. 6,71e-06;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 155 CCACCACACGACGACGAG 173
 /organism="Caenorhabditis elegans"
 Cp 684 CCACCACACGACGACGAG 666

RESULT 6
 LOCUS M75869 415 bp mRNA EST 16-SEP-1992
 DEFINITION CE006a11 Caenorhabditis elegans cDNA clone cm06a11 5'.
 ACCESSION M75869
 MID 9275214
 KEYWORDS EST.
 SOURCE Nematodes clone=cm06a11 library=Chris Martin sorted cDNA library strain=Bristol N2 vector=lamdaphage SHMX2 host=MC1061 Mixed stage hermaprodite cDNA library. Partially normalized by successively picking groups of clones that didn't hybridize to previously picked clones. Vector: lamdaphage SHMX2 (liphiltz, D.H. et al., Gene 88:25-36 (1990)). Host: MC1061.
 ORGANISM Caenorhabditis elegans
 Eukaryota; Animalia; Eumetazoa; Nematoda; Secernentea; Rhabdillidae; Rhabdillina; Rhabdillidae; Rhabdillidae.
 REFERENCE 1 (bases 1 to 415)
 AUTHORS Waterston,R., Martin,C., Craxton,M., Huynh,C., Coulson,A., Hillier,L., Durbin,R.K., Green,P., Showkeen,R., Halloran,N., Hawkins,T., Wilson,R., Berts,M., Du,Z., Thomas,K., Thierry-Mieg,J. and Sulston,J.
 TITLE A survey of expressed genes in Caenorhabditis elegans
 JOURNAL Nature Genet. 1, 114-123 (1992)
 COMMENT
 Contact: Waterston R.H. (USA) and Sulston J.E. (UK)
 (USA) Dept. of Genetics or (UK)
 (USA) Washington Univ. School of Medicine or (UK) MRC Laboratory of Molecular Biology
 Box 8232, 4566 Scott Ave., St. Louis, MI 63110, USA, or, Hills Road, Cambridge CB2 2QH, UK
 Tel: (USA) (314)3627072 or (UK) (0223)248011
 Fax: (USA) (314)3624137 or (UK) (0223)402008

FEATURES
 source
 1..415
 /organism="Caenorhabditis elegans"
 /clone="cm06a11"
 /strain="Bristol N2"
 BASE COUNT 123 a 69 c 95 g 125 t 3 others
 ORIGIN
 Query Match 1.9%; Score 19; DB 9; Length 415;
 Best Local Similarity 100.0%; Pred. No. 6,71e-06;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 78 CCTCATCATCATCGCTGCG 96
 /organism="Caenorhabditis elegans"
 QY 560 CCTCATCATCATCGCTGCG 578

RESULT 7
 LOCUS AA447244 521 bp mRNA EST 03-JUN-1997
 DEFINITION ZW93C04.F1 Soares total fetus NB2HF8 9w Homo sapiens cDNA clone 784518 5'.
 ACCESSION AA447244
 MID 92159909
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryotes; Mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 521)
 AUTHORS Hillier,L., Allen,M., Bowles,L., Dubugue,T., Geisel,G., Jost,S., Kucada,T., Jacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellendberg,K., Stepoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
 TITLE WashU-Merck EST Project 1997
 JOURNAL Unpublished (1997)
 COMMENT
 Contact: Wilson RK
 WashU-Merck EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@wustl.edu
 This clone is available royalty-free through LIND; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
 Seq primer: -28ml3 rev2 ET from Amersham
 High quality sequence stop: 490.
 Location/Qualifiers
 1..521
 /organism="Homo sapiens"
 /note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was prepared from mRNA obtained from pooled 8-9 week (total) fetus material with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGAGCGCGCGCTAATTTTCTTTTCTT 3']. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."
 /db_xref="taxon:9606"
 /clone="784518"
 /clone_id="Soares total fetus NB2HF8 9w"
 /dev_stage="8-9 weeks"
 /lab_host="DH10B"
 <1..>521
 /db_xref="GDB:5982136"
 BASE COUNT 142 a 128 c 127 g 124 t
 ORIGIN
 Query Match 1.9%; Score 19; DB 23; Length 521;

COMMENT

FEATURES

Location/Qualifiers

SOURCE 1. .261
/organism="Homo sapiens"
/note="Organ: Embryo; 8 weeks; Vector: pBluescript SK-;
Site_1: ECORI; Site_2: XhoI
/db_xref="ATCC (inhost):133016"
/db_xref="taxon:9606"
/clone_lib="Embryo, 8 week I"
/dev_stage="embryo, 8 wks"
<1. .>261

BASE COUNT 59 a 90 c 54 g 56 t 2 others

ORIGIN

Query Match 1.8%; Score 18; DB 18; Length 261;
Best Local Similarity 100.0%; Pred. No. 3.21e-04;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 205 ATGACGTGACCGCTAC 222
|||||
297 ATGACGTGACCGCTAC 314

Qy

RESULT 11
LOCUS H38470 261 bp mRNA EST 16-AUG-1995
DEFINITION YP69D06.r1 Homo sapiens cDNA clone 192659 5'.
ACCESSION H38470
NID 9907965
KEYWORDS EST.
SOURCE human clone=192659 library=Soares adult brain N2d-HB5Y
vector=PT73D (Pharmacia) with a modified polylinker host=DH10B
(ampicillin resistant) primer=M13P1 Rs1tel=Not I Rs1tel2=Eco RI
55-year old male; 1st strand cDNA was primed with a Not I -
oligo(4T) primer [5'
TGTTACCAATCTGAGTGGAGCGCGCGCTTTTCTTTTCTTTT 3']
double-stranded cDNA was size selected, ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I and Eco
RI sites of a modified PT73 vector (Pharmacia). Library went
through one round of normalization to a Cot = 53. Library
constructed by Bento Soares and M. Fatima Ronaldo. The adult brain
RNA was provided by Dr. Donald H. Gilden. Tissue was acquired 17-18
hours after death which occurred in consequence of a ruptured
aortic aneurysm. RNA was prepared from a pool of tissues
representing the following areas of the brain: frontal, parietal,
temporal and occipital cortex from the left and right hemispheres,
subcortical white matter, basal ganglia, thalamus, cerebellum,
midbrain, pons and medulla.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygia; Chondata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 261)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Merrit, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Tretasakis, E., Waterston, R., Williamson, A., Wohlmann, P. and
Wilson, R. R. W. EST Project
The WASHU-Merck EST Project
Unpublished (1995)

TITLE
JOURNAL
COMMENT
Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu
High quality sequence stops: 203
Source: IMAGE Consortium, LNL
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Location/Qualifiers
1. .261
/organism="Homo sapiens"

BASE COUNT 39 a 72 c 76 g 63 t 11 others
ORIGIN
Query Match 1.8%; Score 18; DB 11; Length 261;
Best Local Similarity 94.7%; Pred. No. 3.21e-04;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 153 GTCCTCATCATCATCGNCT 171
|||||
Qy 558 GTCCTCATCATCATCGTCT 576

RESULT 12
LOCUS AA296456 316 bp mRNA EST 18-APR-1997
DEFINITION EST11038 Umbilical vein endothelial cells T1 Homo sapiens cDNA 5'
end similar to vasodilative intestinal peptide receptor RDC1.
ACCESSION AA296456
NID 91948859
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Eukaryota; Eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea;
Homo.
1 (bases 1 to 316)
Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,
Bult, C.J., Lee, R.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
White, O., Sutton, G., Blake, J.A., Brannon, R.C., Mai, Wai, C.,
Clayton, R.A., Cline, J.R., Cotton, M.D., Earle-Hughes, E., Fine, L.D.,
Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Georgagen, N.S.,
Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr.,
Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,
Moreno, Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,
Phillips, C.A., Ryder, S.E., Scott, J.L., Sauder, D.M., Shirley, R.,
Small, K.V., Spriggs, T.A., Uterback, T.R., Weidman, J.F., Yi, X.,
Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
Dirke, D., Feng, D.-F., Ferris, A., Fischer, C., Hastings, G.A.,
He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K.,
Kozak, D.L., Kunsch, C., Hunsjun, J., Li, H., Meisner, P.S., Olsen, H.,
Raymond, L., Wei, F.F., Wang, J., Xu, C., Yu, G.L., Rubin, S.M.,
Dillon, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C.,
Fraser, C.M. and Venter, J.C.
Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cDNA sequence
Nature 377 (6547 Suppl), 3-174 (1995)
96026280
Other ESTs: EST11039 EST183921 TRC105954
Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (<http://www.tigr.org/tdb/hgi/hgi.html>)
Seq primer: M13 Reverse
Location/Qualifiers
1. .316
/organism="Homo sapiens"
/note="Organ: umbilical vein; Vector: pBluescript SK-;
Site_1: ECORI; Site_2: XhoI"
/db_xref="ATCC (inhost):194234"
/db_xref="taxon:9606"
/clone_lib="Umbilical vein endothelial cells T1"
/cell_type="endothelial cell"
/dev_stage="fetus"
<1. .>316

BASE COUNT 67 a 106 c 72 g 71 t
ORIGIN

Query Match 1.8%; Score 18; DB 18; Length 316;
 Best Local Similarity 100.0%; Pred. No. 3.21e-04;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 230 ATGAGCGTGACCGCTAC 247
 ||||||||||||||||
 Qy 297 ATGAGCGTGACCGCTAC 314

RESULT 13
 LOCUS AA361360 337 bp mRNA EST 21-APR-1997
 DEFINITION EST10628 T-cell lymphoma Homo sapiens cDNA 5' end.
 ACCESSION AA361360
 NID 92013678
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryotae; Mitochondrial eukaryotes; Metazoa; Chordata;
 Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae;

REFERENCE 1 (bases 1 to 337)
 AUTHORS Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fulder,R.A.,
 Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
 White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wei,C.,
 Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
 Fitzgerald,L.M., Fitzhugh,W.M., Fitchman,J.L., Geoghagen,N.S.,
 Glodek,A., Gnehm,C.U., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr.,
 Kelley,J.M., Kelley,J.C., Liu,B.-I., Marmaros,S.M., Merrick,J.M.,
 Moreno-Balances,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
 Phillips,C.A., Ryder,S.E., Scott,J.L., Saudke,D.M., Shirley,R.,
 Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,X.,
 Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.-J.,
 Dinko,D., Feng,D.-F., Ferris,A., Fischer,C., Hastings,G.A.,
 He,M.W., Hu,S.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.R.,
 Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Weisner,P.S., Olsen,H.,
 Raymond,L., Wei,Y.F., Wang,J., Xu,C., Yu,G.L., Ruben,S.M.,
 Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
 Fraser,C.M. and Venter,J.C.

TITLE Initial assessment of human gene diversity and expression patterns
 JOURNAL based upon 83 million nucleotides of cDNA sequence
 MEDLINE Nature 377 (6547 Suppl), 3-174 (1995).
 COMMENT 96026280

CONTACT: Kerlavage, AR
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 9712 Medical Center Drive, Rockville, MD 20850 USA
 Tel: 3018699056
 Fax: 3018699423
 Email: arkerlav@tigr.org

FEATURES
 source
 1. .337
 /organism="Homo sapiens"
 /note="Vector: plnuescript SK-; site_1: EcoRI; site_2:
 XhoI"
 /db_xref="ATCC (inhost):165502"
 /db_xref="taxon:9606"
 /clone_lib="T-cell lymphoma"
 /cell_type="T-lymphocyte"
 <1. .>337
 60 a 90 c 103 g 75 t 9 others

BASE COUNT
 ORIGIN
 Query Match 1.8%; Score 18; DB 19; Length 337;
 Best Local Similarity 100.0%; Pred. No. 3.21e-04;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 11 GTGACCGCTACATTGCC 28
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Qy 303 GTGACCGCTACATTGCC 320

RESULT 14
 LOCUS FR0019360 364 bp DNA GSS 10-DEC-1997
 DEFINITION F.rubripes GSS sequence, clone 028B15A7.
 ACCESSION AL012252
 NID 92678620
 KEYWORDS GSS; genome survey sequence.
 SOURCE Fugu rubripes.
 ORGANISM Fugu rubripes.
 Eukaryotae; Metazoa; Chordata; Vertebrata; Actinopterygii;
 Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha;
 Tetraodontiformes; Tetraodontidae; Tetraodontidae; Fugu.
 1 (bases 1 to 364)
 Elgar,G., Clark,M., Smith,S., Meek,S., Warner,S., Umrana,S.,
 Williams,G. and Brenner,S.
 Direct Submission
 Submitted (08-DEC-1997) MRC Human Genome Mapping Project Resource
 Centre Hinxton, Cambridge, CB10 1SB. Email: biohelp@hmp.mrc.ac.uk
 Vector: plnuescript II KS
 V type: phagemid
 PRIMER: KS
 DESC: One pass dye-terminator sequencing of cosmid cloned genomic
 sequence.

FEATURES
 source
 1. .364
 /organism="Fugu rubripes"
 /db_xref="taxon:31033"
 /clone_lib="cosmid 028B15"
 /clone="028B15A7"

BASE COUNT
 ORIGIN
 Query Match 1.8%; Score 18; DB 21; Length 364;
 Best Local Similarity 100.0%; Pred. No. 3.21e-04;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 202 CATCGCTGCTACACCGT 219
 ||||||||||||||||
 Qy 569 CATCGCTGCTACACCGT 586

RESULT 15
 LOCUS T01065 367 bp mRNA EST 10-NOV-1992
 DEFINITION W85T01786 Caenorhabditis elegans cDNA clone CEESM36.
 ACCESSION T01065
 NID 9277546
 KEYWORDS EST.
 SOURCE Nematodes clone=CEESM36 library=Early embryo, Stragene (cat.
 #937007) primer=M13 forward.
 ORGANISM Caenorhabditis elegans

REFERENCE 1 (bases 1 to 367)
 AUTHORS McCombie,W.R., Kelley,J.M., Aubin,L., Goscoechea,M.,
 Fitzgerald,M.G., Wu,A., Adams,M.D., Dubnick,M., Kerlavage,A.R.,
 Venter,J.C. and Fields,C.A.
 Unpublished (1993)

JOURNAL
 COMMENT

CONTACT: Kerlavage AR
 The Institute for Genomic Research
 932 Clopper Road, Gaithersburg, MD 20878
 Tel: 3018699056
 Fax: 3018699423
 Email: arkerlav@tigr.org

FEATURES
 source
 1. .367
 /organism="Caenorhabditis elegans"
 /clone="CEESM36"

BASE COUNT
 ORIGIN
 141 a 75 c 57 g 94 t

Query Match 1.8%; Score 18; DB 9; Length 367;
Best Local Similarity 100.0%; Pred. No. 3.21e-04;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 323 GCCCTTCAGAGTAGGT 340
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QY 179 GCCCTTCAGAGTAGGT 196

Search completed: Tue Apr 21 01:24:37 1998
Job time : 901 secs.